Gene	p-value	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
			No.	No.	No.
201280 s at	0.018222	gb:NM_001343.1 /DEF=Homo	NM 001343	110.	NP_001334
		sapiens disabled (Drosophila)			
;		homolog 2 (mitogen-responsive	. 1	,	į
		phosphoprotein) (DAB2), mRNA.		·	[
		/FEA=mRNA /GEN=DAB2	1 .		1
	,	/PROD=disabled (Drosophila)			
		homolog 2		,	
	,	/DB_XREF=gi:4503250			1
		//UG=Hs.81988 disabled			
(')		(Drosophila) homolog 2 (mitogen-			1
• •		1	Ì	Ī	1 .
		responsive phosphoprotein)			1 .
No. 1		/FL=gb:U39050.1 gb:U53446.1	[1
		gb:BC003064.1 gb:NM_001343.1			,
	2 2 12 2 12			 	110 700 10
201281_at	0.046/49	gb:NM_007002.1 /DEF=Homo	NM_007002		NP_783163
		sapiens cell membrane	ł		
	1 1 1	glycoprotein, 110000M(r) (surface			1
		antigen) (GP110), mRNA.			
		/FEA=mRNA /GEN=GP110	, ,		
		/PROD=cell membrane	\	•	1
		glycoprotein, 110000M(r)		ļ	1
		(surfaceantigen)			1
		/DB_XREF=gi:5901959	}		. }
		/UG=Hs.90107 cell membrane		1	·
		glycoprotein, 110000M(r) (surface		•	1
-		antigen) /FL=gb:NM_007002.1	1		
!		gb:D64154.1	1	.[1
201299 s_at	0.034721	gb:NM_018221.1 /DEF=Homo	NM_018221		NP_06069
		sapiens hypothetical protein			1
	}	FLJ10788 (FLJ10788), mRNA.	• • • • • • • • • • • • • • • • • • • •	} .	
		/FEA=mRNA /GEN=FLJ10788	1		1
		/PROD=hypothetical protein			
	i .	FLJ10788 /DB XREF=gi:8922670		,	
		/UG=Hs.196437 hypothetical			
	{	protein FLJ10788	1		
		/FL=gb:AB016839.1	}	.	
		gb:BC003398.1 gb:NM_018221.1	,	1	
1 .	1	Tapy Doggood 1 April 1 in To Los ST. 1	1	1	1
		, *	1 .	1	1

Gene	p-value	ng to Figure 19 - Coronary Artery l Description	Gene	Unigene	Protein
ld ntifier	p value		Accession	Accession	Accession
ia iltiilei			No.		
201313_at	0.02008	gb:NM_001975.1 /DEF=Homo	NM 001975	No.	No. NP 001966
201313_at	0.02008	1 - · ·	NIVI_001973		INF_00 1900
	1	sapiens enolase 2, (gamma,		ļ	1
		neuronal) (ENO2), mRNA.			
	4	/FEA=mRNA /GEN=ENO2			
		/PROD=enolase 2, (gamma,			
	1	neuronal) /DB_XREF=gi:5803010	:		ł
	! *	/UG=Hs.146580 enolase 2,			1
	ļ	(gamma, neuronal)		* •	1
	l	/FL=gb:BC002745.1			1
		gb:NM_001975.1 gb:M22349.1			
201314_at	0.03002	gb:NM_006374.1 /DEF=Homo	NM_006374		NP_006365
		sapiens serinethreonine kinase	(Table 1	1	-
	1	25 (Ste20, yeast homolog)			
		(STK25), mRNA. /FEA=mRNA			
1		/GEN=STK25			
		/PROD=serinethreonine kinase	4		•
	* -	25 (Ste20, yeasthomolog)	1	· .	
		/DB_XREF=gi:5454173	[1
	,				1
		/UG=Hs.155206 serinethreonine			1
		kinase 25 (Ste20, yeast			
		homolog) /FL=gb:D63780.1	·		
	L	gb:NM_006374.1	 	<u> </u>	1
201321_s_at	0.046749	gb:NM_003075.1 /DEF=Homo	NM_003075		NP_620706
•		sapiens SWISNF related, matrix	·	1	
		associated, actin dependent		.}	
	1	regulator of chromatin, subfamily		1	
		c, member 2 (SMARCC2),			
	· .	mRNA. /FEA=mRNA			
	· ·	/GEN=SMARCC2			
	1	/PROD=SWISNF related, matrix			
		associated, actindependent	1		
l je je		regulator of chromatin, subfamily		}	
		c member 2			
		/DB_XREF=gi:4507080	ľ		1
		/UG=Hs.236030 SWISNF related,		1	
	1		• •		
	1.	matrix associated, actin		1	
·	\	dependent regulator of	}	}	
٠.		chromatin, subfamily c, member			
		2 /FL=gb:U66616.1		}	1
		gb:NM_003075.1			
	1 .	1	ŀ	1	1 .

		ng to Figure 19 - Coronary Artery I		llmina	Ducto
Gene	p-value	D scription	Gene	Unigene	Protein
ldentifier			Accession	Accession	Acc ssion
			No.	No.	No.
201388 at	0.026842	gb:NM_002809.1 /DEF=Homo	NM_002809		NP_002800
_		sapiens proteasome (prosome,	.		_
	• -	macropain) 26S subunit, non-			
•	•	ATPase, 3 (PSMD3), mRNA			į.
		/FEA=mRNA /GEN=PSMD3			
1. Sec. 14.	İ	/PROD=proteasome (prosome,			1
	• •	macropain) 26\$ subunit,non-			
		ATPase, 3		İ	
	.	I to the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of			•
		/DB_XREF=gi:4506228	[[
		/UG=Hs.9736 proteasome		· .	
	['	(prosome, macropain) 26S			[
		subunit, non-ATPase, 3	· ·		
		/FL=gb:BC000074.1	[
		gb:BC004859.1 gb:D67025.1		4	l :
<u> </u>	[gb:AF091075.1 gb:NM_002809.1			<u> </u>
201432_at	0.034721	gb:NM_001752.1 /DEF=Homo	NM_001752		NP_00174
- .		sapiens catalase (CAT), mRNA.	1		
		/FEA=mRNA /GEN=CAT			
•	1	/PROD=catalase			
•		/DB XREF=gi:4557013	•		į
		/UG=Hs.76359 catalase			
*		/FL=gb:NM_001752.1	,		
201439_at	0.025284		NM_004193	 	NP 00418
20 1439_at	0.023264	10 =	14141_004193		1115_00410
		sapiens golgi-specific brefeldin A		· '	
		resistance factor 1 (GBF1),		<u>,</u>	}
		mRNA /FEA=mRNA			
]	/GEN=GBF1 /PROD=golgi-]	j
		specific brefeldin A resistance	*		
	,	factor 1 /DB_XREF=gi:4758415	1	j :	
		/UG=Hs.155499 golgi-specific			
		brefeldin A resistance factor 1			ļ
		/FL=gb:AF068755.1			
		gb:NM_004193.1		1	
201458_s_at	0.034721	gb:NM 004725.1 /DEF=Homo	NM_004725		NP 00471
	1	sapiens BUB3 (budding	ļ - '		ļ -
		uninhibited by benzimidazoles 3,			
	1	yeast) homolog (BUB3), mRNA.	1.		į.
		/FEA=mRNA /GEN=BUB3	. ,		
	ļ	//PROD=BUB3 (budding		}	
- 1 - A	•	1			
		uninhibited by benzimidazoles		1	
		3,yeast) homolog			1 .
		/DB_XREF=gi:4757879			
		/UG=Hs.40323 BUB3 (budding			
		uninhibited by benzimidazoles 3,		1.	1
		yeast) homolog		1	
	1	/FL=gb:BC005138.1			1
		gb:AF047472.1 gb:AF053304.1			
	1 .	gb:AF081496.1 gb:NM_004725.1	ļ	J	1

Gene List Co	rrespondir	ng to Figure 19 - Coronary Artery I	Disease		
Gene Identifier	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
201462_at	0.028893	gb:NM_014766.1 /DEF=Homo	NM_014766		NP_055581
. 1		sapiens KIAA0193 gene product			
		(KIAA0193), mRNA. /FEA=mRNA			•
		/GEN=KIAA0193			
•		/PROD=KIAA0193 gene product			
	•	/DB_XREF=gi:7661983	,		
ı	1 1	/UG=Hs.75137 KIAA0193 gene	1		ł
1	~	product /FL=gb:D83777.1			
201511 04	0.036054	gb:NM_014766.1	NIM 004007		ND 004070
201511_at	0.036254	gb:NM_001087.1 /DEF=Homo	NM_001087		NP_001078
		sapiens angio-associated, migratory cell protein (AAMP),			
		mRNA. /FEA=mRNA		.:	
		/GEN=AAMP /PROD=angio-			
	ļ	associated, migratory cell protein			
	• • •	/DB_XREF=gi:4557228			
		/UG=Hs.83347 angio-associated,			
•		migratory cell protein			
		/FL=gb:NM_001087.1			1
	}	gb:M95627.1		٠.	
201516_at	0.018023	gb:NM_003132.1 /DEF=Homo	NM_003132		NP 003123
		sapiens spermidine synthase	_		
		(SRM), mRNA /FEA=mRNA			
,	•	/GEN=SRM /PROD=spermidine			
		synthase /DB_XREF=gi:4507208			
		/UG≃Hs.76244 spermidine			Ì
] .	synthase /FL=gb:BC000309.1			
004500	0.04000	gb:NM_003132.1 gb:M34338.1		<u> </u>	
201522_x_at	0.018023	gb:NM_003097.2 /DEF=Homo	NM_003097	· .	NP_073719
		sapiens small nuclear			
	ŀ	ribonucleoprotein polypeptide N			1
*.		(SNRPN), transcript variant 1, mRNA /FFA=mRNA			
		/GEN=SNRPN /PROD=small			
ı		nuclear ribonucleoprotein	٠.		
		polypeptide N			
		/DB_XREF=gi:13027651	l to a]
		/UG=Hs.48375 small nuclear			·
	1	ribonucleoprotein polypeptide N	1		
	1	/FL=gb:U41303.1			
		gb:NM_003097.2 gb:BC003180.1	,		1
		gb:J04615.1			
201528_at	0.046749	replication protein A1, 70kDa	BG398414	Hs.84318	NP_002936

Cno	متاذيدها	Decemention	Cono	Unidono	Protein
G ne	p-value	Description	Gene	Unigene	
ldentifi r			Accession	Accession	Accession
			No.	No.	No.
201532_at	0.046749	gb:NM_002788.1 /DEF=Homo	NM_002788		NP_687033
	-	sapiens proteasome (prosome,	·		1
		macropain) subunit, alpha type,			
	''	3 (PSMA3), mRNA. /FEA=mRNA			
*	,	/GEN=PSMA3	4.		
		/PROD=proteasome (prosome,			
		macropain) subunit, alphatype, 3	٠	•	
		/DB_XREF=gi:4506182		·	
S		/UG=Hs.167106 proteasome			· .
		· ·		i	
		(prosome, macropain) subunit,	,		
	,	alpha type, 3			
		/FL=gb:BC005265.1	3		
		gb:NM_002788.1			
201544_x_at		poly(A) binding protein, nuclear 1	BF675004	Hs.117176	NP_004634
201545_s_at	0.034721	1~ -	NM_004643		NP_004634
į.	ļ	sapiens poly(A)-binding protein,	· ·		
		nuclear 1 (PABPN1), mRNA.			
		/FEA=mRNA /GEN=PABPN1			
	1	/PROD=poly(A)-binding protein,			
	}	nuclear 1 /DB_XREF=gi:4758875	·	,	
* - F		/UG=Hs.117176 poly(A)-binding		1	
	ļ	protein, nuclear 1			
		/FL=gb:NM_004643.1			
201548_s_at	0.025284	putative DNA/chromatin binding	AA729218	Hs.143323	NP_006609
201040_3_at	0.020204	motif	701720210	1113.14,0020	111 _000000
201555 at	0.034721	gb:NM 002388.2 /DEF=Homo	NM_002388		NP 002379
201333_at	0.034721	,	NIVI_002300	ł	141002379
		sapiens minichromosome			
		maintenance deficient (S.			
		cerevisiae) 3 (MCM3), mRNA.	·		
		/FEA=mRNA /GEN=MCM3	1	ł	
	1	/PROD=minichromosome			
		maintenance deficient		20	
-	'	(S.cerevisiae) 3			
	1	/DB_XREF=gi:6631094	1	1	
4		/UG=Hs 179565 minichromosome			· ·
		maintenance deficient (S.			
		cerevisiae) 3 /FL=gb:BC001626.1			
				1	
	i .	gb:NM_002388.2 gb:D38073.1			1

G ne		ng to Figur 19 - Coronary Artery [D scription	Gene	Unigene	Protein
Identifier	p-valu	D scription	Acc ssion	Accession	Accession
identilier		,			No.
2045CEt	0.024704	gb:NM 002166.1 /DEF=Homo	No. NM 002166	No.	NP_002157
201565_s_at	0.034721		11111_002 100	**	NF_002137
		sapiens inhibitor of DNA binding	•		
	'	2, dominant negative helix-loop-	е '	. 1	
		helix protein (ID2), mRNA.	٠		
• •		/FEA=mRNA /GEN=ID2	*		
		/PROD=inhibitor of DNA binding		, i	
		2, dominant negativehelix-loop-			
,		helix protein			
		/DB_XREF=gi:4504570		'	`.
		/UG=Hs.180919 inhibitor of DNA	A.		
		binding 2, dominant negative			
		helix-loop-helix protein		:	
		/FL=gb:M97796.1			
		gb:NM_002166.1 gb:D13891.1			
201572 x at	0.046749	gb:NM 001921.1 /DEF=Homo	NM 001921		NP_00191
- -		sapiens dCMP deaminase	_		
	1.	(DCTD), mRNA. /FEA=mRNA		•	
		/GEN=DCTD /PROD=dCMP			
*		deaminase			
		/DB_XREF=gi:4503276		• • •	
	1	/UG=Hs.76894 dCMP deaminase			
		/FL=gb:L12136.1			· .
	· ·	gb:NM_001921.1			
201584 s at	0.019022	gb:NM_005804.1 /DEF=Homo	NM 005804		NP 62055
201004_S_at	0.016023	sapiens nuclear RNA helicase,	TVIVI_003004	•	NF _02033
		•			
		DECD variant of DEAD box		· ·	ļ
		family (DDXL), mRNA.	1, 1		
	1	/FEA=mRNA /GEN=DDXL			* * * * * * * * * * * * * * * * * * * *
		/PROD=nuclear RNA helicase,	1		
		DECD variant of DEAD			
		boxfamily /DB_XREF=gi:5031658			1
	•	/UG=Hs.179606 nuclear RNA			
		helicase, DECD variant of DEAD			
		box family /FL=gb:BC001009.1	A 1		
	1	gb:U90426.1 gb:NM_005804.1			
				l	-
201606_s_at	0.046749	nuclear phosphoprotein similar to	BE796924	Hs.172589	NP_00899
		S. cerevisiae PWP1			•

		ng to Figure 19 - Coronary Artery I		 	D-4-1-
Gene	p-value	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
			No.	No.	No.
201608_s_at	0.046749	gb:NM_007062.1 /DEF=Homo	NM_007062	1	NP_008993
		sapiens nuclear phosphoprotein	55.552		
N.	•	similar to S. cerevisiae PWP1		,	
	-	(PWP1), mRNA /FEA=mRNA			
		/GEN=PWP1 /PROD=nuclear			·
·		phosphoprotein similar to S.	* -		at .
*.		cerevisiaePWP1			
	* · · · · ·	/DB_XREF=gi:5902033			
**	-	/UG=Hs.172589 nuclear			
		phosphoprotein similar to S.	* ·		
		cerevisiae PWP1	,		
1 1		/FL=gb:BC001652.1 gb:L07758.1			
		gb:NM 007062.1			
201613_s_at	0.046740	gb:BC000519.1 /DEF=Homo	BC000519		
201013_5_at	0.046749		IBC000519		
	***	sapiens, RuvB (E coli homolog)-	i		
		like 1, clone MGC:8557, mRNA,	,		
		complete cds. /FEA=mRNA			1 .
· ·		/PROD=RuvB (E coli homolog)-			
		like 1 /DB_XREF=gi:12653494			
		/UG=Hs.272822 RuvB (E coli		•	,
		homolog)-like 1			
		/FL=gb:BC000519.1	,		
•	*	gb:BC002993.1 gb:AB012122.1			
* * * * * * * * * * * * * * * * * * * *	•	gb:AF070735.1 gb:AF099084.1	2.4		_
	٠,	gb:NM_003707.1			
		gb.141W_003707.1			
201623 s at	0.046740	gb:BC000629.1 /DEF=Homo	BC000629	* *	ND 001240
201023_S_at	0.046749				NP_001340
		sapiens, Similar to aspartyl-tRNA			
		synthetase, clone MGC:1562,			
		mRNA, complete cds.			
		/FEA=mRNA /PROD=Similar to	,	İ	
		aspartyl-tRNA synthetase			4.
. *		/DB_XREF=gi:12653688			
		/UG=Hs.80758 aspartyl-tRNA			
		synthetase /FL=gb:BC000629.1			
		gb:J05032.1 gb:NM 001349.1]		5.
		garage and a garage and the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control			
201630 s at	0.046740	gb:NM_004300.1 /DEF=Homo	NM_004300		NP_808222
	0.040140	sapiens acid phosphatase 1,	1004000		-000222
	٠.				1,
* :		soluble (ACP1), transcript variant	-		
		a, mRNA. /FEA=mRNA			
-		/GEN=ACP1 /PROD=acid	:		1
		phosphatase 1 isoform a			
	'	/DB_XREF=gi:4757713			
		/UG=Hs.75393 acid phosphatase	. '	1	· '
	1	1, soluble /FL=gb:M83653.1			•
		II, Soluble /I L-qb.Wi03033.1			1
		gb:NM_004300.1			

		ng to Figure 19 - Coronary Artery		<u> </u>	
G ne	p-value	Description	Gene	Unigene	Protein
ld ntifier			Accession	Accession	Accession
			No.	No.	No.
201633_s_at	0.027792	cytochrome b5 outer mitochondrial	AW235051	Hs.381218	NP_085056
		membrane precursor	•		-
		• • • • • • • • • • • • • • • • • • • •			
201635_s_at	0.018222	fragile X mental retardation,	AI990766	Hs.82712	NP_005078
	·	autosomal homolog 1			_
201647_s_at	0.046749	gb:NM_005506.1 /DEF=Homo	NM_005506		NP_005497
: — · — · —		sapiens CD36 antigen (collagen			
		type I receptor, thrombospondin			
		receptor)-like 2 (lysosomal	,		
		integral membrane protein II)			
		(CD36L2), mRNA. /FEA=mRNA			
		/GEN=CD36L2 /PROD=CD36			
			, '		
		antigen (collagen type I			
		receptor,thrombospondin		·	
		receptor)-like 2 (lysosomal			
		integralmembrane protein II)			
*		/DB_XREF=gi:5031630			
		/UG=Hs.323567 CD36 antigen		1	
		(collagen type I receptor,	:		
		thrombospondin receptor)-like 2			
		(lysosomal integral membrane	:		2
		protein II) /FL=gb:D12676.1			**
, 		gb:NM_005506.1			
201649_at	0.034721	gb:NM_004223.1 /DEF=Homo	NM_004223		NP 004214
		sapiens ubiquitin-conjugating	_		
		enzyme E2L 6 (UBE2L6),			
		mRNA. /FEA=mRNA			
		/GEN=UBE2L6 /PROD=ubiquitin-			
		conjugating enzyme E2L 6	ļ ·		
	-	/DB_XREF=gi:4759281	'		
		/UG=Hs.169895 ubiquitin-			
		conjugating enzyme E2L 6			
		/FL=gb:AF031141.1			
	1	gb:AF061736.1 gb:NM_004223.1			
201661_s_at	0.024724	gb:NM 004457.2 /DEF=Homo	NIM 004457		NP 004448
201001_5_at	0.034721	. –	NM_004457		INP_004446
		sapiens fatty-acid-Coenzyme A			
-		ligase, long-chain 3 (FACL3),			* .
	4 1	mRNA. /FEA=mRNA			*
		/GEN=FACL3 /PROD=long-chain			
		fatty-acid-Coenzyme A ligase 3		,	
		/DB_XREF=gi:12669907			
•		/UG=Hs.268012 fatty-acid-			
	ľ	Coenzyme A ligase, long-chain			1
		3 /FL=gb:NM_004457.2	<u> </u>		
	,	gb:D89053.1 gb:AF116690.1			
	l .				

Gene	p-value	Description	Gene	Unigene 🔪	Protein
Identifier	P 14.45		Accession	Accession	Accession
iggildilei			No.	No.	No.
201680 x at	0.046749	gb:NM_015908.1 /DEF=Homo	NM_015908	140.	NP_056992
201000_x_at	0.010710	sapiens arsenate resistance	10.10000		00,000.
		protein ARS2 (ARS2), mRNA.			2 0
		/FEA=mRNA /GEN=ARS2			
		/PROD=arsenate resistance			
		protein ARS2	·	İ	
		/DB_XREF=gi:7706237			
		/UG=Hs.111801 arsenate	1	1	
*		resistance protein ARS2	'		
		/FL=gb:BC000082.1			
-		gb:AF082871.1 gb:NM_015908.1		,	
201683_x_at	0.038017	KIAA0737 gene product	BE783632	Hs.194035	NP 05564:
201690 s at		tumor protein D52	BE974098	Hs.2384	NP 005070
201697 s at		gb:NM_001379.1 /DEF=Homo	NM 001379	11.5.2007	NP 00137
201001_5_4	0.920294	sapiens DNA (cytosine-5-)-	11111_001070		
•		methyltransferase 1 (DNMT1),			1
		mRNA. /FEA=mRNA			
Commence of Section		/GEN=DNMT1 /PROD=DNA			-
		(cytosine-5-)-methyltransferase 1			-
		/DB_XREF=gi:4503350	14 .	•	
		/UG=Hs.77462 DNA (cytosine-5-)-		·	
		methyltransferase 1	_		
•		/FL=gb:NM_001379.1			
201711 x at	0.025284	RAN binding protein 2	Al681120	Hs.179825	NP 00625
201720 s at		Lysosomal-associated	AI589086	Hs.79356	NP 00675
201720_0_0	0.001721	multispanning membrane protein-5	1	110.10000	
		Transparring membrario protoni o			,
201728 s at	0.018693	KIAA0100 gene product	AA904674	Hs.151761	
201739 at		gb:NM_005627.1 /DEF=Homo	NM_005627		NP 00561
		sapiens serumglucocorticoid			
		regulated kinase (SGK), mRNA.			
a.		/FEA=mRNA /GEN=SGK			
		/PROD=serumglucocorticoid			
		regulated kinase			1.0
		/DB_XREF=gi:5032090			
		/UG=Hs.296323	1		100
		serumglucocorticoid regulated			
		kinase /FL=gb:BC001263.1		•	
		gb:NM_005627.1 gb:AF153609.1			,

		ng to Figure 19 - Coronary Artery			· · · · · · · · · · · · · · · · · · ·
Gene	p-value	Description	Gene	Unigene	Protein
dentifier			Accession	Accession	Accession
			No.	No.	No.
201748 s at	0.036354	gb:NM 002967.1 /DEF=Homo	NM_002967	140.	NP_002958
101740_S_at	0.030254	I T -	141VI_002907		INF_002930
		sapiens scaffold attachment		ł	1
		factor B (SAFB), mRNA.			
•	·	/FEA=mRNA /GEN=SAFB			
		/PROD=scaffold attachment			1:2
		factor B /DB_XREF=gi:4506778		į .	
		/UG=Hs.23978 scaffold			İ
			1	· .	
,		attachment factor B	:		
	,	/FL=gb:U72355.1		ļ.	
		gb:NM_002967.1			
01775_s_at	0.046749	Consensus includes	AK001487		NP_055589
		gb:AA676790 /FEA=EST		· ·	
. •		/DB_XREF=gi:2657312			:
		/DB_XREF=est:zj64h12.s1	1	1	
	•	. –		4	
-		/CLONE=IMAGE:455111			
	٠,	/UG=Hs.62515 KIAA0494 gene			
		product /FL=gb:BC002525.1	1		1
* .		gb:AB007963.1 gb:NM_014774.1			
01853 s at	0.018023	gb:NM 021873.1 /DEF=Homo	NM_021873		NP_068660
0 1000_s_a	0.010023	, -	14141_02 1073	, , ,	111 _000000
		sapiens cell division cycle 25B] .
		(CDC25B), transcript variant 3,			
	·	mRNA. /FEA=mRNA			
		/GEN=CDC25B /PROD=cell			
•		division cycle 25B, isoform 3			
	,	/DB_XREF=gi:11641412			
	. ~	/UG=Hs.153752 cell division			
· · · · · ·					*
		cycle 25B /FL=gb:NM_021873.1] .		<u> </u>
01856_s_at	0.034721	gb:BC000376.1 /DEF=Homo	BC000376		
		sapiens, clone MGC:8379,			
		mRNA, complete cds.	1		1
		/FEA=mRNA /PROD=Unknown	-	,	,
			,		
		(protein for MGC:8379)		1	
	•	/DB_XREF=gi:12653216			'
		/UG=Hs.173518 M-phase	* *		
		phosphoprotein homolog			
		/FL=gb:BC000376.1			
(x,y) = (x,y) + (x,y)		gb:BC000746.1 gb:AF100742.1		l	
		I =			
04050	0.004704	gb:NM_016107.1	100000		ND 0007/0
201858_s_at	0.034721	13	J03223		NP_002718
		secretory granule proteoglycan			
	1	peptide core mRNA, complete		1	1
		cds. /FEA=mRNA /GEN=PRG1		1	
		/DB_XREF=gi:190419			,
		/UG=Hs 1908 proteoglycan 1,		{	
		secretory granule			
		/FL=gb:J03223.1		1	
	1	gb:NM_002727.1	1	1	1 .

Gene List Col	rrespondir	ng to Figure 19 - Coronary Artery I	<u>Disease</u>	<u></u>	
Gene	p-value	Description	Gene	Unigene	Protein
Identifier	•		Accession	Accession	Accession
			No.	No.	No.
201861_s_at	0.018023	leucine rich repeat (in FLII)	BF965566	Hs.326159	NP 004726
		interacting protein 1		1.0.020100	_00 ,,20
201878 at	0.046749	Consensus includes gb:N25546	NM 005744		NP_005735
-01010_qt	0.0 101, 10	/FEA=EST			
		/DB_XREF=gi:1139894			
•		/DB_XREF=est:yx76e05.s1		e.	
	-	/CLONE=IMAGE:267680			
	1 .	/UG=Hs.181461 ariadne			
4.4		(Drosophila) homolog, ubiquitin-			
		conjugating enzyme E2-binding			
		protein, 1 /FL=gb:AF072832.1		,	
		T T T T T T T T T T T T T T T T T T T		·	
201970 at	0.024724	gb:NM_005744.2	NIM OOF744		ND 005725
201879_at	0.034721	Consensus includes gb:Al694332	NIVI_005744		NP_005735
		/FEA=EST			* .
		/DB_XREF=gi:4971672			
•		/DB_XREF=est:wd45e11.x1		,	
		/CLONE=IMAGE:2331116			
		/UG=Hs.181461 ariadne		-	
•		(Drosophila) homolog, ubiquitin-	•		
*		conjugating enzyme E2-binding			
		protein, 1 /FL=gb:AF072832.1			**
		gb:NM_005744.2			
201883_s_at	0.049425	gb:D29805.1 /DEF=Human	D29805		NP_001488
		mRNA for beta-1,4-			
·		galactosyltransferase, complete			
	•	cds. /FEA=mRNA /PROD=beta-			
		1,4-galactosyltransferase		· ·	
·		/DB_XREF=gi:474986			
	٠	/UG=Hs.198248 UDP-			
		Gal:betaGlcNAc beta 1,4-			•
		galactosyltransferase, polypeptide			
,		1 /FL=gb:NM_001497.1			
. •	,	gb:D29805.1			
-		the transfer of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of th			
201888_s_at	0.034721	gb:U81379.3 /DEF=Homo	U81379		NP_001551
		sapiens interleukin-13 receptor	,		
		mRNA, complete cds.			
	*	/FEA=mRNA /PROD=interleukin-			
		13 receptor			
		/DB_XREF=gi:5870850			
		/UG=Hs.285115 interleukin 13			
		receptor, alpha 1			
•		/FL=gb:NM_001560.1			*.
		gb:U81379.3			

Gene List Co		ng to Figure 19 - Coronary Artery	Dis ase		
Gen	p-value	Description	Gene	Unigene	Protein
Identifier	[Acc ssion	Accession	Accession
	100		No.	No.	No.
201953 at	0.046740	gb:NM 006384.2 /DEF=Homo	NM 006384	110.	NP 006375
201900_ai	0.040743	,	14141_000304		NF_000373
		sapiens calcium and integrin	<u>.</u>		
		binding protein (DNA-dependent		· ·	•
		protein kinase interacting protein)			
		(SIP2-28), mRNA /FEA=mRNA			
	·	/GEN=SIP2-28 /PROD=calcium		•	
		and integrin binding protein			
	l c	/DB_XREF=gi:9951921).	
		/UG=Hs.10803 calcium and			e
	•	1			
	.	integrin binding protein (DNA-			4.
		dependent protein kinase	1		
		interacting protein)	1		
		/FL=gb:BC000846:1 gb:U83236.1			ļ
•		gb:U82226.1 gb:U85611.1			
		gb:NM_006384.2			
		gb.14W_000004.2			
204050	0.000043	KIA A 0040	A A 400000	11- 454444	ND OFFORD
201959_s_at		KIAA0916 protein	AA488899	Hs.151411	NP_055872
201967_at	0.046749	gb:NM_005777.1 · /DEF=Homo	NM_005777	·	NP_005768
· · .	,	sapiens RNA binding motif			`.
	-	protein 6 (RBM6), mRNA.	1		1
		/FEA=mRNA /GEN=RBM6		. ,	*
		/PROD=RNA binding motif			
	4 12 1	protein 6 /DB_XREF=gi:5032032			
٠.,		/UG=Hs.173993 RNA binding			
			~		
		motif protein 6		:	-
- '		/FL=gb:AF042857.1			
No.		gb:AF069517.1 gb:U50839.1			
•		gb:AF091264.1 gb:NM_005777.1	1		
			1		
201980 s at	0.046749	gb:NM 012425.2 /DEF=Homo	NM 012425		NP 036557
		sapiens Ras suppressor protein			
,		1 (RSU1), mRNA. /FEA=mRNA			•
•	-		•		
		/GEN=RSU1 /PROD=ras			1
		suppressor protein 1			
		/DB_XREF=gi:10800408	[·		
		/UG=Hs.75551 Homo sapiens			+ 1
		Ras suppressor protein 1			
		(RSU1), mRNA			1
[·		/FL=gb:NM_012425.2	· .		1
201002+	0.025204		NM 004504		ND 004540
201992_s_at	0.025284	•	NM_004521		NP_004512
,	[sapiens kinesin family member			1
		5B (KIF5B), mRNA. /FEA=mRNA			
	· '	/GEN=KIF5B /PROD=kinesin			
		family member 5B			
		/DB_XREF=gi:4758647			1
, .		/UG=Hs.149436 kinesin family		1	1
	l .			}	{
		member 5B			
	l	/FL=gb:NM_004521.1			

Gene	p-valu	ng to Figure 19 - Coronary Art ry Description	Gene	Unigene	Protein
Identifier	p vuiu	Boomption	Accession	Accession	Accession
identifici			No.	No.	No.
201996 s_at	0.019292	SMART/HDAC1 associated	AL524033	Hs.184245	NP_055816
a.	0.0.0202	repressor protein	7.202.000	10.10.12.10	-000070
201998 at	0.034721	sialyltransferase 1 (beta-	AI743792	Hs.374528	NP 775324
_		galactoside alpha-2,6-	·		
· · · · · · · · · · · · · · · · · · ·		sialytransferase)			
202000_at	0.034721	gb:BC002772.1 /DEF=Homo	BC002772		NP 002481
· -		sapiens, NADH dehydrogenase			
		(ubiquinone) 1 alpha		•	
		subcomplex, 6 (14kD, B14),		,	
		clone MGC:3686, mRNA,			
		complete cds. /FEA=mRNA			
		/PROD=NADH_dehydrogenase			
	,	(ubiquinone) 1 alphasubcomplex,			+
•		6 (14kD, B14)			Ρ.
		/DB_XREF=gi:12803858			
		/UG=Hs.274416 NADH			
		dehydrogenase (ubiquinone) 1			
		alpha subcomplex, 6 (14kD,			
		B14) /FL=gb:BC002772.1			
	•	gb:AF047182.1 gb:NM_002490.1			
202028 s at	0.046749	Consensus includes	BC000603		NP 000990
		gb:BC000603.1 /DEF=Homo		· ·	
		sapiens, ribosomal protein L38,			
		clone MGC:1637, mRNA,	:		
		complete cds. /FEA=mRNA			
		/PROD=ribosomal protein L38		*	
		/DB_XREF=gi:12653644			,
-	5	/UG=Hs.2017 ribosomal protein			
		L38 /FL=gb:BC000603.1			
		gb:NM 000999.1			
202073 at	0.018023	optineurin	AV757675	Hs.278898	NP 068815

		ng to Figure 19 - Coronary Artery			<u> </u>
Gene	p-value	Description	G ne	Unigene	Protein
ldentifier		e e e e e e e e e e e e e e e e e e e	Accession	Accession	Accession
			No.	No.	No.
202074_s_at	0.040064	gb:NM_021980.1 /DEF=Homo	NM_021980	PROJECT STORY	NP_068815
	-	sapiens tumor necrosis factor			_
		alpha-inducible cellular protein			
	·	containing leucine zipper			
		domains; Huntingtin interacting			
		protein L; transcrption factor IIIA-		the same of	
2.00			1		
	l	interacting protein (FIP2), mRNA.	1	, '	
		/FEA=mRNA /GEN=FIP2	<u> </u>		4.1
		/PROD=tumor necrosis factor			
		alpha-inducible cellularprotein			
		containing leucine zipper			
		domains: Huntingtininteracting			
•		protein L; transcrption factorIIIA-			
	,	interacting protein			
		/DB_XREF=gi:11415041			
• • •		/UG=Hs.278898 tumor necrosis			
	ŀ	factor alpha-inducible cellular			
		protein containing leucine zipper			
		domains; Huntingtin interacting	1		
		protein L; transcrption factor IIIA-	, ,		
		interacting protein			ar i
		/FL=gb:NM_021980.1	· .	-	5.
202118_s_at			AA541758	Hs.14158	NP_003900
202136_at	0.025284	adenovirus 5 E1A binding protein	BE250417	Hs.301449	NP_006615
202138_x_at	0.018023	gb:NM_006303.2 /DEF=Homo	NM_006303		NP_006294
		sapiens JTV1 gene (JTV1),			
		mRNA. /FEA=mRNA /GEN=JTV1			
		/PROD=JTV1			
•		/DB_XREF=gi:11125769			
	:	/UG=Hs.301613 JTV1 gene			*
		/FL=gb:NM 006303.2			* * *
000447	0.046740	gb:U24169.1 gb:BC002853.1	NINA 004550		NID 004544
202147_s_at	0.046749	gb:NM_001550.1 /DEF=Homo	NM_001550		NP_001541
		sapiens interferon-related		ļ	
		developmental regulator 1			·, ·
		(IFRD1), mRNA. /FEA=mRNA		1	
		/GEN=IFRD1 /PROD=interferon-			
		related developmental regulator			9.5
		1 /DB_XREF=gi:4504606			
		/UG=Hs.7879 interferon-related	Į.		1
		developmental regulator 1	1.		
		/FL=gb:BC001272.1	1	1.0	
		I = -		1	
	L	gb:NM_001550.1	L		<u>L</u>

		ng to Figure 19 - Coronary Artery		 	
Gene Identifi r	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
dentili i			No.	No.	No.
202151 s at	0.027239	gb:NM_016172.1 /DEF=Homo	NM_016172	110.	NP 057256
-02 101_5_dt	0.021200	sapiens putative glialblastoma	""_"		-00.200
		cell differentiation-related			
	• •	(GDBR1), mRNA. /FEA=mRNA			
a		1.			
		/GEN=GDBR1 /PROD=putative			
		glialblastoma celldifferentiation-			
		related protein	,		
		/DB_XREF=gi:7705380			
	-	/UG=Hs.9194 putative		e "	į
		glialblastoma cell differentiation-	-		
,		related /FL=gb:BC004967.1			
		gb:AF176796.1 gb:NM_016172.1			
202156_s_at	0.046749	CUG triplet repeat, RNA binding	N36839	Hs.211610	NP_006552
		protein 2			
202161_at	0.018222	gb:NM_002741.1 /DEF=Homo	NM_002741		NP_002732
; ;		sapiens protein kinase C-like 1			
* * *		(PRKCL1), mRNA. /FEA=mRNA			
		/GEN=PRKCL1 /PROD=protein			
• ;	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	kinase C-like 1			
		/DB_XREF=gi:4506072			
		/UG=Hs 2499 protein kinase C-			
		like 1 /FL=gb:U33053.1		•	
		gb:NM_002741.1 gb:D26181.1			
202166_s_at	0.025284	gb:NM_0027411 gb:D2510111	NM 006241		NP 006232
202100_3_at	0.020204	sapiens protein phosphatase 1,	11111_000241		_000232
•	1	regulatory (inhibitor) subunit 2			. '
	<u>'</u>	(PPP1R2), mRNA /FEA=mRNA			
		/GEN=PPP1R2 /PROD=protein			,
•		phosphatase 1, regulatory	,		,
a to the]	(inhibitor)subunit 2		ı]
		/DB_XREF=gi:5453945	,	•	**
	-	/UG=Hs.267819 protein		4 .	
		phosphatase 1, regulatory			
		(inhibitor) subunit 2			
		/FL=gb:NM_006241.1			
202171_at	0.025284	Consensus includes	NM_007146		NP_00907
		gb:AU146275 /FEA=EST			• '
		/DB_XREF=gi:11007796			
		/DB_XREF=est:AU146275			
		/CLONE=HEMBB1000004			
•		/UG=Hs.6557 zinc finger protein			
		161 /FL=gb:D28118.1			
	1	1101 /1 E 90.020110.1	1	1	1

		ng to Figure 19 - Coronary Artery I			
Gene Identifier	p-value	Description	Gen Accession No.	Unigene Accession No.	Protein Accession No.
202207 at	0.046749	Consensus includes	NM 005737	ino.	NP_005728
202201_at	0.0-07-13	gb:BG435404 /FEA=EST	14101_000707		147 _000720
		/DB_XREF=gi:13341910]	,
		/DB_XREF=gt: 63341910 /DB_XREF=est:602507678F1			
		/CLONE=IMAGE:4605066			
				· ·	N 1
•		/UG=Hs.111554 ADP-ribosylation			
		factor-like 7 /FL=gb:BC001051.1			1:
		gb:AB016811.1 gb:NM_005737.2			
202208_s_at	0.018222	gb:BC001051.1 /DEF=Homo	BC001051		NP_005728
:		sapiens, ADP-ribosylation factor-			
		like 7, clone MGC:1575, mRNA,	ļ		· ·
4	, i	complete cds. /FEA=mRNA			
		/PROD=ADP-ribosylation factor-			1
		like 7 /DB_XREF=gi:12654450			1
, `	Α,	/UG=Hs.111554 ADP-ribosylation] .
		factor-like 7 /FL=gb:BC001051.1		:	
		gb:AB016811.1 gb:NM_005737.2		N. Company	\
1.*.					*
		·	ľ	:	
202216_x_at	0.036254	gb:BC005003.1 /DEF=Homo	BC005003		NP_055038
2022 10_X_0t	0.000201	sapiens, nuclear transcription			-000000
		factor Y, gamma, clone		1	
		MGC:792, mRNA, complete cds.			
	,	/FEA=mRNA /PROD=nuclear		•	
		transcription factor Y, gamma			
		/DB_XREF=gi:13436472		[· ·	
w , ;		/UG=Hs.168157 nuclear			
		transcription factor Y, gamma	1		
		/FL=gb:NM_014223.2			
		gb:D85425.1 gb:BC005003.1		5	-
•		gb:D89986.1			
· .					
202220_at	0.034721	gb:NM_014949.1 /DEF=Homo	NM_014949		NP_055764
	,	sapiens KIAA0907 protein			
		(KIAA0907), mRNA. /FEA=mRNA			
·		/GEN=KIAA0907			
•	, ,	/PROD=KIAA0907 protein		.* .	
		/DB XREF=gi:7662371			
		/UG=Hs.24656 KIAA0907 protein		1	
		/FL=gb:AB020714.1			1.
		gb:NM_014949.1	1 .	1	1

		ng to Figur 19 - Coronary Artery		<u> </u>	
Gene	p-value	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
			No.	No.	No.
202230_s_at	0.046749	gb:NM_006387.2 /DEF=Homo	NM_006387		NP_006378
		sapiens protein with			
		polyglutamine repeat; calcium			<u> </u>
		(ca2+) homeostasis endoplasmic		* *	
		reticulum protein (ERPROT213-			4.
		21), mRNA. /FEA=mRNA			,
F		/GEN=ERPROT213-21			
		/PROD=protein with			
		polyglutamine repeat;	*	1	
	ļ	calcium(ca2+) homeostasis			
	İ	endoplasmic reticulum protein	· '	[
		/DB_XREF=gi:11055968			
		/UG=Hs.6430 protein with			
	•	polyglutamine repeat; calcium			
,		(ca2+) homeostasis endoplasmic			•
		reticulum protein	,		
		/FL=gb:U94836.2		7	/
		gb:NM_006387.2			
202265_at	0.025284	gb:NM_005180.1 /DEF=Homo	NM_005180		NP 005171
	ļ. ·	sapiens murine leukemia viral	_ ,		_
		(bmi-1) oncogene homolog			
		(BMI1), mRNA. /FEA=mRNA			
		/GEN=BMI1 /PROD=murine		ļ.·	·
* · · · · · · · · · · · · · · · · · · ·		leukemia viral (bmi-1) oncogene	·		1
,		homolog /DB_XREF=gi:4885094			
		/UG=Hs.431 murine leukemia		,	l .
*		viral (bmi-1) oncogene homolog			
•					
		/FL=gb:L13689.1			
000004	0.005004	gb:NM_005180.1		11. 01010	N.B. 075000
202301_s_at	0.025284	hypothetical protein FLJ11021	BE396879	Hs.81648	NP_075388
*. * * * * * * * * * * * * * * * * * *		similar to splicing factor,			
		arginine/serine-rich 4			
202369_s_at	0.027792	gb:NM_012288.1 /DEF=Homo	NM_012288		NP_036420
	*	sapiens TRAM-like protein]	
,		(KIAA0057), mRNA. /FEA=mRNA			
		/GEN=KIAA0057 /PROD=TRAM-			
		like protein			
		/DB_XREF=gi:6912449	1		
		/UG=Hs.153954 TRAM-like		,	
٠.		protein /FL=gb:D31762.1	,		
	I	gb:NM_012288.1	1	1	l .

		ng to Figure 19 - Coronary Artery I	Gene	Unigene	Protein
Gen	p-value	Description		1 '	
Identifier			Accession	Accession	Accession
	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		No.	No.	No.
202378_s_at	0.049425	gb:NM_017526.1 /DEF=Homo	NM_017526	·	NP_059996
•		sapiens leptin receptor gene-	*	1	
		related protein (HSOBRGRP),		*	
	1.9	mRNA. /FEA=mRNA			
		/GEN=HSOBRGRP /PROD=leptin		*.*	2
		receptor gene-related protein			
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		/DB_XREF=gi:8923784			,
		/UG=Hs.23581 leptin receptor			
		gene-related protein			· · ·
(·	/FL=gb:NM_017526.1 \			
202393 s at	0.046749	gb:NM 005655.1 /DEF=Homo	NM_005655	<u> </u>	NP_005646
a	1 0.0 107 10	sapiens TGFB inducible early			
A Comment	, ,	growth response (TIEG), mRNA			,
		/FEA=mRNA /GEN=TIEG			
		1			
		/PROD=TGFB inducible early			
		growth response		·	
		/DB_XREF=gi:5032176	1		
*	4	/UG=Hs.82173 TGFB inducible		,	,
		early growth response			
		/FL=gb:U21847.1			
	1,	gb:NM_005655.1		1	
202426_s_a	t 0.018023	Consensus includes	NM_002957		NP_00294
		gb:BE675800 /FEA=EST	,		
		/DB_XREF=gi:10036341			
		/DB_XREF=est:7f16c05.x1		4.	
*		/CLONE=IMAGE:3294824		i.	
		/UG=Hs.20084 retinoid X			
	4.5	receptor, alpha		'	
10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg - 10 mg		/FL=gb:NM_002957.2)
202438_x_a	0.034721	iduronate 2-sulfatase (Hunter	BF346014	Hs.172458	1
		syndrome)			
202439_s_a	0 034721	gb:NM_000202.2 /DEF=Homo	NM 000202		NP_00611
	,	sapiens iduronate 2-sulfatase			
		(Hunter syndrome) (IDS),		[· ·
		transcript variant 1, mRNA.			
		/FEA=mRNA /GEN=IDS			
•					
	12	/PROD=iduronate-2-sulfatase	,		
. 1	1	isoform a precursor			1
		/DB_XREF=gi:5360215			1
	1.	/UG=Hs.172458 iduronate 2-	,		
		sulfatase (Hunter syndrome)			
		/FL=gb:M58342.1			
		gb:NM 000202.2	1		,

Gene	p-value	ng to Figure 19 - Coronary Artery Description	Gene	Unigene	Protein
Identifier	p-value	Description	Accession	Accession	Accession
			No.	No.	No.
202461 at	0.046749	gb:NM_014239.1 /DEF=Homo	NM 014239		NP 05505
-	1	sapiens eukaryotic translation	_		
		initiation factor 2B, subunit 2	,		
		(beta, 39kD) (EIF2B2), mRNA.			
		/FEA=mRNA /GEN=EIF2B2			
		/PROD=eukaryotic translation			
			,		
		initiation factor 2B,subunit 2]		
	1	(beta, 39kD)			
-		/DB_XREF=gi:7657057	÷ •		
**		/UG=Hs.170001 eukaryotic		1	
		translation initiation factor 2B,			
1.0		subunit 2 (beta, 39kD)	,		
i i	1	/FL=gb:BC000494.1	1.		
		gb:BC003165.1 gb:AF035280.1			
	1	gb:NM_014239.1			
202466_at	0:034721	gb:NM_006999.2 /DEF=Homo	NM 006999	 	NP_00893
		sapiens topoisomerase-related			
	and the second	function protein 4-1 (TRF4),			
		mRNA. /FEA=mRNA	ļ		ļ
· · · · · · · · · · · · · · · · · · ·					
	· ·	/GEN=TRF4			
		/PROD=topoisomerase-related			
:		function protein 4-1			
	;	/DB_XREF=gi:6631114			
		/UG=Hs.225951 topoisomerase-			
5	· ·	related function protein 4-1			
		/FL=gb:AB005754.3	4.3		
		gb:NM_006999,2			
202491 s at	0.018023	gb:NM_003640.1 /DEF=Homo	NM_003640		NP 00363
		sapiens inhibitor of kappa light		-	
:		polypeptide gene enhancer in B-	1	1	1.
·		cells, kinase complex-associated			,
		protein (IKBKAP), mRNA.			<i>f</i>
* '	:	/FEA=mRNA /GEN=IKBKAP			
	·	/PROD=inhibitor of kappa light			
		polypeptide geneenhancer in B-	1		
		cells, kinase complex-associated			
		protein /DB_XREF=gi:4504628	,		Ī
		/UG=Hs.31323 inhibitor of kappa			
• • •		light polypeptide gene enhancer			
		in B-cells, kinase complex-			
		associated protein			}
•		/FL=gb:AF153419.2			
•		gb:AF044195.1 gb:NM_003640.1	1 a		
	1	J			1

Identifier	Gene List Co	rr spondir	ig to Figure 19 - Coronary Artery I	Diseas		
No. No. No. No. No. No. No. No. No. No.	Gene	p-value	Description	Gene	Unigen	Protein
No. No. No. No. No. No. No. No. No. No.	Identifier	-		Accession	Accession	Accession
0.046749 Consensus includes gb.BG251175 /FEA=EST //DB_XREF=gi:12760991 //DB_XREF=gi:12760991 //DB_XREF=gi:12760991 //DB_XREF=gi:12760991 //DB_XREF=gi:12760991 //DB_XREF=gi:12760991 //DB_XREF=gi:1473165 //UG=Hs.154294 discs, large (Drosophila) homolog 1 //FL=gb:NM_004087.1 gb:U13896.1 O.018023 gb:NM_014767.1 //DEF=Homo sapiens KIAA0275 gene product (KIAA0275), mRNA //FEA=mRNA //GEN=KIAA0275 //PROD=KIAA0275 gene product //DB_XREF=gi:7662035 //UG=Hs,74583 KIAA0275 gene product //DB_XREF=gi:7662035 //UG=Hs,74583 KIAA0275 gene product //DEF=Human homozygous deletion target in pancreatic carcinoma (DPC4) mRNA, complete cds //FEA=mRNA //GEN=DPC4 //PROD=Dpc4 //DB_XREF=gi:1163233 //UG=Hs.75862 MAD (mothers against decapentaplegic, Drosophila) homolog 4 //FL=gb:D44378.1 gb:BC002379.1 gb:NM_003899.1 //DEF=Homo sapiens PAK-interacting exchange factor beta (P8SSPR), mRNA //FEA=mRNA //GEN=P8SSPR //PROD=PAK-interacting exchange factor beta //PL=gb:D63476.1 gb:NM_003899.1						
gb:BG251175 /FEA=EST //DB_XREF=gi:12760991 //DB_XREF=gest602364982F1 //CLONE=IMAGE:4473165 //UG=Hs.154294 discs, large (Drosophila) homolog 1 /FL=gb:NM_004087.1 gb:U13896.1 202524_s_at	202515 at	0.046749	Consensus includes			NP 004078
DB_XREF=gi:12760991	2020.0_00	0.0.0.	·			
DB_XREF=est602364982F1			,		· ·	
/CLONE=IMAGE:4473165 //UG=Hs.154294 discs, large (Drosophila) homolog 1 /FL=gb:NM_004087.1 gb:U13896.1 202524_s_at			_ ,			
/UG=Hs.154294 discs, large (Drosophila) homolog 1 /FL=gb:NM_004087.1 gb:U13896.1 202524_s_at			_			
(Drosophila) homolog 1 /FI=gb:NM_004087.1 gb:U13896.1 202524_s_at		-		,		
FL=gb:NM_004087.1 gb:U13896.1 gb:U13896.1 gb:NM_014767.1 DEF=Homo sapiens KIAA0275 gene product (KIAA0275) mRNA. /FEA=mRNA /GEN=KIAA0275 gene product (BEN=KIAA0275 gene product /DB_XREF=gi:7662035 /UG=Hs,74583 KIAA0275 gene product /DB_XREF=gi:7662035 /UG=Hs,74583 KIAA0275 gene product /FL=gb:D87465.1 gb:NM_014767.1 DEF=Human homozygous deletion target in pancreatic carcinoma (DPC4) mRNA, complete cds. /FEA=mRNA /GEN=DPC4 /PROD=Dpc4 /DB_XREF=gi:1163233 /UG=Hs.75862 MAD (mothers against decapentaplegic, Drosophila) homolog 4 /FL=gb:U44378.1 gb:BC002379.1 gb:NM_005359.1 DEF=Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA /FEA=mRNA /GEN=P85SPR /PROD=PAK-interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1 DEF=Homo sapiens PAK-interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1 DEF=Homo sapiens PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1 DEF=Homo sapiens PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1 DEF=Homo sapiens PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1 DEF=Homo sapiens PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1 DEF=Homo sapiens PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1 DEF=Homo sapiens PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1 DEF=Homo sapiens PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1 DEF=Homo sapiens PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1 DEF=Homo sapiens PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1 DEF=Homo sapiens PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1 DEF=Homo sapiens PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1 DEF=Homo sapiens PAK-interacting exchange factor beta /FL=gb:D63476.1 DEF=Homo sapiens PAK-interacting	-					
gb:U13896.1 gb:NM_014767.1 /DEF=Homo NM_014767 NP_0558 Sapiens KIAA0275 gene product (KIAA0275), mRNA. /FEA=mRNA /GEN=KIAA0275 /PROD=KIAA0275 gene product /DB_XREF=gi:7662035 /UG=Hs.74583 KIAA0275 gene product /FL=gb:D87465.1 gb:NM_014767.1 U44378.1 U44378 DEF=Human homozygous deletion target in pancreatic carcinoma (DPC4) mRNA, complete cds. /FEA=mRNA /GEN=DPC4 //PROD=Dpc4 /DB_XREF=gi:1163233 /UG=Hs.75862 MAD (mothers against decapentaplegic, Drosophila) homolog 4 /FL=gb:U44378.1 gb:BC002379.1 gb:NM_005359.1 DEF=Homo Sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. /FEA=mRNA /GEN=P85SPR /PROD=PAK-interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1 //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF=Homo //DEF						
202524_s_at	*	* .	_ :			
sapiens KIAA0275 gene product (KIAA0275), mRNA. /FEA=mRNA /GEN=KIAA0275 /PROD=KIAA0275 gene product /DB_XREF=gi:7662035 /UG=Hs.74583 KIAA0275 gene product /FL=gb:D87465.1 gb:NM_014767.1 202526_at 0.034721 Consensus includes gb:U44378.1 /DEF=Human homozygous deletion target in pancreatic carcinoma (DPC4) mRNA, complete cds. /FEA=mRNA /GEN=DPC4 /PROD=Dpc4 //DB_XREF=gi:1163233 /UG=Hs.75862 MAD (mothers against decapentaplegic, Drosophila) homolog 4 //FL=gb:U44378.1 gb:BC002379.1 gb:NM_005359.1 202548_s_at 0.025284 gb:NM_003899.1 /DEF=Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. /FEA=mRNA /GEN=P85SPR /PROD=PAK- interacting exchange factor beta //DB_XREF=gi:4505572 //G=Hs.172813 PAK-interacting exchange factor beta //FL=gb:D63476.1 gb:NM_003899.1						
(KIAA0275), mRNA. /FEA=mRNA /GEN=KIAA0275 //PROD=KIAA0275 gene product //DB_XREF=gi:7662035 //UG=Hs.74583 KIAA0275 gene product /FL=gb:D87465.1 gb:NM_014767.1 202526_at 0.034721 Consensus includes gb:U44378.1 //DEF=Human homozygous deletion target in pancreatic carcinoma (DPC4) mRNA, complete cds. /FEA=mRNA //GEN=DPC4 //ROD=Dpc4 //DB_XREF=gi:1163233 //UG=Hs.75862 MAD (mothers against decapentaplegic, Drosophila) homolog 4 //FL=gb:U44378.1 gb:BC002379.1 gb:NM_005359.1 202548_s_at 0.025284 gb:NM_003899.1 //DEF=Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. /FEA=mRNA //GEN=P85SPR //PROD=PAK- interacting exchange factor beta //DB_XREF=gi:4505572 //UG=Hs.172813 PAK-interacting exchange factor beta //FL=gb:D63476.1 gb:NM_003899.1	202524_s_at	0.018023	gb:NM_014767.1 /DEF=Homo	NM_014767		NP_055582
(KIAA0275), mRNA. /FEA=mRNA /GEN=KIAA0275 /PROD=KIAA0275 gene product //DB_XREF=gi:7662035 /UG=Hs,74583 KIAA0275 gene product /FL=gb:D87465.1 gb:NM_014767.1 Consensus includes gb:U44378.1 //DEF=Human homozygous deletion target in pancreatic carcinoma (DPC4) mRNA, complete cds. /FEA=mRNA //GEN=DPC4 /PROD=Dpc4 //DB_XREF=gi:1163233 /UG=Hs.75862 MAD (mothers against decapentaplegic, Drosophila) homolog 4 //FL=gb:U44378.1 gb:BC002379.1 gb:NM_005359.1 202548_s_at	7		sapiens KIAA0275 gene product			
/GEN=KIAA0275 //PROD=KIAA0275 gene product //DB_XREF=gi:7662035 //UG=Hs.74583 KIAA0275 gene product /FL=gb:D87465.1 gb:NM_014767.1 202526_at 0.034721 Consensus includes gb:U44378.1 //DEF=Human homozygous deletion target in pancreatic carcinoma (DPC4) mRNA, complete cds. /FEA=mRNA //GEN=DPC4 //PROD=Dpc4 //DB_XREF=gi:1163233 //UG=Hs.75862 MAD (mothers against decapentaplegic, Drosophila) homolog 4 //FL=gb:U44378.1 gb:BC002379.1 gb:NM_005359.1 202548_s_at 0.025284 gb:NM_003899.1 //DEF=Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. /FEA=mRNA //GEN=P85SPR //PROD=PAK- interacting exchange factor beta //DB_XREF=gi:4505572 //UG=Hs.172813 PAK-interacting exchange factor beta //FL=gb:D63476.1 gb:NM_003899.1						
/PROD=KIAA0275 gene product /DB_XREF=gi:7662035 /UG=Hs.74583 KIAA0275 gene product /FL=gb:D87465.1 gb:NM_014767.1 202526_at 0.034721 Consensus includes gb:U44378.1 /DEF=Human homozygous deletion target in pancreatic carcinoma (DPC4) mRNA, complete cds. /FEA=mRNA /GEN=DPC4 /PROD=Dpc4 /DB_XREF=gi:1163233 /UG=Hs.75862 MAD (mothers against decapentaplegic, Drosophila) homolog 4 /FL=gb:U44378.1 gb:BC002379.1 gb:NM_005359.1 202548_s_at 0.025284 gb:NM_003899.1 /DEF=Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. /FEA=mRNA /GEN=P85SPR /PROD=PAK- interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1			`			
/DB_XREF=gi:7662035 /UG=Hs.74583 KIAA0275 gene product /FL=gb:D87465.1 gb:NM_014767.1 202526_at		•	· · · · · · · · · · · · · · · · · · ·			
/UG=Hs.74583 KIAA0275 gene product /FL=gb:D87465.1 gb:NM_014767.1 202526_at				A CONTRACTOR		- '
product /FL=gb:D87465.1 gb:NM_014767.1 202526_at						
gb:NM_014767.1			,	· .		
202526_at 0.034721 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus includes gb:U44378.1 Consensus i			I .	**		
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deletion target in pancreatic carcinoma (DPC4) mRNA, complete cds. /FEA=mRNA /GEN=DPC4 /PROD=Dpc4 /DB_XREF=gi:1163233 /UG=Hs.75862 MAD (mothers against decapentaplegic, Drosophila) homolog 4 /FL=gb:U44378.1 gb:BC002379.1 gb:NM_005359.1 202548_s_at 0.025284 gb:NM_003899.1 /DEF=Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. /FEA=mRNA /GEN=P85SPR /PROD=PAK-interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1	202526_at	0.034721		U44378		NP_005350
carcinoma (DPC4) mRNA, complete cds. /FEA=mRNA /GEN=DPC4 /PROD=Dpc4 /DB_XREF=gi:1163233 /UG=Hs.75862 MAD (mothers against decapentaplegic, Drosophila) homolog 4 /FL=gb:U44378.1 gb:BC002379.1 gb:NM_005359.1 202548_s_at 0.025284 gb:NM_03899.1 /DEF=Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. /FEA=mRNA /GEN=P85SPR /PROD=PAK- interacting exchange factor beta //DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta //FL=gb:D63476.1 gb:NM_003899.1						
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//GEN=DPC4 /PROD=Dpc4 //DB_XREF=gi:1163233 //UG=Hs.75862 MAD (mothers against decapentaplegic, Drosophila) homolog 4 //FL=gb:U44378.1 gb:BC002379.1 gb:NM_005359.1 202548_s_at		*	carcinoma (DPC4) mRNA,			
//GEN=DPC4 /PROD=Dpc4 //DB_XREF=gi:1163233 //UG=Hs.75862 MAD (mothers against decapentaplegic, Drosophila) homolog 4 //FL=gb:U44378.1 gb:BC002379.1 gb:NM_005359.1 202548_s_at	,		complete cds. /FEA=mRNA			
/DB_XREF=gi:1163233 /UG=Hs.75862 MAD (mothers against decapentaplegic, Drosophila) homolog 4 /FL=gb:U44378.1 gb:BC002379.1 gb:NM_005359.1 202548_s_at 0.025284 gb:NM_003899.1 /DEF=Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. /FEA=mRNA /GEN=P85SPR /PROD=PAK-interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1						
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against decapentaplegic, Drosophila) homolog 4 /FL=gb:U44378.1 gb:BC002379.1 gb:NM_005359.1 202548_s_at 0.025284 gb:NM_003899.1 /DEF=Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. /FEA=mRNA /GEN=P85SPR /PROD=PAK- interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1						
Drosophila) homolog 4 //FL=gb:U44378.1 gb:BC002379.1 gb:NM_005359.1 202548_s_at 0.025284 gb:NM_003899.1 /DEF=Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. //FEA=mRNA //GEN=P85SPR //PROD=PAK- interacting exchange factor beta //DB_XREF=gi:4505572 //UG=Hs.172813 PAK-interacting exchange factor beta //FL=gb:D63476.1 gb:NM_003899.1			· · · · · · · · · · · · · · · · · · ·	·		
/FL=gb:U44378.1 gb:BC002379.1 gb:NM_005359.1 202548_s_at			1 -		,	
gb:NM_005359.1 202548_s_at 0.025284 gb:NM_003899.1 /DEF=Homo						
202548_s_at 0.025284 gb:NM_003899.1 /DEF=Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. /FEA=mRNA /GEN=P85SPR /PROD=PAK-interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1					s\$	
sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. /FEA=mRNA /GEN=P85SPR /PROD=PAK- interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1		l .	gb:NM_005359.1			
sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. /FEA=mRNA /GEN=P85SPR /PROD=PAK- interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1						
sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. /FEA=mRNA /GEN=P85SPR /PROD=PAK- interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1		,				
exchange factor beta (P85SPR), mRNA. /FEA=mRNA /GEN=P85SPR /PROD=PAK- interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1	202548_s_at	0.025284	gb:NM_003899.1 /DEF=Homo	NM_003899		NP_663788
mRNA. /FEA=mRNA /GEN=P85SPR /PROD=PAK- interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1			sapiens PAK-interacting			
/GEN=P85SPR /PROD=PAK- interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1			exchange factor beta (P85SPR),			
/GEN=P85SPR /PROD=PAK- interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1			mRNA. /FEA=mRNA			
interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1			1 '			. ·
/DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1			1		,	
/UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1						
exchange factor beta /FL=gb:D63476.1 gb:NM_003899.1			_ · · · — · · · · · · · · · · · · · · ·		,	
/FL=gb:D63476.1 gb:NM_003899.1			1			
gb:NM_003899.1			1 ' -			
	٠,		1			,
202554 s. at 10.042466 glutathione S-transferase M3			gp:MM_003899.1			
CONTAINS A REAL OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRAC	202554 c ct	0.042466	dutathione S. transferace M3	ΔΙ 527/20	Hs 2006	NP_000840
	202004_5_dl	0.042400	17	ALUZ1430	113.2000	_000040
(brain) (brain) AW005776 Hs.323817 NP_056	202550 ··· -+	0.000050		A)A/OCE77C	Un 222017	NP_056422

		ng to Figure 19 - Coronary Artery I			
Gene	p-value	Description	Gene	Unigene	Protein
ldentifier			Accession	Accession	Accession
			No.	No.	No.
202561_at	0.018023	Consensus includes	AF070613		NP_003738
		gb:AF070613.1 /DEF=Homo			√
		sapiens clone 24585 mRNA			:
]	sequence. /FEA=mRNA	,		
	ļ	/DB_XREF=gi:3387995			
	·	/UG=Hs.131814 tankyrase, TRF1-	a.		
İ	•	interacting ankyrin-related ADP-		1.	1
	· ·	ribose polymerase	•		
-			1	ĺ	
	ļ ·	/FL=gb:AF082556.1			
000004	0.010710	gb:NM_003747.1	1		100 20/22
202621_at	0.046749	gb:NM_001571.1 /DEF=Homo	NM_001571		NP_001562
		sapiens interferon regulatory			
		factor 3 (IRF3), mRNA.	•		1
	ļ	/FEA=mRNA /GEN=IRF3		1 74	
		/PROD=interferon regulatory			
	1.0	factor 3 /DB_XREF=gi:4504724			1
		/UG=Hs.75254 interferon			
		regulatory factor 3			
: •		/FL=gb:NM_001571.1			
202642_s_at	0.034721	gb:NM 003496.1 /DEF=Homo	NM 003496		NP_003487
		sapiens		•	
		transformationtranscription		•	
÷	1	domain-associated protein			1
Į		(TRRAP), mRNA. /FEA=mRNA			
		/GEN=TRRAP			
1	}	1 *			1
ŀ		/PROD=transformationtranscription	1		1
· . ·		domain-associatedprotein	. ,		
		/DB_XREF=gi:4507690			
		/UG=Hs 203952			
		transformationtranscription		f .	
		domain-associated protein			
	i .	/FL=gb:AF076974.1	'		1
<u> </u>		gb:NM_003496.1			
202687_s_at	0.046749	gb:U57059.1 /DEF=Homo	U57059		NP_003801
1		sapiens Apo-2 ligand mRNA,			_
•	er.	complete cds. /FEA=mRNA			
		/PROD=Apo-2 ligand			1
,	ł	/DB_XREF=gi:1336207			L
	1	/UG=Hs.83429 tumor necrosis		*	1
	1	factor (ligand) superfamily,			1
] .	member 10 /FL=gb:U37518.1			
	1 *	gb:U57059.1 gb:NM_003810.1_	<u> </u>	i .	1

Gene Identifier 202747 s at	p-value	Description	Gene	Unig n	Protein
	1		I A A A A C C I A B	I A accesion	According
202747 s at			Accession	Accession	Accession
202/4/ s at	0.010000		No.	No.	No.
-v-1 -1 _0_at	0.018693	gb:NM_004867.1 /DEF=Homo	NM_004867		NP_004858
		sapiens integral membrane	-, n ->		
		protein 2A (ITM2A), mRNA.			
		/FEA=mRNA /GEN=ITM2A	·		
		/PROD=integral membrane			
		protein 2A			
		/DB_XREF=gi:4758223		i	
		/UG=Hs.17109 integral	1	i	
		membrane protein 2A			
		/FL=gb:AF038953.1			
	ļ	gb:NM_004867.1			
202759_s_at	0.026842	A kinase (PRKA) anchor protein 2	BE879367	Hs.42322	NP_671492
	0.5255 12	/ Thinass (Frag ly anone) protein =	2.		_ , , , , , , ,
202771_at	0.026013	gb:NM 014745.1 /DEF=Homo	NM 014745	H	NP 055560
202111_at	0.020010	sapiens KIAA0233 gene product	11111_01_11		-000000
		(KIAA0233), mRNA. /FEA=mRNA			
		/GEN=KIAA0233			
*]			•	
] ' ' ,	/PROD=KIAA0233 gene product		1	
		/DB_XREF=gi:7662013		•	, ÷
		/UG=Hs.79077 KIAA0233 gene		*	
		product /FL=gb:D87071.1			
		gb:NM_014745.1		 	1,15, 222.2
202775_s_at	0.034721	gb:NM_004592.1 /DEF=Homo	NM_004592		NP_689421
		sapiens splicing factor,			1
•		arginineserine-rich 8 (suppressor-	-		ļ
		of-white-apricot, Drosophila		- 10	
		homolog) (SFRS8), mRNA.			
		/FEA=mRNA /GEN=SFRS8			
		/PROD=splicing factor,			ľ
		arginineserine-rich 8(suppressor-			1
•	. /	of-white-apricot, Drosophila			·
		homolog) /DB_XREF=gi:4759101		.5	
		/UG=Hs.84229 splicing factor,			
•		arginineserine-rich 8 (suppressor-			
	,	of-white-apricot, Drosophila	100		1
	1	homolog) /FL=gb:NM 004592.1	(İ
:		gb:U08377.1			
		95.00077.1		ŀ	1
				. *	1

		ng to Figure 19 - Coronary Artery			
Gene	p-value	D scription	Gen	Unigene	Protein
Identifier			Acc ssion	Accession	Accession
			No.	No.	No.
202780_at	0.035763	gb:NM 000436.1 /DEF=Homo	NM_000436		NP_000427
' '		sapiens 3-oxoacid CoA			
		transferase (OXCT), nuclear			
		gene encoding mitochondrial	V 2		
		protein, mRNA. /FEA=mRNA	*		
		/GEN=OXCT /PROD=3-oxoacid			
		CoA transferase precursor			,
		/DB_XREF=gi:4557816			ľ
		/UG=Hs.177584 3-oxoacid CoA	•		
		transferase /FL=gb:U62961.1			
*		I =		•	·
000700 -+	0.046746	gb:NM_000436.1	NIA 040000		NE 007005
202786_at	0.046749	gb:NM_013233.1 /DEF=Homo	NM_013233		NP_037365
		sapiens Ste-20 related kinase			
		(SPAK), mRNA. /FEA=mRNA	. *		
	·	/GEN=SPAK /PROD=Ste-20	<u>'</u>		
		related kinase			
		/DB_XREF=gi:7019542	ļ		
		/UG=Hs.199263 Ste-20 related			• .
		kinase /FL=gb:AF017635.1			
to the second of the second		gb:AF099989.1 gb:AF030403.1			
		gb:NM_013233.1			
202787_s_at√	0.034721	gb:U43784.1 /DEF=Human	U43784		NP 004626
	ľ	mitogen activated protein kinase	•		-
		activated protein kinase-3			
		mRNA, complete cds.		*	
		/FEA=mRNA /PROD=mitogen			
•		activated protein kinase			-
		activatedprotein kinase-3			
		/DB_XREF=gi:1256004			
		/UG=Hs.227789 mitogen-			
		activated protein kinase-activated			(
	,	protein kinase 3			
		/FL=gb:U09578.1 gb:U43784.1	·		
		gb:BC001662.1 gb:NM_004635.1	* · ·		
		gb.bcccc1002.1			
202822 at	0.025394	LIM domain containing preferred	AL044018	Hs.180398	NP 005569
202022_at	0.023264		AL044010	100390	NP_005569
202900_s_at	0.020002	translocation partner in lipoma gb:NM_002532.2 /DEF=Homo	NIM OOSESS		ND 000Ē0Š
202900_5_at	0.020093		NM_002532	İ	NP_002523
:		sapiens nucleoporin 88kD		1	
		(NUP88), mRNA. /FEA=mRNA			
		/GEN=NUP88	1		
\sim . \sim		/PROD=nucleoporin 88kD	l · ·	1	
		/DB_XREF=gi:5729954	I .		
	,	/UG=Hs.172108 nucleoporin	[
		88kD /FL=gb:BC000335.1	1		
		gb:NM 002532.2		1	1

Gene List Co	rr spondir	ng to Figur 19 - Coronary Artery [Disease		1
Gn	p-value	D scription	Gene	Unigene	Protein
ld ntifi r			Acc ssion	Acc ssion	Accession
	•		No.	No.	No.
202902 s at	0.025284	gb:NM_004079.1 /DEF=Homo	NM_004079		NP_004070
		sapiens cathepsin S (CTSS),	- -		
		mRNA. /FEA=mRNA			
,		/GEN=CTSS /PROD=cathepsin S			
÷		/DB_XREF=gi:4758097		٠	
	V	/UG=Hs.181301 cathepsin S	4, 1		
		/FL=gb:BC002642.1 gb:M86553.1			
•		gb:NM 004079.1 gb:M90696.1			-
	ļ				
202917 s at	0.034721	gb:NM_002964.2 /DEF=Homo	NM 002964		NP 002955
· — —		sapiens S100 calcium-binding	. -	:	- *.**
		protein A8 (calgranulin A)			
		(S100A8), mRNA. /FEA=mRNA			- 16
		/GEN=S100A8 /PROD=S100		1	
	**	calcium-binding protein A8			- ·
		/DB_XREF=gi:9845519			
	* ,	/UG=Hs.100000 S100 calcium-	• ** • • • *		
	;	binding protein A8 (calgranulin			
		A) /FL=gb:NM_002964.2		:	
202943 s at	0.046749	gb:M38083.1 /DEF=Human alpha	M38083		NP_000253
		N-acetylgalactosaminidase		. **	
	,	mRNA, complete cds.			
		/FEA=mRNA /PROD=alpha-N-		:	
,		acetylgalactosaminidase			
	· ·	/DB_XREF=gi:189054	,		1
		/UG=Hs.75372 N-			
		acetylgalactosaminidase, alpha-			
		/FL=gb:BC000095.1 gb:M62783.1			
		gb:M38083.1 gb:NM_000262.1			
	¥	gs			
202962_at	0.036254	gb:NM_015254.1 /DEF=Homo	NM_015254		NP_056069
		sapiens kinesin family member			
		13B (KIF13B), mRNA.	3		1
		/FEA=mRNA /GEN=KIF13B			
		/PROD=kinesin family member			·
1		13B /DB_XREF=gi:13194196			1 1
		/UG=Hs.15711 kinesin family			
1.		member 13B /FL=gb:AL583912.1			
		gb:NM_015254.1_gb:AF279865.1		,	
		gs			
202975_s_at	0.019657	Rho-related BTB domain	N21138	Hs.10432	† · · · · · · · · · · · · · · · · · · ·
	1	containing 3	· ·		1

		ng to Figur 19 - Coronary Artery	Dis ase		
Gene	p-value	D scription	Gene	Unigene	Protein
ld ntifier			Accession	Accession	Accession
		*	No.	No.	No.
203007_x_at	0.018023	gb:AF077198.1 /DEF=Homo	AF077198		NP_006321
		sapiens lysophospholipase			
		mRNA, complete cds.			
, <u>, , , , , , , , , , , , , , , , , , </u>		/FEA=mRNA			
		/PROD=lysophospholipase			
٠,		/DB XREF=qi:4679009		1	
	1	/UG=Hs 12540 lysophospholipase		ļ. ,	
		I /FL=gb:AF081281.1	٠		* *
		1			
		gb:AF077198.1 gb:NM_006330.1		1	
		gb:AF291053.1	•	·	
000000 -4	0.040000		NA '04 4070		N.D. 055005
203026_at	0.018023	gb:NM_014872.1 /DEF=Homo	NM_014872		NP_055687
	* 5	sapiens KIAA0354 gene product			ŀ
		(KIAA0354), mRNA. /FEA=mRNA			, ·
		/GEN=KIAA0354			·
		/PROD=KIAA0354 gene product		, ,	11
		/DB_XREF=gi:7662073	ì		
		/UG=Hs.3682 KIAA0354 gene			
		product /FL=gb:AB002352.1		`	
		gb:NM_014872.1		*	
203062 s at	0.018023	gb:NM_014641.1 /DEF=Homo	NM_014641		NP_055456
		sapiens KIAA0170 gene product	_	* 15	
	ļ	(KIAA0170), mRNA. /FEA=mRNA			
		/GEN=KIAA0170			
		/PROD=KIAA0170 gene product	[
		/DB_XREF=gi:7661965			
		/UG=Hs.277585 KIAA0170 gene		4 fu 1	
	J	product /FL=gb:D79992.1]	<i>}</i> , '	
		gb:NM 014641.1			
202002 04	0.019022		NINA 044750		ND OFFE
203082_at	0.016023	gb:NM_014753.1 /DEF=Homo	NM_014753		NP_055568
	ļ ·	sapiens KIAA0187 gene product		= -	<u>.</u>
		(KIAA0187), mRNA. /FEA=mRNA			
		/GEN=KIAA0187			
		/PROD=KIAA0187 gene product			
		/DB_XREF=gi:7661979			
		/UG=Hs.10848 KIAA0187 gene			
*		product /FL=gb:D80009.1		,	
• •		gb:NM_014753.1	·		
203159_at	0.034721	gb:NM_014905.1 /DEF=Homo	NM_014905		NP_055720
•	,	sapiens glutaminase (GLS),			
		mRNA. /FEA=mRNA /GEN=GLS			·
		/PROD=glutaminase C			
,	,	/DB_XREF=gi:7662327	1		
_		/UG=Hs.239189 glutaminase		2.4	
	1,	/FL=gb:AF327434.1		1	• *
-		gb:AB020645.1 gb:AF097493.1		1	
		gb:AF223943.1 gb:NM_014905.1	1	1	1
203164 of	0.025204		DE464750	Uo 205470	NID 004704
203164_at		acetyl-Coenzyme A transporter	BE464756	Hs.285176	NP_004724
203181_x_at-	_U.U3b254	SFRS protein kinase 2	AW149364	Hs.78353	NP_003129

Gene	p-value	ng to Figure 19 - Coronary Artery ID scription	Gene	Unigene	Protein
	p-value	Scription		_	
ldentifier			Accession	Accession	Accession
			No.	No.	No.
203184_at	0.034721	gb:NM_001999.2 /DEF=Homo	NM_001999		NP_001990
		sapiens fibrillin 2 (congenital			
		contractural arachnodactyly)	;		1 .
		(FBN2), mRNA. /FEA=mRNA			
		/GEN=FBN2 /PROD=fibrillin 2			
		/DB_XREF=gi:4755135			•
		/UG=Hs.79432 fibrillin 2	•		
	•	(congenital contractural			
		arachnodactyly) /FL=gb:U03272.1	ŀ		
		gb:NM_001999.2	1		
4	·	gb.NM_001999.2 			
200400	0.040054	LI NIM 000 400 4 4DEE III	NIM 000 400		ND 00040
203189_s_at	0.046651	gb:NM_002496.1 /DEF=Homo	NM_002496		NP_002487
		sapiens NADH dehydrogenase		3° .	
		(ubiquinone) Fe-S protein 8	*		
	1	(23kD) (NADH-coenzyme Q			
		reductase) (NDUFS8), mRNA.			:
		/FEA=mRNA /GEN=NDUFS8	**		
		/PROD=NADH dehydrogenase			
		(ubiquinone) Fe-S protein			
		8(23kD) (NADH-coenzyme Q			
		reductase)	1.		1
	,	/DB_XREF=gi:4505370		**	
	*	//UG=Hs.90443 NADH	a de la companya de la companya de la companya de la companya de la companya de la companya de la companya de		·
		dehydrogenase (ubiquinone) Fe-			
	-		1 1		
*		S protein 8 (23kD) (NADH-			
		coenzyme Q reductase)			
		/FL=gb:U65579.1			
		gb:NM_002496.1			
203217_s_at	0.025284	gb:NM_003896.1 /DEF=Homo	NM_003896	-	NP_00388
		sapiens sialyltransferase 9 (CMP			1.
		NeuAc:lactosylceramide alpha-2,3	•	,	
•		sialyltransferase; GM3 synthase)			
		(SIAT9), mRNA. /FEA=mRNA			
1.		/GEN=SIAT9		l	
-		/PROD=sialyltransferase 9 (CMP-		·	
		NeuAc:lactosylceramidealpha-2,3-			
	1.	sialyltransferase; GM3 synthase)			
	**	/DB_XREF=gi:4506954		10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to 10 to	
	* *	/UG=Hs.225939 sialyltransferase			
		9 (CMP-NeuAc:lactosylceramide	1		1
		alpha-2,3-sialyltransferase; GM3			
		synthase) /FL=gb:AB018356.1	1 -		
		gb:NM_003896.1 gb:AF119415.1			
•	, ,				
	1 .		1	1	1

		ng to Figure 19 - Coronary Artery I			
Gene	p-value	Description	Gene	Unigene	Protein
ldentifier			Accession	Accession	Accession
	,		No.	No.	No.
203262_s_at	0.025284	gb:NM_004699.1 /DEF=Homo	NM_004699		NP_004690
	ļ., , , <u>, ,-</u> ,,	sapiens DNA segment on			
		chromosome X (unique) 9928			
		expressed sequence			
		(DXS9928E), mRNA.			
		/FEA=mRNA /GEN=DXS9928E		4	
		/PROD=XAP-5 protein			*
		/DB_XREF=gi:4758219			
		/UG=Hs.54277 DNA segment on			
		chromosome X (unique) 9928			\$ m
		expressed sequence			
	•	/FL=gb:BC000028.1 gb:D83260.1		. 1	
		gb:AD001530.1 gb:NM_004699.1			
		J			
203281 s at	0.035763	gb:NM_003335.1 /DEF=Homo	NM_003335	·	NP 003326
 		sapiens ubiquitin-activating			-
		enzyme E1-like (UBE1L), mRNA.			
		/FEA=mRNA /GEN=UBE1L			
		/PROD=ubiquitin-activating			
		enzyme E1-like			
		/DB_XREF=gi:4507766		. :	
		/UG=Hs.16695 ubiquitin-activating			:
		enzyme E1-like			
		/FL=gb:NM_003335.1			, .
		gb:L13852.1			
203314 at	0.034721	gb:NM_012227.1 /DEF=Homo	NM_012227		NP_036359
 -		sapiens Pseudoautosomal GTP-	, -		=
		binding protein-like (PGPL),			
		mRNA. /FEA=mRNA			
	*	/GEN=PGPL	•		
		/PROD=Pseudoautosomal GTP-			
		binding protein-likeprotein	-		
		/DB_XREF=gi:6912587			,
<i>i</i> *		/UG=Hs.101033			
	,	Pseudoautosomal GTP-binding			
	,	protein-like /FL=gb:NM_012227.1			
	1	•		1	L .

		ig to Figure 19 - Coronary Artery [7.45		<u></u>
" · · · · · · · · · · · · · · · · · · ·	p-valu	D scription	Gene	Unigene	Protein
Identifier	-		Accession	Accession	Accession
			No.	No.	No.
203338_at	0.034721	gb:NM_006246.1 /DEF=Homo	NM_006246		NP_006237
		sapiens protein phosphatase 2,			
		regulatory subunit B (B56),			
		epsilon isoform (PPP2R5E),			
-		mRNA. /FEA=mRNA			
		/GEN=PPP2R5E /PROD=protein			
		phosphatase 2, regulatory		5	
		subunit B(B56), epsilon isoform		1	
		/DB_XREF=gi:5453955		4 W	
		/UG=Hs.173328 protein	· · · · · · · · · · · · · · · · · · ·		
	,	phosphatase 2, regulatory	*		·
		subunit B (B56), epsilon isoform			
		/FL=gb:L76703.1	,		ļ
		gb:NM 006246.1			i .
		gb.14W_000240.1	· i	~	,
202275	0.046740		NIM 000004		ND 00000
203375_s_at	0.046749	gb:NM_003291.1 /DEF=Homo	NM_003291		NP_003282
		sapiens tripeptidyl peptidase II			
		(TPP2), mRNA. /FEA=mRNA	*]
	• • •	/GEN=TPP2 /PROD=tripeptidyl		ļ ·	,
× .		peptidase II			
*		/DB_XREF=gi:4507656			
		/UG=Hs.1117 tripeptidyl			
	1	peptidase II /FL=gb:M73047.1	:		
	'	gb:NM_003291.1			
203377_s_at	0.018222	gb:NM_015891.1 /DEF=Homo	NM_015891		NP_056975
		sapiens pre-mRNA splicing			
* 1		factor (PRP17), mRNA.			
•		/FEA=mRNA /GEN=PRP17			
		/PROD=pre-mRNA splicing factor			
		/DB_XREF=gi:7706656	}		
		/UG=Hs.116674 pre-mRNA			
		splicing factor 17			, i
		/FL=gb:AF038392.1	-		
		gb:AF061241.1 gb:NM_015891.1	,		
203434 s at	0.046749	membrane metallo-endopeptidase	Al433463	Hs.1298	NP 009220
	3.5.3.75	(neutral endopeptidase,		1.3233	-555220
				1	
		enkephalinase, CALLA, CD10)		1 >	1 '

Gene List Co	rrespondir	ng to Figure 19 - Coronary Artery I	Disease		E //
Gene ld ntifier	p-value	D scription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
203504 s at	0.046749	gb:NM_005502.1 /DEF=Homo	NM_005502		NP 005493
		sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), mRNA. /FEA=mRNA /GEN=ABCA1 /PROD=ATP- binding cassette, sub-family A			
		member 1 /DB_XREF=gi:5915657 /UG=Hs.211562 ATP-binding cassette, sub-family A (ABC1), member 1 /FL=gb:AF165281.1 gb:NM_005502.1 gb:AF285167.1			
203515_s_at	0.049425	gb:NM_006556.1 /DEF=Homo sapiens phosphomevalonate kinase (PMVK), mRNA. /FEA=mRNA /GEN=PMVK	NM_006556		NP_006547
		/PROD=phosphomevalonate kinase /DB_XREF=gi:5729979 /UG=Hs:30954 phosphomevalonate kinase			
		/FL=gb:L77213.1 gb:NM_006556.1			
203531 at	0.046749		BF435809	Hs.101299	
203600_s_at		gb:NM_003704.1 /DEF=Homo sapiens gene with multiple splice variants near HD locus on 4p16.3 (RES4-22), mRNA. /FEA=mRNA /GEN=RES4-22 /PROD=gene with multiple splice variants near HD locuson 4p16.3 /DB_XREF=gi:4506480 /UG=Hs.325987 gene with multiple splice variants near HD locus on 4p16.3 /FL=gb:AB000459.1 gb:NM_003704.1	NM_003704	15.101299	NP_003695
203660_s_at	0.045316	gb:NM_006031.1 /DEF=Homo sapiens pericentrin (PCNT), mRNA. /FEA=mRNA /GEN=PCNT /PROD=pericentrin /DB_XREF=gi:5174478 /UG=Hs.15896 pericentrin /FL=gb:U52962.1 gb:NM_006031.1	NM_006031		NP_006022

Gene	p-value	Description	Gen	Unigene	Protein
ldentifier	•		Accession	Accession	Accession
			No.	No.	No.
203711 s_at	0.035763	gb:NM_014362.1 /DEF=Homo	NM 014362		NP 055177
		sapiens 3-hydroxyisobutyryl-			-
		Coenzyme A hydrolase (HIBCH),	4.1	V	e .
		mRNA. /FEA=mRNA		1 .	
		/GEN=HIBCH /PROD=3-			
	· .	hydroxyisobutyryl-Coenzyme A		3	
		hydrolase /DB XREF=gi:7657159			
		/UG=Hs.236642 3-			
		hydroxyisobutyryl-Coenzyme A	ŕ		
		hydrolase /FL=gb:BC005190.1			
		gb:U66669.1 gb:NM_014362.1		* .	
		gb.000009.1	t.		
203738 at	0.046749	hypothetical protein FLJ11193	Al421192	Hs.151046	NP 060826
203730_at 203742 s at		thymine-DNA glycosylase	BF674842	Hs.173824	141_000020
203788 s at		sema domain, immunoglobulin	Al962897	Hs.171921	NP 006370
200700_3_at	0.010020	domain (lg), short basic domain,	7 (1002007)	113.17 1321	-000070
N .	1.0	secreted, (semaphorin) 3C			
203793 x at	0.042466	gb:NM_007144.1 /DEF=Homo	NM 007144		NP_009075
200100_x_a(0.042400	sapiens zinc finger protein 144	1444_007 1444		
į.		(Mel-18) (ZNF144), mRNA.			,
	:	/FEA=mRNA /GEN=ZNF144			
		/PROD=zinc finger protein 144	· ·		
		(Mel-18) /DB_XREF=gi:6005963	41		, A
•		/UG=Hs.184669 zinc finger			
		protein 144 (Mel-18)	• •	*,	
		/FL=gb:BC004858.1 gb:D13969.1		3	
		gb:NM_007144.1	1		
203817 at	0.034721	guanylate cyclase 1, soluble, beta	W93728	Hs.77890	NP_000848
200017_at	0.004721	3	1.00,20	110.71000	111 _000010
203828 s at	0.02008	gb:NM 004221.1 /DEF=Homo	NM 004221		NP 004212
a.	0.02000	sapiens natural killer cell			
		transcript 4 (NK4), mRNA.		to the second	
		/FEA=mRNA /GEN=NK4	, w		·
		/PROD=natural killer cell		1	276
		transcript 4		1 ′ .	
		/DB_XREF=gi:4758811		1	
	,	//UG=Hs.943 natural killer cell		1	
1	! . ,	transcript 4 /FL=gb:M59807.1	,	1	
		gb:NM_004221.1			1.

		ng to Figure 19 - Coronary Artery I			
Gene	p-valu	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
	j		No.	No	No.
203832_at	0.046749	gb:NM 003095.1 /DEF=Homo	NM 003095		NP_003086
		sapiens small nuclear	<u> </u>		J
	,	ribonucleoprotein polypeptide F			
		(SNRPF), mRNA. /FEA=mRNA			}
].	/GEN=SNRPF /PROD=small			
. *	ļ ·	nuclear ribonucleoprotein			j
		polypeptide F			
	}	/DB_XREF=gi:4507130	}		
		/UG=Hs.105465 small nuclear			
		ribonucleoprotein polypeptide F	. .	} .**	
* *		/FL=gb:BC002505.1			
	}	gb:NM_003095.1			}
203843_at	0.046740	ribosomal protein S6 kinase,	AA906056	He 472065	ND 004577
203043_at	0.046749 		IAA900036	Hs.173965	NP_004577
202964 a at	0.036054	90kDa, polypeptide 3	NINA 004400	<u> </u>	NID 004004
203864_s_at	0.030254	gb:NM_001103.1 /DEF=Homo	NM_001103	(NP_001094
	÷	sapiens actinin, alpha 2			<u> </u>
		(ACTN2), mRNA. /FEA=mRNA			j
		/GEN=ACTN2 /PROD=actinin,	p		
		alpha 2 /DB_XREF=gi:4501892	[· ·	1
		/UG≃Hs.83672 actinin, alpha 2			
		/FL=gb:M86406.1			
		gb:NM_001103.1	,		
203888_at	0.019292	gb:NM_000361.1 /DEF=Homo	NM_000361		NP_000352
		sapiens thrombomodulin (THBD),		1.	1
		mRNA. /FEA=mRNA			
		/GEN=THBD		1	ļ
	٠.	/PROD=thrombomodulin	٠.		
		/DB_XREF=gi:4507482			
		/UG=Hs.2030 thrombomodulin			
		/FL=gb:M16552.1		ľ	1 .
		gb:NM_000361.1			
203893_at	0.046749	gb:NM_016283.1 /DEF=Homo	NM 016283		NP_057367
	1 1	sapiens adrenal gland protein	1		· = ·
,	,	AD-004 (LOC51578), mRNA.	1		
,		/FEA=mRNA /GEN=LOC51578	·		
	ĺ	/PROD=adrenal gland protein AD	i.	1	
_	1 · ·	004 /DB_XREF=gi:7706211			
		/UG=Hs.279586 adrenal gland		·	i , ·
	,	protein AD-004			
	[·	/FL=gb:AF151895.1		1	[.
		gb:AF110777.1 gb:NM_016283.1			
203922_s at	0.034721		Al308863	Hs.88974	NP_000388
a.	0.004721	polypeptide (chronic	/ 11000000	1.13.00374	
		granulomatous disease)]	
203975_s at	0.042057	chromatin assembly factor 1,	BEOOGSSO	He 70019	ND 005474
2009/0_5_at -	0.042037		BF000239	Hs.79018	NP_005474
202001	0.000000	subunit A (p150)	A1 574000	No.04005	ND 004704
203981_s_at	0.028893	ATP-binding cassette, sub-family D	AL5/4660	Hs.94395	NP_064731
	1	(ALD), member 4	<u> </u>	L	L

		ng to Figure 19 - Coronary Artery I	Disease		
G ne	p-value	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
			No.	No.	No.
204020 at	0.025284	purine-rich element binding protein		Hs.29117	NP 005850
· · · · -		A			. -
204021_s_at	0.041795	gb:NM_005859.1 /DEF=Homo	NM_005859		NP 005850
		sapiens purine-rich element	· · · · · - · · · · · · · ·		<u> </u>
		binding protein A (PURA),		,	
	· .	mRNA. /FEA=mRNA		1	
		/GEN=PURA /PROD=purine-rich	:		
	,	element binding protein A		a. 1	,
		/DB_XREF=gi:5032006			
		/UG=Hs.29117 purine-rich			
		element binding protein A		,	
		/FL=gb:M96684.1	İ		
		gb:NM 005859.1	ļ ·		
204023_at	0.018023	gb:NM_003839.1 gb:NM_002916.1 /DEF=Homo	NM_002916		NP 002907
204023_at	0.010023	sapiens replication factor C	14141_002910		NF_002907
		(activator 1) 4 (37kD) (RFC4),			
		(activator 1) 4 (37kD) (RFC4), ImRNA. /FEA=mRNA		· 1	
	. '	/GEN=RFC4 /PROD=replication]-
· · · · · · · · · · · · · · · · · · ·		factor C (activator 1) 4 (37kD)	J. A. Carlotte		
		/DB_XREF=gi:4506490		1	
	!	/UG=Hs.35120 replication factor			,
		C (activator 1) 4 (37kD)		1	
		/FL=gb:M87339.1			
		gb:NM_002916.1			
204055_s_at	0.038017	gb:NM_005930.1 /DEF=Homo	NM_005930		NP_005921
	1	sapiens meningioma expressed	1		
		antigen 6 (coiled-coil proline-rich)	,		
	1	(MGEA6), mRNA. /FEA=mRNA	ł *		
		/GEN=MGEA6			
ł ⁱ	<u> </u>	/PROD=meningioma expressed		₩· ·	,
		antigen 6 (coiled-coilproline-rich)			
		/DB_XREF=gi:5174560			
1	: -	/UG=Hs.117242 meningioma		,	·
	[expressed antigen 6 (coiled-coil	\$.		
		proline-rich) /FL=gb:U94780.1			
		gb:NM_005930.1			
] .]
204057_at	0.046749	interferon consensus sequence	AI073984	Hs.14453	NP_002154
		binding protein 1	,	ļ	_
204060_s_at	0.025284	gb:NM_005044.1 /DEF=Homo	NM_005044	7	NP_005035
		sapiens protein kinase, X-linked	_	1	l
		(PRKX), mRNA. /FEA=mRNA			r
1	1	/GEN=PRKX /PROD=protein			'
		kinase, X-linked			
]	1	/DB_XREF=gi:4826947			
		/UG=Hs.147996 protein kinase,	,		
		X-linked /FL=gb:NM_005044.1	! :		1
L	L.,	IN-mined /inc-go.tvivi 000044.1	 	L	L

		ng to Figure 19 - Coronary Artery I			
Gene	p-value	Description	Gene	Unigene	Protein
Identifier		· · · · · · · · · · · · · · · · · · ·	Accession	Accession	Accession
		···	No.	No.	No.
204061_at	0.025284	gb:NM 005044.1 /DEF=Homo	NM 005044	** * ** **	NP_005035
204001_at	0.020204	IY —	14141_000044		_000009
	l	sapiens protein kinase, X-linked			
		(PRKX), mRNA. /FEA=mRNA	7		
		/GEN=PRKX /PROD=protein		•	1 .
		kinase, X-linked			
		/DB XREF=gi:4826947			-
		/UG=Hs.147996 protein kinase,			
		X-linked /FL=gb:NM_005044.1		-	
204070 at	0.018023	gb:NM 004585.2 /DEF=Homo	NM 004585		NP_004576
204070_at	0.016023	15 =	NIN _004303		141-004370
		sapiens retinoic acid receptor			1
		responder (tazarotene induced) 3			
		(RARRES3), mRNA.			
		/FEA=mRNA /GEN=RARRES3			
		/PROD=retinoic acid receptor			
* * *	}	responder (tazaroteneinduced) 3		- · ·	
		/DB XREF=gi:8051633			
		/UG=Hs.17466 retinoic acid			
· ·		l i			1.0
		receptor responder (tazarotene			
		induced) 3 /FL=gb:AF060228.1			
		gb:AF092922.1 gb:NM_004585.2	· ·	4.1	
		gb:AB030815.1			
204081 at	0.034721		NM 006176		NP_006167
· - ·		sapiens neurogranin (protein			
		kinase C substrate, RC3)			
		(NRGN), mRNA. /FEA=mRNA		·	
		I S C C C C C C C C C C C C C C C C C C	,		
		/GEN=NRGN /PROD=neurogranin			
		/DB_XREF=gi:5453799			
•		/UG=Hs.26944 neurogranin			
		(protein kinase C substrate,	· ·		
		RC3) /FL=gb:BC002835.1	•		
		gb:U89165.1 gb:NM 006176.1			
		g			
204100 c at	0.034721	ab NM 002505.2 /DEE-Homo	NIM 002505	 	ND 068351
204 109_5_at	0.034721	gb:NM_002505.2 /DEF=Homo	NM_002505		NP_06835 ²
	:	sapiens nuclear transcription	,		
		factor Y, alpha (NFYA),	:		
:		transcript variant 1, mRNA.		;	
	-	/FEA=mRNA /GEN=NFYA	·		
	1	/PROD=nuclear transcription			
		factor Y, alpha, isoform1	1		* -
		/DB_XREF=gi:11496975			
		/UG=Hs 797 nuclear transcription		•	
		factor Y, alpha			
		/FL=gb:NM_002505.2			
	1	gb:M59079.1			

Gene	p-value	ng to Figure 19 - Coronary Artery Description	Gen	Unigene	Protein
Identifier	p value	Description	Accession	Accession	Accession
luciunei			No.	No	* · · · · · · · · · · · · · · · · · · ·
204151_x_at	0.026842	gb:NM_001353.2 /DEF=Homo	NM 001353	INO.	No. NP 001344
204101_X_at	0.0200-2	sapiens aldo-keto reductase	111111_001000		[M 00 1044
		family 1, member C1			
,	}	(dihydrodiol dehydrogenase 1; 20			
,		alpha (3-alpha)-hydroxysteroid			·
	ĺ				1
	,	dehydrogenase) (AKR1C1),	·		Ì
	ļ	mRNA. /FEA=mRNA	[
	h , '	/GEN=AKR1C1 /PROD=aldo-keto	ł		
	1	reductase family 1, member			
	1	C1(dihydrodiol dehydrogenase 1;		_	
]	20-alpha(3-alpha)-hydroxysteroid]]	}
		dehydrogenase)	, t		
		/DB_XREF=gi:5453542	} :	1	ļ
		/UG=Hs.306098 aldo-keto			
		reductase family 1, member C1	{		1.
		(dihydrodiol dehydrogenase 1; 20			} .
. '		alpha (3-alpha)-hydroxysteroid	<u> </u> -		
		dehydrogenase) /FL=gb:U05684.1			Į.
		gb:NM_001353.2 gb:M86609.1			l
·					
					1
204153_s_at	0.046749	gb:NM 002405.1 /DEF=Homo	NM 002405		NP_002396
	t	sapiens manic fringe	÷.		_
]· · · ·	(Drosophila) homolog (MFNG),			
		mRNA. /FEA=mRNA			
,	ļ	/GEN=MFNG /PROD=manic			1
ļ		fringe (Drosophila) homolog	•		
,		/DB_XREF=gi:4505158	1	· .	
· ·	j	/UG=Hs.31939 manic fringe	<i>e.</i>		
1)	(Drosophila) homolog	,		
	} * *	/FL=gb:U94352.1			1
		gb:NM_002405.1			1
204184 c at	0.040064	gb:NM_005160.2 /DEF=Homo	NM_005160		NP_005151
204104_5_at	0.040004		14M_002 160		NF_005151
	/	sapiens adrenergic, beta,			
	ŀ	receptor kinase 2 (ADRBK2),	}	·	}
		mRNA. /FEA=mRNA			
•		/GEN=ADRBK2 /PROD=beta		1	1
		adrenergic receptor kinase 2	_]	J
		/DB_XREF=gi:6138972	· .		,
		/UG=Hs.13944 adrenergic, beta,		}	
		receptor kinase 2		ľ	h 1
	(/FL=gb:NM 005160.2	1 .	1	1

		ng to Figure 19 - Coronary Artery			ļ
Gene	p-value	Description	Gene	Unigene /	Protein
Identifier			Accession	Accession	Accession
	}		No.	No.	No.
204190 at	0.046749	gb:NM_005800.1 /DEF≂Homo	NM_005800	1	NP_005791
		sapiens highly charged protein		} i =	1
(m)		(D13S106E), mRNA.			· .
;	ļ	/FEA=mRNA /GEN=D13S106E	* * ·	1	1
	ł	I .			
	ł	/PROD=highly charged protein	İ		ļ
	i	/DB_XREF=gi:5031648			<i>*</i>
	,	/UG=Hs 151236 highly charged	· ·	·	\
		protein /FL=gb:NM_005800.1			
204197_s_at	0.018023	gb:NM_004350.1 /DEF=Homo	NM_004350	1	NP_004341
1		sapiens runt-related transcription			ĺ
	1	factor 3 (RUNX3), mRNA.	1		
	_	/FEA=mRNA /GEN=RUNX3			
		/PROD=runt-related transcription	,	1	1 .
		factor 3 /DB XREF=gi:4757917	1		ŀ
		/UG=Hs.170019 runt-related			ì
* *		transcription factor 3			İ
	ì	/FL=gb:NM_004350.1	1		1
204198 s at	0.034721	runt-related transcription factor 3	AA541630	Hs.170019	NP 004341
204275 at		small optic lobes homolog	AI796687	Hs.55836	NP_005623
201210_40	0.010222	(Drosophila)	1 11 30001	113.00000	_000020
204331_s_at	0.045316	gb:NM_021107.1 /DEF=Homo	NM 021107	 	NP_203527
204001_3_at	0.040010	sapiens mitochondrial ribosomal	14W_021107		-20332 <i>1</i>
		· ·			
]	protein S12 (MRPS12), mRNA.	1		
	1	/FEA=mRNA /GEN=MRPS12		ľ	1
,		/PROD=mitochondrial ribosomal	· ·	· ·	
	!	protein S12			
	l	/DB_XREF=gi:11056055			
	Į.	/UG=Hs.9964 mitochondrial			
•		ribosomal protein S12			ľ
		/FL=gb:NM_021107.1			
204346_s_at	0.026013	gb:NM_007182.2 /DEF=Homo	NM_007182		NP_733835
	ļ	sapiens Ras association	· ·		
	· .	(RalGDSAF-6) domain family 1			
	ļ	(RASSF1), mRNA. /FEA=mRNA		ļ	\ .
		/GEN=RASSF1 /PROD=Ras			
·		association (RalGDSAF-6)			1
	1	domain family 1			
		/DB_XREF=gi:9256633			1
4:		/UG=Hs.26931 Ras association			
	}	(RalGDSAF-6) domain family 1		1	1
		I/FL=gb:AF061836.1			
			1		}
		gb:AF132676.1 gb:AF040703.2			
L	L	gb:NM_007182.2	<u> </u>	L	I

<u>~</u>		ng to Figur 19 - Coronary Art ry I		I Indiana	Danta
· · ·	p-value	Description	G ne	Unigene	Protein
ldentifi r			Accession	Accession	Accession
			No.	No.	No.
204352_at	0.040064	gb:NM_004619.1 /DEF=Homo	NM_004619		NP_665702
<u> </u>		sapiens TNF receptor-associated			
		factor 5 (TRAF5), mRNA.			.
		/FEA=mRNA /GEN=TRAF5			
		/PROD=TNF receptor-associated			
	-	factor 5 /DB_XREF=gi:11321602			
÷		/UG=Hs.29736 TNF receptor-			
•		I			-
	4	associated factor 5			
100	*	/FL=gb:NM_004619.1		1	
d exe		gb:AB000509.1	4 4	1	
			<u> </u>		
204355_at	0.026842	gb:NM_014966.1 /DEF=Homo	NM_014966		NP_61952
**	-	sapiens KIAA0890 protein			# T
		(KIAA0890), mRNA. /FEA=mRNA			
		/GEN=KIAA0890		**	*
		/PROD=KIAA0890 protein		,	-
	4	/DB_XREF=gi:7662361			
		/UG=Hs.323462 KIAA0890	a think a second	* · · · · · · · · · · · · · · · · · · ·	
•		protein /FL=gb:AB020697.1		,	
		gb:NM_014966.1			
204260 ot	0.046740		NM_006218		NP_00620
204369_at	0.046749	gb:NM_006218.1 /DEF=Homo	NINI_0002 10		NP_00020
		sapiens phosphoinositide-3-		•	
] -	kinase, catalytic, alpha			
		polypeptide (PIK3CA), mRNA.			
		/FEA=mRNA /GEN=PIK3CA		1.	
	1	/PROD=phosphoinositide-3-			* •
		kinase, catalytic,		,	ľ
•		alphapolypeptide			
		/DB_XREF=gi:5453891			
		/UG=Hs.85701 phosphoinositide-3			
		kinase, catalytic, alpha			
		polypeptide /FL=gb.U79143.1			
		, · · · · · · · · · · · · · · · · · · ·	r .	-	
004000 -+	0.040466	gb:NM_006218.1	NINA 000740		ND 07224
204383_at	0.042466	gb:NM_022719.1 /DEF=Homo	NM_022719		NP_07321
		sapiens DiGeorge syndrome			
		critical region gene DGSI			
44		(DGSI), mRNA. /FEA=mRNA	<u> </u>		
		/GEN=DGSI /PROD=DiGeorge			
		syndrome critical region gene	5.	1	
		DGSIprotein		Ĺ	1
		/DB_XREF=gi:13027629	•		
*		/UG=Hs.154879 DiGeorge			
	1	syndrome critical region gene	, ,	1	1
			1	1	

Gene		ng to Figure 19 - Coronary Artery ID scription	G ne	Unigene	Protein
	p-value	D scription		, -	J
ldentifier	l ·	•	Accession	Accession	Acc ssion
			No.	No.	No.
204396_s_at	0.046749	gb:NM_005308.1 /DEF=Homo	NM_005308		NP_005299
· · · · · · · · · · · · · · · · · · ·	en y en engliste	sapiens G protein-coupled			}
	1	receptor kinase 5 (GPRK5),	1		
C.		mRNA. /FEA=mRNA			,
		/GEN=GPRK5 /PROD=G protein-			1
		coupled receptor kinase 5	·		1
		/DB_XREF=gi:4885348			
		/UG=Hs.211569 G protein-) n - 1 - 1	ļ	1
		coupled receptor kinase 5			Ť
		/FL=qb:L15388.1] .	
		gb:NM_005308.1			
004400	0.040004		NIM 014710	 	ND 05552
204403_x_at	0.040064	gb:NM_014719.1 /DEF=Homo	NM_014719		NP_055534
		sapiens KIAA0738 gene product		}	1.
		(KIAA0738), mRNA. /FEA=mRNA			
		/GEN=KIAA0738		}	
		/PROD=KIAA0738 gene product			
	ļ	/DB_XREF=gi:7662275		· ·	
1	100	/UG=Hs.107479 KIAA0738 gene		, ´ .	
		product /FL=gb:AB018281.1			
	·	gb:NM 014719.1	3,		
	ł				1
204481_at	0.034721	gb:NM_004634.1 /DEF=Homo	NM 004634		NP 004625
		sapiens bromodomain and PHD			_
		finger containing, 1 (BRPF1),			
e de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de l		mRNA. /FEA=mRNA	21.5	1	
	-	/GEN=BRPF1			
	- "	/PROD=bromodomain-containing	·	ì	
		1	,	A	
1.		protein /DB_XREF=gi:4757865	1.	l l	†
	<u> </u>	/UG=Hs 1004 bromodomain and		*	ł
	, ,	PHD finger containing, 1		1	ł
		/FL=gb:M91585.1			
	<u> </u>	gb:NM_004634.1	1.	<u> </u>	
204490_s_at	0.025284	gb:M24915.1 /DEF≃Human	M24915		NP_000601
		CDw44 antigen, complete cds.	}		ł
	1	/FEA=mRNA			, ,
	1	/DB XREF=gi:180196			1
		/UG=Hs.169610 CD44 antigen	ر ا		
	1	(homing function and Indian			·
4. *		blood group system)			1
	ŀ	/FL=gb:NM 000610.1	1		1
		1 - /	1		
	1 1	gb:U40373.1 gb:M59040.1	1		1
	1 / _	gb:M24915.1		<u> </u>	1

Gene	p-value	ng to Figure 19 - Coronary Artery Description	Gene	Unigene	Protein
Identifier	h-vaine	Description			1 '
identifier		,	Accession	Accession	Accession
			No.	No.	No.
204493_at	0.034721	gb:NM_001196.1 /DEF=Homo	NM_001196		NP_001187
, , , ,		sapiens BH3 interacting domain	*	·	1
ı.,	,	death agonist (BID), mRNA.			47
,		/FEA=mRNA /GEN=BID			
	· -	/PROD=BH3 interacting domain			
		death agonist	- '	ļ	
		/DB_XREF=gi:4557360	·		
		/UG=Hs.172894 BH3 interacting			1
		domain death agonist			ł .
i		/FL=gb:AF042083.1	<u> </u>		1
		gb:NM_001196.1	<u> </u>		
204524_at	0.045316	gb:NM_002613.1 /DEF=Homo	NM_002613		NP_002604
		sapiens 3-phosphoinositide			
		dependent protein kinase-1			
	İ	(PDPK1), mRNA /FEA=mRNA			
	: .	/GEN=PDPK1 /PROD=3-			
		phosphoinositide dependent		1	
		protein kinase-1			,
	·	/DB_XREF=gi:4505694	,		
		/UG=Hs.154729 3-			
		phosphoinositide dependent)	
		protein kinase-1			
		/FL=gb:AF017995.1			**
		gb:NM_002613.1		1	ł
204529_s_at	0.025284	thymus high mobility group box	AI961231	Hs.184297	NP_055544
		protein TOX		1	i
204549_at	0.025284	gb:NM_014002.1 /DEF=Homo	NM_014002		NP_054721
	٠.	sapiens IKK-related kinase	_		_
		epsilon; inducible IkappaB kinase		1	
		(IKKE), mRNA. /FEA=mRNA		[
	1 .	/GEN=IKKE /PROD=IKK-related		j]
		kinase epsilon	1.	1.	}
1		/DB_XREF=gi:7661945			
* .	ı	/UG=Hs.321045 IKK-related] .	1
	l	1/00~ns.321043 INN-related			
			3]	ļ -
		kinase epsilon, inducible IkappaB	3		
		kinase epsilon; inducible lkappaB kinase /FL=gb:D63485.1	3		
		kinase epsilon, inducible IkappaB			

Gen	p-value	ng to Figure 19 - Coronary Artery I Description	Gene	Unigene	Prot in
Identifier			Accession	Accession	Accession
			No.	No.	No.
204610 s at	0.018693	gb:NM 006848.1 /DEF=Homo	NM 006848	140.	NP 006839
201010_0_0_4	0.01000	sapiens hepatitis delta antigen-	555515		
		interacting protein A (DIPA),			
	1	mRNA. /FEA=mRNA /GEN=DIPA			
	ŀ	/PROD=hepatitis delta antigen-	ļ	}	
)	interacting protein A	i		
		/DB_XREF=gi:5803004			1
		/UG=Hs.66713 hepatitis delta	ĺ		
		antigen-interacting protein A			`
	:	/FL=gb:U63825.1		-	1
	Ī	gb:NM_006848.1		ĺ .	
204617 s at	0.025203	gb:NM 022914.1 /DEF=Homo	NM_022914		NP 075065
204017_3_at	0.020200	sapiens hypothetical protein	022314		1111 _075005
		24432 (24432), mRNA.		1, 1	
	i	/FEA=mRNA /GEN=24432			
		//PROD=hypothetical protein			
		24432 /DB XREF=gi:12597658			
er i		/UG=Hs.78019 hypothetical			
		protein 24432			.
		/FL=gb:NM_022914.1		<u>]</u>	
204622 x_at	0.034317	gb:NM 006186.1 /DEF=Homo	NM_006186		NP 775265
204022_X_at	0.034317	sapiens nuclear receptor	114141_000100		INF_115205
		1			
•	·	subfamily 4, group A, member 2			
100	İ.	(NR4A2), mRNA. /FEA=mRNA		1	1
,		/GEN=NR4A2 /PROD=nuclear	1		}
•		receptor subfamily 4, group A,			
	,	member 2			1
		//DB_XREF=gi:5453821	a e		ľ
•		/UG=Hs.82120 nuclear receptor		1)
		subfamily 4, group A, member 2			
004000 -4	0.040004	/FL=gb:NM_006186.1	1111 000000	 	NID 000046
204639_at	0.040064	gb:NM_000022.1 /DEF=Homo	NM_000022		NP_000013
		sapiens adenosine deaminase			
•		(ADA), mRNA. /FEA=mRNA			
		/GEN=ADA /PROD=adenosine	ì		1
	,	deaminase			1
		/DB_XREF=gi:4557248		1	
*1		/UG=Hs.1217 adenosine			
į,		deaminase /FL=gb:K02567.1		}	1 .
* * * * * * * * * * * * * * * * * * * *	1	gb:NM_000022.1		1	1

Gene List Co		ng to Figure 19 - Coronary Artery	Disease		
Gene	p-value	Description	Gene	Unig ne	Protein
ldentifi r			Accession	Acc ssion	Accession
	,		No.	No.	No.
204655_at	0.018023	gb:NM 002985.1 /DEF=Homo	NM 002985		NP_002976
		sapiens small inducible cytokine		}	-
	} '	A5 (RANTES) (SCYA5), mRNA.			
		/FEA=mRNA /GEN=SCYA5)	}	ł
· ·		/PROD=small inducible cytokine	Ì	ł	(
		A5 (RANTES)			
,		/DB_XREF=gi:4506846	ĺ	ļ	
		/UG=Hs.241392 small inducible	·		
		cytokine A5 (RANTES)	[·	·	
		/FL=gb:AF043341.1 gb:M21121.1			
	·	gb:NM_002985.1 gb:AF266753.1	[· ·	
•	· .	gb.74W_002303.1 gb.74 200730.1]	}	
]]	
204683_at	0.025284	gb:NM_000873.2 /DEF=Homo	NM 000873		NP 000864
20 1000_at	0.020204	sapiens intercellular adhesion	1111_000070		
		molecule 2 (ICAM2), mRNA.			
	}	/FEA=mRNA /GEN=ICAM2		}	1
		/PROD=intercellular adhesion			ŀ
÷ .		molecule 2 precursor		ł .	
		/DB_XREF=gi:12545398	*		1
		/UG=Hs.83733 intercellular	·		·
1000	1	ladhesion molecule 2	Ì	9).	
		/FL=gb:NM_000873.2			
		gb:BC003097.1		(.	
204698_at	0.034721	gb:NM_002201.2 /DEF=Homo	NM 002201	 	NP 002192
201000_41	0.00 1721	sapiens interferon stimulated	11111_002201		_002132
		gene (20kD) (ISG20), mRNA.)	.
•	}	//FEA=mRNA /GEN=ISG20	ļ·		
		/PROD=interferon stimulated		}	1
· ·		gene (20kD)		ļ	
	ì	/DB_XREF=gi:6857799	1		:
	Ì	/UG=Hs.183487 interferon	} '	1	
		stimulated gene (20kD)	1		
		/FL=gb:U88964.1	1	l	1
		gb:NM_002201.2	1		
204699_s_at	0.022752	novel putative protein similar to	N30910	Hs.194754	NP_055203
204000_0_4	0.022702	YIL091C yeast hypothetical 84 kD	1100010	113.104104	147 _000200
	}	protein from SGA1-KTR7			
204718_at	0.045316	gb:NM_004445.1 /DEF=Homo	NM_004445	 	NP_004436
	3.070010	sapiens EphB6 (EPHB6) mRNA.	1111_004440	1	-004400
	1	I/FEA=mRNA /GEN=EPHB6	}	}	}
		/PROD=EphB6		ł	}
- !	}	/DB_XREF=gi:4758291	ł	1	1
		/UG=Hs.3796 EphB6	}		}
		//FL≈gb:D83492.1	ł ·	1	1
	1	gb:NM_004445.1	1	l	1
	L	IGD.IAINI_004440. I		<u>L'</u> :	<u></u>

Gene	p-value	ng to Figure 19 - Coronary Artery Description	G ne	Unigene	Protein
Identifier	p-value	Description	. "	_	
igentiller		,	Accession	Accession	Accession
204721° ot	0.010022	shiNIM 002242.4 (DEE-Home	No.	No.	No.
204731_at	0.018023	gb:NM_003243.1 /DEF=Homo	NM_003243		NP_003234
		sapiens transforming growth	- ,	1	
		factor, beta receptor III			
		(betaglycan, 300kD) (TGFBR3),	·		
		mRNA. /FEA=mRNA			
		/GEN=TGFBR3			
	,	/PROD=transforming growth			
	1	factor, beta receptor	Ì	Ì	
		III(betaglycan, 300kD)			
		/DB_XREF=gi:4507470			
		/UG=Hs.79059 transforming			
		growth factor, beta receptor III			
7		(betaglycan, 300kD)			
		/FL=gb:NM_003243.1			
		gb:L07594.1			
204788 s at	0.018023	gb:NM 000309.1 /DEF=Homo	NM 000309	1 E 1	NP_000300
	,	sapiens protoporphyrinogen	-		_
e e e e e e e e e e e e e e e e e e e		oxidase (PPOX), mRNA.			
		/FEA=mRNA /GEN=PPOX	1	1 .	
	3	/PROD=protoporphyrinogen	}		
4		oxidase /DB XREF=gi:4506000	•		
		/UG=Hs.100016			
		protoporphyrinogen oxidase			
		/FL=gb:NM_000309.1			
		gb:D38537.1			
204791 at	0.018023	gb:NM 003297.1 /DEF=Homo	NM_003297		NP 003288
		sapiens nuclear receptor			
		subfamily 2, group C, member			
		1 (NR2C1), mRNA. /FEA=mRNA		l	
		/GEN=NR2C1 /PROD=nuclear			
		receptor subfamily 2, group C,			
		Imember 1			
		//DB_XREF=gi:4507672			
		, – •			
		/UG=Hs.108301 nuclear receptor		٠	
		subfamily 2, group C, member			
		1 /FL=gb:M29960.1			
	ŀ	gb:NM_003297.1]

		ng to Figure 19 - Coronary Artery I		 	B
Gn	p-value	Description	Gene	Unigene	Protein
Identifier	*'		Accession	Accession	Accession
			No.	No.	No.
204811_s_at	0.021876	gb:NM_006030.1 /DEF=Homo	NM 006030		NP 006021
	0.52.5	sapiens calcium channel, voltage		1 .	
		dependent, alpha 2delta subunit			
		2 (CACNA2D2), mRNA.			
			,		
		/FEA=mRNA /GEN=CACNA2D2			
	,	/PROD=calcium channel, voltage-	18.1		
		dependent, alpha2delta subunit 2	i .		
		/DB_XREF=gi:5174402			
		/UG=Hs.127436 calcium channel,			
•		voltage-dependent, alpha 2delta			
		subunit 2 /FL=gb:AF040709.1			
		gb:NM_006030.1		[-	
) .]-
1 g ' 					
			4		
204828_at	0.025284	gb:NM 004584.1 /DEF=Homo	NM 004584		NP 00457
	, 0,04020 .	sapiens RAD9 (S. pombe)		j	
· ·		homolog (RAD9), mRNA.			
		/FEA=mRNA /GEN=RAD9			5.0
		/PROD=RAD9 (S. pombe)	j		
,		homolog /DB_XREF=gi:4759021	Transfer of the second		
]	/UG=Hs.240457 RAD9 (S.			,
-		pombe) homolog			
	1	/FL=gb:U53174.1]
	·	gb:NM_004584.1			
204837_at	0.025284	Consensus includes	AL080178		NP_05627
		gb:AL080178.1 /DEF=Homo			
		sapiens mRNA, cDNA	ļ		
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		DKFZp434K171 (from clone	İ	·	
		DKFZp434K171), partial cds.			÷.
		/FEA=mRNA			,
		/GEN=DKFZp434K171	1	}	•
		/PROD=hypothetical protein			
	-	//DB_XREF=gi:5262652			
	* * * *	1			· ·
		/UG=Hs.27194 DKFZP434K171	1		
		protein /FL=gb:NM_015458.1	1		
204838_s_at	0.033533	gb:NM_014381.1 /DEF=Homo	NM_014381		NP_05519
		sapiens mutL (E. coli) homolog			
		3 (MLH3), mRNA. /FEA=mRNA		ļ.	1
		/GEN=MLH3 /PROD=mutL (E.		ľ	
		coli) homolog 3	,	1 .	
		/DB_XREF=gi:7657336	· ·	-	
ł		/UG=Hs.279843 mutL (E. coli)			1
`.		homolog 3 /FL=gb:AF195657.1			,
	,	gb:NM 014381.1			
204860_s_at	0.046749	baculoviral IAP repeat-containing 1	AI817801	Hs.79019	NP_00452
1204000_5_at	0.040749	Pacciovital IAF Tepeat-containing T	71017001	113.73013	JINF_00452
	L	1	<u> </u>	<u> </u>	<u> </u>

		ng to Figure 19 - Coronary Artery I		<u> </u>	<u> </u>
Gene	p-value	Description	Gene	Unigene	Protein
ld ntifier			Accession	Accession	Accession
		ď	No.	No.	No.
204891_s_at	0.018023	gb:NM_005356.1 /DEF=Homo	NM_005356		NP_005347
		sapiens lymphocyte-specific)
		protein tyrosine kinase (LCK),			
	-	mRNA. /FEA=mRNA /GEN=LCK		1	
		/PROD=lymphocyte-specific			-
		protein tyrosine kinase		. `	
		/DB_XREF=gi:4885448			
		/UG=Hs.1765 lymphocyte-specific			
		protein tyrosine kinase			
		/FL=gb:M36881.1 gb:U07236.1		1	ł ,
		gb:NM_005356.1			2
204912 at	0.034721	gb:NM_001558.1 /DEF=Homo	NM_001558		NP 001549
	100	sapiens interleukin 10 receptor,			
		alpha (IL10RA), mRNA.		·	
	4. P	/FEA=mRNA /GEN=IL10RA			
		/PROD=interleukin 10 receptor,		·	1
		alpha /DB_XREF=gi:4504632	1		1
	:.	/UG≈Hs.327 interleukin 10			
		receptor, alpha			
		/FL=gb:NM_001558.1		1.	
		gb:U00672.1			
204972 at	0.046749		NM 016817		NP 058197
204972_at	0.040749	sapiens 2-5oligoadenylate	14141_010017	<u>:</u>	ME_020197
		synthetase 2 (OAS2), transcript			
		variant 1, mRNA /FEA=mRNA		·	}
		/GEN=OAS2 /PROD=2-			
		5oligoadenylate synthetase 2,			1
		lisoform p71		·	
,		•			
		/DB_XREF=gi:8051624			
	,	/UG=Hs.264981 2-5oligoadenylate	1		Ì
		synthetase 2 /FL=gb:M87434.1	1		ļ
		gb:NM_016817.1			1
004070	0.040000		A1(000000	 	ND 05046
204976_s_at	0.018023	Consensus includes	AK023637		NP_056180
ļ	,	gb:AK023637.1 /DEF=Homo	J .].
- %		sapiens cDNA FLJ13575 fis,	·		1
		clone PLACE1008630.	, ,		ļ
		/FEA=mRNA			
		/DB_XREF=gi:10435621	1		
	,	/UG=Hs.326142 Alport syndrome,	1.		
		mental retardation, midface			1
		hypoplasia and elliptocytosis		1	
		chromosomal region, gene 1			1
	4	/FL≈gb:NM_015365.1			
,				1	

		ng to Figure 19 - Coronary Artery I		Unigona	Broto
Gene	p-value	Description	Gen	Unigene	Protein
ldentifier			Accession	Accession	Accession
			No.	No.	No.
204980_at	0.018222	gb:NM_004898.1 /DEF=Homo	NM_004898		NP_004889
		sapiens clock (mouse) homolog			
		(CLOCK), mRNA. /FEA=mRNA		,	
		/GEN=CLOCK /PROD=clock			
	·	(mouse) homolog	ļ ,		
,		/DB_XREF=gi:4758009	}		
		/UG=Hs.50722 clock (mouse)	!		
		homolog /FL=gb:AB002332.1)	
	-	gb:AF011568.1 gb:NM_004898.1			- ,
205022_s at	0.025284	gb:NM 005197.1 /DEF=Homo	NM 005197	 	NP_005188
203022_s_at	0.023204	sapiens checkpoint suppressor 1	14141_003197	· .	14E_002 100
	1				
•	l	(CHES1), mRNA. /FEA=mRNA	N		
	1	/GEN=CHES1 /PROD=checkpoint			
		suppressor 1			
	. .	/DB_XREF=gi:4885136	ł		
		/UG=Hs.211773 checkpoint	F14		
	}	suppressor 1 /FL=gb:U68723.1	1		
		gb:NM_005197.1			
205042_at	0.034721	gb:NM_005476.2 /DEF=Homo	NM_005476		NP_005467
		sapiens UDP-N-	-] =
	}	acetylglucosamine-2-epimeraseN-			1
		acetylmannosamine kinase			
•	ł	(GNE), mRNA /FEA=mRNA	·	1	
		/GEN=GNE /PROD=UDP-N-			
	ł	acetylglucosamine-2-epimeraseN-	٠	1	
		acetylmannosamine kinase			
T.	i	/DB_XREF=gi:6382074			
	į				
	i ·	/UG=Hs.5920 UDP-N-	}	-	
		acetylglucosamine-2-epimeraseN-			
	1	acetylmannosamine kinase		1 *	
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1		/FL=gb:AF051852.1			
		gb:AF155663.1 gb:NM_005476.2			
205081_at	0.034721	gb:NM_001311.1 /DEF=Homo	NM_001311		NP_001302
'		sapiens cysteine-rich protein 1			
'		(intestinal) (CRIP1), mRNA			
)	[/FEA=mRNA /GEN=CRIP1	[1
		/PROD=cysteine-rich protein 1	+ 1	, ,	
· 		(intestinal) /DB_XREF=gi:4503046		1	
	;	/UG=Hs.17409 cysteine-rich			
	[,	protein 1 (intestinal)			
	[·	/FL≈gb:BC002738.1 gb:U58630.1			
4		gb:NM_001311.1 gb:U09770.1	4.5	[
				,	1
		n.		· ·	
	 _	<u> </u>		L	<u></u>

Gene	p-value	ng to Figure 19 - Coronary Artery Description	Gene	Unigene	Protein
Identifier	p-value	Description	Accession	T	1
identinei				Accession	Accession
205105_at	0.018023	gb:NM_002372.1 /DEF=Homo	No. NM_002372	No.	NP 002363
200 100_at	0.010023	sapiens mannosidase, alpha,	14141_002372		MP_002363
		class 2A, member 1 (MAN2A1),			
· •	j	mRNA. /FEA=mRNA	1		
		I/GEN=MAN2A1	l ·	1	
	<u> </u>	1)	} .	1
•	·	/PROD=mannosidase, alpha,	}	}	}
		class 2A, member 1	1		
	ļ	//DB_XREF=gi:4758697			
		/UG=Hs.32965 mannosidase,			
•	• •	alpha, class 2A, member 1			[
		/FL=gb:U31520.1	1	1	
005400	0.004704	gb:NM_002372.1 gb:D63998.1	1114 000000	<u> </u>	
205126_at	0.031/04	gb:NM_006296.1 /DEF=Homo	NM_006296		NP_006287
To a contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract		sapiens vaccinia related kinase	1	ļ	
	}	2 (VRK2), mRNA. /FEA=mRNA			
*	<u> </u>	/GEN=VRK2 /PROD=vaccinia	}	_	
		related kinase 2			
		/DB_XREF=gi:5454163		<u>, </u>	
	·	/UG=Hs.82771 vaccinia related			
	Í	kinase 2 /FL=gb:AB000450.1		1	
	 	gb:NM_006296.1			
205128_x_at	0.046749	gb:NM_000962.1 /DEF=Homo	NM_000962		NP_542158
		sapiens prostaglandin-			
	}	endoperoxide synthase 1			
		(prostaglandin GH synthase and		,	
		cyclooxygenase) (PTGS1),			
	. ,	mRNA. /FEA=mRNA		ř :	İ
		/GEN=PTGS1			1
		/PROD=prostaglandin-	· 5.		1
		endoperoxide synthase		1	
		1(prostaglandin GH synthase			
		and cyclooxygenase)			
		/DB_XREF=gi:11386140	~		
		/UG=Hs.88474 prostaglandin-			
•		endoperoxide synthase 1			[
		(prostaglandin GH synthase and			
		cyclooxygenase)	1		
	٠.	/FL=gb:NM_000962.1	1, 11		1
	1	gb:M59979.1	1	1	ļ

		ng to Figure 19 - Coronary Artery		triaina n	Droto!=
G ne	p-value	Description	Gene	Ünigene	Protein
Identifier	1		Accession	Accession	Accession
	ļ	,	No.	No.	No.
205176_s_at	0.034721	gb:NM 014288.1 /DEF=Homo	NM 014288		NP_055103
		sapiens integrin beta 3 binding		l.	-
*		protein (beta3-endonexin)			
					,
**		(ITGB3BP), mRNA. /FEA=mRNA			
		/GEN=ITGB3BP /PROD=integrin			ľ
		beta 3 binding protein(beta3-			
		endonexin)		•	
		/DB_XREF=gi:7657205			,
		/UG=Hs.82084 integrin beta 3			
		binding protein (beta3-endonexin)		1	
	1.	/FL=gb:BC005301.1			
,	1		,		1
005040	0.000047	gb:AF175306.1 gb:NM_014288.1	NIM 04 474C	<u> </u>	ND OFFEOA
205212_s_at	0.038017	gb:NM_014716.1 /DEF=Homo	NM_014716		NP_055531
	ļ ·	sapiens KIAA0050 gene product			
		(ACAP1), mRNA. /FEA=mRNA	·		1.
1)	/GEN=ACAP1 /PROD=centaurin			.
	**	beta1 /DB_XREF=gi:7661879	•	,	>
	1	/UG=Hs.108947 KIAA0050 gene	}		
		product /FL=gb:D30758.1			
	ŀ	I'			
		gb:NM_014716.1		, i	
			l	ļ	1
205214_at	0.034/21	gb:NM_004226.1 /DEF=Homo	NM_004226		NP_004217
		sapiens serinethreonine kinase			
}		17b (apoptosis-inducing)	Ų		
		(STK17B), mRNA. /FEA=mRNA			
		/GEN=STK17B			
		/PROD=serinethreonine kinase			
		17b(apoptosis-inducing)			
	1	1			
١.		/DB_XREF=gi:4758193	*	,	
}	-	/UG=Hs.120996 serinethreonine		.]	
•		kinase 17b (apoptosis-inducing)			
*		/FL=gb:AB011421.1	1 '		ł
		gb:NM_004226.1	• •		
205250_s_at	0.031704	gb:NM_014684.1 /DEF=Homo	NM_014684	T	NP 055499
	3,55,115.	sapiens KIAA0373 gene product			
[-		(KIAA0373), mRNA. /FEA=mRNA			
			1	.,	
		/GEN=KIAA0373			· ·
		/PROD=KIAA0373 gene product			;
1		/DB_XREF=gi:7662079			
ł	ł	/UG=Hs.150444 KIAA0373 gene	1	1. 1	* .
<u>'</u>	1	product /FL=gb:AB002371.1			
1		gb:NM_014684.1	1	Ì	
1.5		3201.001			
L	1	<u> </u>		<u> </u>	<u> </u>

Gene	p-value	Description	Gene	Unigene	Protein
Identifier	1		Accession	Accession	Accession
			No.	No.	No.
205267 at	0.018444	gb:NM 006235.1 /DEF=Homo	NM 006235	110.	NP 006226
	1 - E	sapiens POU domain, class 2,		1	
	1	associating factor 1 (POU2AF1),			
	1	mRNA. /FEA=mRNA		1	
		/GEN=POU2AF1 /PROD=POU	}		
		Idomain, class 2, associating	Ì		
٠.	{	factor 1 /DB_XREF=gi:5453933	{		
		/UG=Hs.2407 POU domain,	1		,
		class 2, associating factor 1			1
		/FL=gb:NM_006235.1	l		1
	1	L=gb.14141_000233.1	1		
205282 at	0.046749	gb:NM_004631.1 /DEF=Homo	NM 004631	 	NP_150643
-40-05-01	0.0.0	sapiens low density lipoprotein		1	(000 10
й		receptor-related protein 8,	· .		l ·
-	-	apolipoprotein e receptor (LRP8),	1		
		mRNA. /FEA=mRNA	;]
1	7	/GEN=LRP8 /PROD=low density			1
		lipoprotein receptor-related			1
	*	protein8, apolipoprotein e			
	1	receptor /DB_XREF=gi:4758687			
		/UG=Hs.54481 low density		·	Į
		lipoprotein receptor-related		}	
		protein 8, apolipoprotein e			ļ.
		receptor /FL=gb:D50678.1	*		
		gb:NM_004631.1			
		\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		1	1
205297_s_at	0.036254	gb:NM_000626.1 /DEF=Homo	NM_000626		NP_067613
	1	sapiens CD79B antigen		1	· ·
	} .	(immunoglobulin-associated beta)	}		1
	`	(CD79B), transcript variant 1,	1	į	1
	1	mRNA. /FEA=mRNA			
-	İ	/GEN=CD79B /PROD=CD79B		1	
		antigen, isoform 1 precursor	1		}
		/DB_XREF=gi:11038673		1	
		/UG=Hs.89575 CD79B antigen	1		
_	1	(immunoglobulin-associated beta)	1	İ	
	1	/FL=gb:NM_000626.1	{	1	1
		gb:M80461.1 gb:M89957.1	}	}	}

		ng to Figure 19 - Coronary Art ry I		<u> </u>	B
Gene	p-value	Description	Gen	Unigene	Protein
ldentifier			Accession	Accession	Accession
			No.	No.	No.
205301 s at	0.045316	gb:NM 016820.1 /DEF=Homo	NM_016820		NP 058438
		sapiens 8-oxoguanine DNA	l		
	,	glycosylase (OGG1), nuclear			
		gene encoding mitochondrial			
		1 -	·		
		protein, transcript variant 1c,	. 247		
-		mRNA. /FEA=mRNA			1 "
		/GEN=OGG1 /PROD=8-			
		oxoguanine DNA glycosylase,			
		isoform 1c			
		/DB_XREF=gi:8670531			
•		/UG=Hs.96398 8-oxoguanine			
		DNA glycosylase			
		/FL=gb:U96710.1 gb:AF026691.1		J	
		gb:NM 016820.1			
205315_s_at	0.018222	gb:NM_006750.1 /DEF=Homo	NM 006750		NP 570896
2000 10_3_ac	0.0.10222	sapiens syntrophin, beta 2	14141_000730		_370030
		(dystrophin-associated protein			•
		A1, 59kD, basic component 2)			
		(SNTB2), mRNA. /FEA=mRNA			
		/GEN=SNTB2 /PROD=syntrophin,	,		
		beta 2 (dystrophin-			
		associatedprotein A1, 59kD,			
		basic component 2)	*		
1		/DB_XREF=gi:5803176]	:	
		/UG=Hs.172278 syntrophin, beta			20 20
		2 (dystrophin-associated protein			
,		A1, 59kD, basic component 2)			
		/FL=gb:U40572.1	•	[
		1			
005040 -4	0.040057	gb:NM_006750.1	1114 04 4707		ND 055046
205340_at	0.019657	gb:NM_014797.1 /DEF=Homo	NM_014797	*	NP_055612
		sapiens KIAA0441 gene product			
		(KIAA0441), mRNA. /FEA=mRNA		1 ,	
•		/GEN=KIAA0441	1		
		/PROD=KIAA0441 gene product			!
· ·		/DB_XREF=gi:7662127			
		/UG=Hs.32511 KIAA0441 gene			,
		product /FL=gb:AB007901.1	·		
		gb:NM 014797.1	٠		2
205401 at	0.025284	gb:NM_003659.1 /DEF=Homo	NM_003659		NP_003650
200401_at	0.020204	sapiens alkylglycerone phosphate			111 _000000
					٠
	[synthase (AGPS), mRNA			{
		/FEA=mRNA /GEN=AGPS			,
•	1	/PROD=alkylglycerone phosphate			
		synthase precursor			ĺ
		/DB_XREF=gi:4501992			l ·
		/UG=Hs.22580 alkylglycerone			
	1	phosphate synthase			
•		/FL=gb:NM_003659.1			
	l	35.14111_0000000.1	1	1	I

Gene List Co	rrespondir	ng to Figure 19 - Coronary Artery I	Disease		
Gene	p-value	Description	G ne	Unigene	Prot in
Identifier			Accession	Accession	Accession
			No.	No.	No.
205411_at	0.018023	gb:NM 006282.1 /DEF=Homo	NM 006282	101	NP_006273
		sapiens serinethreonine kinase 4			
		(STK4), mRNA. /FEA=mRNA	er e ere e i juger i	***]
		/GEN=STK4	[[
		/PROD=serinethreonine kinase 4	}]
					<u>}</u> .
•		/DB_XREF=gi:5454095	}		} `.
		/UG=Hs.35140 serinethreonine	}		
	•	kinase 4 /FL=gb:U18297.1	ł		
005404		gb:U60207.1 gb:NM_006282.1			
205434_s_at		adaptor-associated kinase 1	AW451954	Hs.135941	NP_055726
205437_at	0.025284	gb:NM_006385.1 /DEF=Homo	NM_006385	·	NP_006376
		sapiens zinc finger protein 211	· ·	[[
		(ZNF211), mRNA. /FEA=mRNA	'		}
		/GEN=ZNF211 /PROD=zinc			}
		finger protein 211			ļ
		/DB_XREF=gi:5454175			
		/UG=Hs.15110 zinc finger protein	,	·	}
		211 /FL=gb:U38904.1	1	ł .	,
		gb:NM_006385.1	!		!
205442 at	0.049425	gb:NM_021647.1 /DEF=Homo	NM 021647		NP 067679
		sapiens KIAA0626 gene product		1	
		(KIAA0626), mRNA. /FEA=mRNA	[
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		/GEN=KIAA0626			[
		/PROD=KIAA0626 gene product])	· ·
,		/DB_XREF=gi:11067364			
:		/UG=Hs.178121 KIAA0626 gene		:	
		product /FL=gb:NM_021647.1			}
		· — · · · · · · · · · · · · · · · · · ·	·		
		gb:AB014526.1		17	ł .
20E462 a at	0.040425	Ch.NIA 000440.4 (DEE-110	NIM 000440		ND COCCC
205462_s_at	0.049425	gb:NM_002149.1 /DEF=Homo	NM_002149		NP_602293
1		sapiens hippocalcin-like 1	1		[
	**	(HPCAL1), mRNA /FEA=mRNA	<u> </u>]	ļ .
		/GEN=HPCAL1	! ,		
,	ļ.	/PROD=hippocalcin-like 1	1	4.7	} -
	,	/DB_XREF=gi:4504474	}		
		/UG=Hs.3618 hippocalcin-like 1			
		/FL=gb:NM_002149.1			ł
		gb:D16227.1			, ,
205483_s_at	0.034721	gb:NM_005101.1 /DEF=Homo	NM_005101		NP_005092
		sapiens interferon-stimulated	1.		_
		protein, 15 kDa (ISG15), mRNA.	[ŀ	
		/FEA=mRNA /GEN=ISG15	1		ļ
		/PROD=interferon-stimulated	1		1
		protein, 15 kDa			}
		/DB_XREF=gi:4826773			ļ
	}	/UG=Hs.833 interferon-stimulated	1		1
	,	protein, 15 kDa			
*		/FL=gb:M13755.1	l .	1	{ ·
					1
	<u> </u>	gb: <u>NM_</u> 005101.1	L'	L	L

		ng to Figure 19 - Coronary Artery		 	la
Gene	p-value	Description	Gene	Unigene	Protein
ldentifier			Accession	Accession	Accession
			No.	No.	No.
205488_at	0.018023	gb:NM_006144.2 /DEF=Homo	NM_006144		NP_006135
		sapiens granzyme A (granzyme		. :	
	· .	1, cytotoxic T-lymphocyte-]:
10 A		associated serine esterase 3)		3	1 - 1
	1	(GZMA), mRNA. /FEA=mRNA			[
		/GEN=GZMA /PROD=granzyme			
	•	A precursor			1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
	•	/DB_XREF=gi:6996012			
		/UG=Hs.90708 granzyme A			
			٠.		
	.1	(granzyme 1, cytotoxic T-			
	· ·	lymphocyte-associated serine		1	
		esterase 3) /FL=gb:M18737.1			
	 	gb:NM_006144.2		 	
205511_at	0.042466	gb:NM_017976.1 /DEF=Homo	NM_017976		NP_060446
		sapiens hypothetical protein		}	
		FLJ10038 (FLJ10038), mRNA.			
	1	/FEA=mRNA /GEN=FLJ10038		**	
	1	/PROD≈hypothetical protein			f
		FLJ10038 /DB_XREF=gi:8922197			· · ·
		/UG=Hs.181202 hypothetical	1		ļ
	,	protein FLJ10038			
		/FL=gb:NM_017976.1			
,	. •				
205525_at	0.048741	gb:NM_018495.3 /DEF=Homo	NM 018495	 -	
		sapiens NAG22 protein			
	1	(LOC55873), mRNA.	1	}	
· ·		/FEA=mRNA /GEN=LOC55873	1		
		/PROD=NAG22 protein	1		
			*.		
	Tell to the	//DB_XREF=gi:13236500	1		,
		/UG=Hs.283080 NAG22 protein			
	\ .	/FL=gb:AF247820.3		,	
 		gb:NM_018495.3		<u> </u>	
205583_s_at	0.046749	gb:NM_024810.1 /DEF=Homo	NM_024810	,	NP_079086
	1	sapiens hypothetical protein]]	
		FLJ23018 (FLJ23018), mRNA.			
	(/FEA=mRNA /GEN=FLJ23018	· .	1	
	1	/PROD=hypothetical protein			
		FLJ23018	}		
		/DB_XREF=gi:13376194			}
] ,]	/UG=Hs.169078 hypothetical			
		protein FLJ23018			
	1	/FL=gb:NM 024810.1		1	

Gene List Co	rr spondir	ng to Figure 19 - Coronary Artery I	Diseas		
Gene	p-value	D scription	Gene	Unig ne	Protein
Identifier	[Accession	Accession	Accession
-	1		No.	No.	No.
205586 x at	0.049425	gb:NM_003378.1 /DEF=Homo	NM 003378		NP 003369
200000_x_ut	0.010120	sapiens VGF nerve growth			
		factor inducible (VGF), mRNA.			
		/FEA=mRNA /GEN=VGF	<u>{</u>		. `
				}	
	1	/PROD=VGF nerve growth factor	ļ		
		inducible /DB_XREF=gi:4507888	· ·		[. ··
		/UG=Hs.171014 VGF nerve	1		
		growth factor inducible			
		/FL=gb:NM_003378.1	K · · · ·		j
**					,
205599_at	0.019657	gb:NM_005658.1 /DEF=Homo	NM_005658		NP_005649
	4.1	sapiens TNF receptor-associated	}	1	
		factor 1 (TRAF1), mRNA.		,	
		/FEA=mRNA /GEN=TRAF1			1
		/PROD=TNF receptor-associated	1		
		factor 1 /DB_XREF=gi:5032192			
		/UG=Hs.2134 TNF receptor-)		
		associated factor 1		•	
		/FL=gb:NM 005658.1			
	ł .	lgb:U19261.1			
* \$	}	190.019261.1 			
0050041	0.005004	abalia 025207 4 /DEE-Hama	NIMA OOFOOT		ND 070400
205661_s_at	0.025284	gb:NM_025207.1 /DEF=Homo	NM_025207		NP_079483
	12.5	sapiens hypothetical protein	· ·	9.	
,		PP591 (PP591), mRNA.	1		
		/FEA=mRNA /GEN=PP591			
		/PROD=hypothetical protein			
	1	PP591 /DB_XREF=gi:13376805	1	•	
	Į.	/UG=Hs.118666 hypothetical			
	ļ	protein PP591			
		/FL=gb:NM_025207.1			
205684_s at	0.034721	gb:NM 017925.1 /DEF=Homo	NM_017925		NP_060395
	1	sapiens hypothetical protein	-		-
		FLJ20686 (FLJ20686), mRNA.	1		
		/FEA=mRNA /GEN=FLJ20686	-		
, .*		/PROD=hypothetical protein	1		
·		FLJ20686 /DB_XREF=gi:8923616		1	}
				1	1
	. ,	/UG=Hs.271480 hypothetical			
		protein FLJ20686		1	j :
} `	}	/FL=gb:NM_017925.1	-	1	1
005740	0.00004=		NINA COCCOS		ND 00000
205718_at	0.038017	1~ ~	NM_000889		NP_000880
		sapiens integrin, beta 7 (ITGB7),			1
		mRNA. /FEA=mRNA			1 4 4
	1	/GEN=ITGB7 /PROD=integrin,			1
] * * .		beta 7 /DB_XREF=gi:4504776].
l		/UG=Hs.1741 integrin, beta 7			
		/FL=gb:M68892.1 gb:M62880.1			1
1] .	gb:NM_000889.1			1

Gene List Co Gene	p-value	Description	Gen	Unigene	Protein
Identifier	p-value	Description	1 7		
identiner		•	Accession	Accession	Accession
205750	0.02040	CD0 addings alaba a dimension	No.	No.	No.
205758_at	0.03018	CD8 antigen, alpha polypeptide	AW006735	Hs.85258	NP_741969
000004		(p32)		ļ	
205821_at	0.018444	gb:NM_007360.1 /DEF=Homo	NM_007360	1	NP_031386
	F .	sapiens DNA segment on			
	·	chromosome 12 (unique) 2489			[
]	expressed sequence			.
	1	(D12S2489E), mRNA.			
٠.		/FEA=mRNA /GEN=D12S2489E]		
		/PROD=NKG2-D type II integral			}
		membrane protein			
- 1		/DB_XREF=gi:6679051			
	2.1	/UG=Hs 74085 DNA segment on		1) · ,
]	chromosome 12 (unique) 2489	}	}	
)	expressed sequence			
		/FL=gb:NM_007360.1	1		
*	ł	gb:AF260135.1 gb:AF260136.1	!	1	}
205831_at	0.018023		NM 001767	1	NP 001758
 -		sapiens CD2 antigen (p50),	· -	1	
		sheep red blood cell receptor	1	1	,
	ł	(CD2), mRNA. /FEA=mRNA	,		1
÷ .	ł	/GEN=CD2 /PROD=CD2 antigen		` '	1
	1	(p50), sheep red blood	1	1	Ì
	1 '	cellreceptor	•		
	ſ.	/DB_XREF=gi:4502652			· .
٠	Í .	/UG=Hs.89476 CD2 antigen			(
	[(p50), sheep red blood cell	;		1
a.		receptor /FL=gb:M16445.1			
		_			1
].	gb:M14362.1 gb:M16336.1]
205972 01	0.010022	gb:NM_001767.1	NIA 004070	 	NID COACCO
205873_at	0.010023	gb:NM_004278.1 /DEF=Homo	NM_004278		NP_004269
ļ	ľ	sapiens phosphatidylinositol			
		glycan, class L (PIGL), mRNA.	1.	A 4 1	1
)	/FEA=mRNA /GEN=PIGL			1.
i i	ļ ·	/PROD=phosphatidylinositol			
\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		glycan, class L	1	1	l
,	<u>.</u>	/DB_XREF=gi:4758921	1	1	1
i	1	/UG=Hs.27008			1
		phosphatidylinositol glycan, class	` .		
,		L /FL=gb:AB017165.1	1	1	
•	,	gb:NM_004278.1	1		
	1		J	J ,	1

Gene List Co		ng to Figure 19 - Coronary Artery I	Disease		
Gene	p-value	Description	Gene	Unigene	Protein
ldentifier		7	Accession	Accession	Accession
		•	No.	No.	No.
205885_s_at	0.018222	gb:L12002.1 /DEF=Human	L12002		NP 000876
		integrin alpha 4 subunit mRNA,			
]	complete cds. /FEA=mRNA		1	
	ļ	/GEN=ITGA4 /PROD=integrin	}		}
	 	alpha 4 subunit	ł	1	ľ
	[li .
	}	/DB_XREF=gi:903743	·		
		/UG=Hs.40034 integrin, alpha 4			
	.	(antigen CD49D, alpha 4 subunit			
	}	of VLA-4 receptor)	ì		1
		/FL=gb:NM_000885.2	·	1	1
		gb:L12002.1			
205988_at	0.018023	gb:NM_003874.1 /DEF=Homo	NM_003874	1	NP_003865
	1	sapiens CD84 antigen (leukocyte	· ·	1	1
-	1	antigen) (CD84), mRNA.			
		/FEA=mRNA /GEN=CD84	1		1
	1	/PROD=CD84 antigen (leukocyte		1	
	}	antigen) /DB_XREF=gi:4502686	}	}	· ·
		/UG=Hs.137548 CD84 antigen	i .	:	
) .	(leukocyte antigen)			
		/FL=gb:U82988.1		ł .	
:	İ	gb:NM_003874.1 gb:AF054815.1	j	1	
		gb.NW_000074.1	ļ ·		
206035_at	0.018603	Consensus includes	NM_002908	 	NP 002899
200000_ar	0.070000	gb:NM_002908.1 /DEF=Homo	14141_002000		141 _002000
		sapiens v-rel avian		}	ł
		1 '	Ì	1	1
. *	ļ	reticuloendotheliosis viral			
		oncogene homolog (REL),		1	
	}	mRNA. /FEA=mRNA /GEN=REL	j	j ·	
		/PROD=v-rel avian			}
•	Ì	reticuloendotheliosis viral		1	ł
	ſ	oncogenehomolog	1		S .
		/DB_XREF=gi:4506472			· ·
	İ	/UG=Hs.44313 v-rel avian		•	
	1	reticuloendotheliosis viral	1		1
	ł	oncogene homolog			į.
		/FL=gb:NM_002908.1	1		1
206049_at	0.038017	gb:NM_003005.2 /DEF=Homo	NM 003005		NP 002996
_		sapiens selectin P (granule		1	-
	į.	membrane protein 140kD,	j	,]
•		antigen CD62) (SELP), mRNA.	} '		ì
		/FEA=mRNA /GEN=SELP	1		1
	1	//PROD=selectin P precursor			1
		//DB XREF=gi:6031196	}	}	1
		, – ,	1	1	1
		/UG=Hs.73800 selectin P			
	}	(granule membrane protein	1		}
		140kD, antigen CD62)			İ
		/FL=gb:M25322.1			1.
) .	gb:NM_003005.2	}	1	1

Gene	p-value	ng to Figure 19 - Coronary Art ry Description	Gene	Unigene	Protein
	p-value	Description			
ldentifi r	1 . 1		Accession	Accession	Accession
	<u> </u>	<u></u>	No.	No.	No.
206050 s_at	0.046749	gb:NM_002939.1 /DEF=Homo	NM_002939	-	NP_002930
) = -	**	sapiens ribonucleaseangiogenin			
	1	inhibitor (RNH), mRNA.		1	1
4.5	1	/FEA=mRNA /GEN=RNH			
	1	/PROD=ribonucleaseangiogenin		 	
· I .		inhibitor /DB_XREF=gi:4506564		[· .
		/UG=Hs.75108]
] .				
		ribonucleaseangiogenin inhibitor	, t		
		/FL=gb:M36717.1		13	7
		gb:NM_002939.1-	1.	 	-
206110_at	0.048741	gb:NM_003536.1 /DEF=Homo	NM_003536		NP_003527
		sapiens H3 histone family,			1
	1	member K (H3FK), mRNA.			
	1	/FEA=mRNA /GEN=H3FK	∤ , ,	1	1
,		/PROD=H3 histone family,			
•		member K			: .
		/DB_XREF=gi:4504294			1.
		/UG=Hs.70937 H3 histone	∮	·[.	1
	İ	family, member K		1	
		/FL=gb:NM_003536.1		1	
200442 = =	0.024704		NM 004162	 	NP 004153
206113_s_at	0.034721	gb:NM_004162.1 /DEF=Homo	NNIVI_004 162		INP_004155
		sapiens RAB5A, member RAS	} · · · ·		
		oncogene family (RAB5A),	}	1	
	1	mRNA. /FEA=mRNA	1		} .
		/GEN=RAB5A /PROD=RAB5A,			1
	} '	member RAS oncogene family			
	.[/DB_XREF=gi:4759003	1	1	
	1 g -2	/UG=Hs.73957 RAB5A, member		1	1
	Ì	RAS oncogene family	1		
	1.	/FL=gb:NM_004162.1			
` .	1	gb:M28215.1			
206118 at	0.018444	gb:NM_003151.1 /DEF=Homo	NM_003151	 	NP 003142
200110_uk) 0.010111	sapiens signal transducer and			
ļ		activator of transcription 4		-	1
	1			,	
	1	(STAT4), mRNA. /FEA=mRNA		,	1
		/GEN=STAT4 /PROD=signal			1 4
	1	transducer and activator of			1
}		transcription4	1	}	1 .
!		/DB_XREF=gi:4507254	1.	1.	
[/UG=Hs.80642 signal transducer	1		1
	,	and activator of transcription 4			
		/FL=gb:L78440.1			
ľ ·	ł	gb:NM_003151.1		1	1

		ng to Figure 19 - Coronary Artery I			
Gene	p-value	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
			No.	No.	No
206132_at	0.042466	gb:NM_002387.1 /DEF=Homo	NM 002387		NP 002378
		sapiens mutated in colorectal			
•		cancers (MCC), mRNA.			
	, ,	/FEA=mRNA /GEN=MCC	ĺ		
		/PROD=mutated in colorectal			
. *		cancers /DB_XREF=gi:4505128			1
		/UG=Hs.1345 mutated in	1.		
r	•	colorectal cancers			
		1		i	Í.
<u> </u>		/FL=gb:M62397.1		· ·	
0004071	0.00040	gb:NM_002387.1	NIM 004474	 	ND 020206
206167_s_at	0.03018	gb:NM_001174.2 /DEF=Homo	NM_001174		NP_038286
l. I	N	sapiens Rho GTPase activating		1	
		protein 6 (ARHGAP6), transcript	[.		[
		variant 2, mRNA. /FEA=mRNA			
		/GEN=ARHGAP6 /PROD=Rho		1	
		GTPase activating protein 6		('	
		isoform 2 /DB_XREF=gi:7382476		1.4	
	1	/UG=Hs:250830 Rho GTPase	1 1		
		activating protein 6			
		/FL=gb:AF022212.2			
•		gb:NM_001174.2		1	
•					1
206194 at	0.034721	homeo box C4	AW299598	Hs.50895	NP 705897
206235 at		gb:NM 002312.1 /DEF=Homo	NM 002312		NP 002303
-		sapiens ligase IV, DNA, ATP-	T -		
	İ	dependent (LIG4), mRNA.	i		
	}	/FEA=mRNA /GEN=LIG4		/	
		/PROD=DNA ligase IV		<u> </u>	. `
		/DB XREF=gi:4504996	}	}	
		/UG=Hs.166091 ligase IV, DNA,			
		ATP-dependent			1
		/FL=gb:NM_002312:1			
200207 - 4	0.007700		NM 002279	 	NP 647612
200267_s_at	0.027792	gb:NM_002378.1 /DEF=Homo	NM_002378		INP_047012
		sapiens megakaryocyte-			ļ.,
		associated tyrosine kinase			
	1	(MATK), mRNA. /FEA=mRNA			•]
	1			L .	1.
		/GEN=MATK			
		/PROD=megakaryocyte-			
		/PROD=megakaryocyte- associated tyrosine kinase			
		/PROD=megakaryocyte- associated tyrosine kinase /DB_XREF=gi:4505108			
		/PROD=megakaryocyte- associated tyrosine kinase			
		/PROD=megakaryocyte- associated tyrosine kinase /DB_XREF=gi:4505108 /UG=Hs 274 megakaryocyte- associated tyrosine kinase			
		/PROD=megakaryocyte- associated tyrosine kinase /DB_XREF=gi:4505108 /UG=Hs 274 megakaryocyte-			
		/PROD=megakaryocyte- associated tyrosine kinase /DB_XREF=gi:4505108 /UG=Hs 274 megakaryocyte- associated tyrosine kinase			

		ng to Figure 19 - Coronary Artery I		 	
Gene Identifier	p-value	Description	G ne Accession	Unigene Accession	Protein Accession
			No.	No.	No.
206296_x_at	0.022752	gb:NM_007181.1 /DEF=Homo	NM_007181	· ·	NP_009112
		sapiens mitogen-activated protein			,
		kinase kinase kinase 1			* *
	1.0	(MAP4K1), mRNA. /FEA=mRNA			
		/GEN=MAP4K1 /PROD=mitogen-			
		activated protein kinase kinase		8	
		kinasekinase 1]		
		/DB_XREF=gi:6005809	**		
		/UG=Hs.86575 mitogen-activated			
		protein kinase kinase kinase			
		kinase 1 /FL=gb:U66464.1			
	•	gb:NM_007181.1			
•	ł .			•	1
206323_x_at	0.034721	gb:NM_002547.1 /DEF=Homo	NM_002547		NP_002538
		sapiens oligophrenin 1 (OPHN1),			
		mRNA. /FEA=mRNA			
		/GEN=OPHN1		•	
		/PROD=oligophrenin 1, Rho-			
		GTPase acivating protein] ,		
	1	/DB_XREF=gi:4505506		ļ,	
		/UG=Hs.128824 oligophrenin 1		4	
	1	/FL=gb:NM_002547.1		É	,
206390 x at	0.046749	gb:NM_002619.1 /DEF=Homo	NM_002619		NP 002610
		sapiens platelet factor 4 (PF4),			
		mRNA. /FEA=mRNA /GEN=PF4			
	•	/PROD=platelet factor 4			
	ł	/DB_XREF=gi:4505732			
	:	/UG=Hs.81564 platelet factor 4			
	1	//FL=gb:M25897.1			
		gb:NM 002619.1			
206398 s at	0.045316	gb:NM_001770.1 /DEF=Homo	NM 001770		NP_001761
200090_s_at	0.043310		14101_001770		_001701
	·	sapiens CD19 antigen (CD19), mRNA. /FEA=mRNA			*.
		/GEN=CD19 /PROD=CD19			
	1 .				
11 11 11 11 11 11 11 11 11 11 11 11 11		antigen /DB_XREF=gi:10835052	•		
		//UG=Hs.96023 CD19 antigen			, .
2 1	j	/FL=gb:NM_001770.1	1.	ļ	
000474	0.040000	gb:M21097.1 gb:M28170.1	NIM 005704		ND 005755
206471_s_at	0.018222	gb:NM_005761.1 /DEF=Homo	NM_005761		NP_005752
		sapiens plexin C1 (PLXNC1),			
		mRNA /FEA=mRNA		}	1
4		/GEN=PLXNC1 /PROD=plexin			
		C1 /DB_XREF=gi:5032222			
		/UG=Hs 286229 plexin C1			
		/FL=gb;AF030339.1	-	1	}
•		gb:NM_005761.1		1	1

Gene	p-value	Description	Gene	Unigene	Protein
Identifier		,	Accession	Acc ssion	Accession
			No.	No.	No.
206478 at	0.034721	gb:NM 014792.1 /DEF=Homo	NM 014792	140.	NP 055607
		sapiens KIAA0125 gene product			
		(KIAA0125), mRNA. /FEA=mRNA			
		/GEN=KIAA0125			·
	· ·	/PROD=KIAA0125 gene product	ļ		
		/DB XREF=gi:7661923			
		/UG=Hs.38365 KIAA0125 gene			
	, ,	product /FL=gb:D50915.1		1	
		gb:NM 014792.1			
206492 at	0.034721	gb:NM 002012.1 /DEF=Homo	NM 002012		NP 002003
200-102_ut	0.001121	sapiens fragile histidine triad	11111_002012		_002000
ı	*	gene (FHIT), mRNA.		, ,	
		/FEA=mRNA /GEN=FHIT	,		
		/PROD=fragile histidine triad			-
**		gene /DB XREF=gi:4503718			1
		/UG=Hs.77252 fragile histidine			1.
	.*	triad gene /FL=gb:U46922.1			
		gb:NM_002012.1			*
206493 at	0.034721	gb:NM_000419.2 /DEF=Homo	NM 000419	 	NP 000410
200 100_0	0.001721	sapiens integrin, alpha 2b	14141_000+10		
		(platelet glycoprotein IIb of IIbIIIa			
		complex, antigen CD41B)	•		*
	1 1	(ITGA2B), mRNA. /FEA=mRNA			
	1	/GEN=ITGA2B /PROD=integrin		46	
		alpha 2b precursor	Î		
		/DB_XREF=gi:6006009		1	
		/UG=Hs.785 integrin, alpha 2b			
· ·		(platelet glycoprotein IIb of IIbIIIa			
		complex, antigen CD41B)			4
1. 7		/FL=gb:M34480.1 gb:J02764.1			
		gb:NM 000419.2			
206507_at	0.035763	gb:NM_014724.1 /DEF=Homo	NM_014724		NP_055539
200001_at	0,000700	sapiens KIAA0426 gene product	14141_014724		141 _000000
		(KIAA0426), mRNA. /FEA=mRNA			
		/GEN=KIAA0426			1
•		/PROD=KIAA0426 gene product			**
		/DB XREF=gi:7662109			
		/UG=Hs.97476 KIAA0426 gene			
		product /FL=gb:AB007886.1			
		1010000t /1 L=UD./\DUU/ 000.1	I .	1	1

Gene	p-value	ng to Figur 19 - Córonary Artery I Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
ide ilitiioi			No	No.	No.
206562 s at	0.018023	gb:NM_001892.1 /DEF=Homo	NM_001892	110.	NP 001883
		sapiens casein kinase 1, alpha			
		1 (CSNK1A1), mRNA.			
	ł	/FEA=mRNA /GEN=CSNK1A1	1	1	
		/PROD=casein kinase 1, alpha 1	, , ,	Í	
		/DB_XREF=gi:4503088			
		/UG=Hs.283738 casein kinase 1,)	}
		alpha 1 /FL=gb:NM_001892.1			1
	į.	gb:L37042.1			1 .
		gb.Lo7042.1		Park Control	
206565 x at	0.018023	gb:NM 006780.1 /DEF=Homo	NM 006780		NP 00677
_00000_x_at	0.010025	sapiens SMA3 (SMA3), mRNA.	1000,00		
• .		/FEA=mRNA /GEN=SMA3		1	
		//PROD=SMA3			
	}	/DB_XREF=gi:5803174	1		
		/UG=Hs 289061 SMA3		·	
		/FL=gb:NM_006780.1			ì
206567_s_at	0.036354	gb:NM 016436.1 /DEF=Homo	NM 016436	 	NP_057520
200507_S_at	0.030234	sapiens hepatocellular carcinoma			_007520
a gara		associated antigen 58	}		1
		(LOC51230), mRNA.			
	[/FEA=mRNA /GEN=LOC51230			
		/PROD=hepatocellular carcinoma-		.	
		associated antigen 58		·	
		/DB_XREF=gi:7705990		1	1
•	ļ.]	1
		/UG=Hs.301055 hepatocellular			ì
	•	carcinoma-associated antigen 58			•
		/FL=gb:AF220416.1			1
DOCCEE a at	0.006940	gb:NM_016436.1	NIM 000407		NP 00039
206655_s_at	0.020842	gb:NM_000407.3 /DEF=Homo	NM_000407	<u>.</u>	JNP_00039
		sapiens glycoprotein lb (platelet),		· .	· ·
		beta polypeptide (GP1BB),		1	
		mRNA. /FEA=mRNA		•	
		//GEN=GP1BB			
	1	/PROD=glycoprotein lb beta	1		
		polypeptide precursor			
		/DB_XREF=gi:9945387			
		/UG=Hs.283743 glycoprotein Ib		1	
		(platelet), beta polypeptide			
		/FL=gb:J03259.1	1	1	1.
	1	gb:NM 000407.3	I	1	1 .

		ng to Figure 19 - Coronary Artery I			
G ne	p-value	Description	Gene	Unigene	Protein
dentifier			Accession	Accession	Accession
	•"		No.	No.	No.
206666_at	0.018444	gb:NM 002104.1 /DEF=Homo	NM 002104	110.	NP 00209
200000_at	0.010444	sapiens granzyme K (serine	14101_002 104	.	-002000
-		, , ,		·	
		protease, granzyme 3; tryptase			
	-	II) (GZMK), mRNA. /FEA=mRNA			
		/GEN=GZMK /PROD=granzyme			
		K precursor		*	
		/DB_XREF=gi:4504234			* .
		/UG=Hs.3066 granzyme K	•		
		(serine protease, granzyme 3,			•
•		tryptase II) /FL=gb:U35237.1		,	
		gb:NM_002104.1 gb:U26174.1	1		
206693 at	0.033533	gb:NM 000880.1 /DEF=Homo	NM_000880		NP_00087
200093_at	0.033333	,	NINI_000000		1415_00007
		sapiens interleukin 7 (IL7),			[
		mRNA. /FEA=mRNA /GEN=IL7			
	*	/PROD=interleukin 7			
		/DB_XREF=gi:4504676			
		/UG=Hs.72927 interleukin 7			· ·
		/FL=gb:J04156.1			
		gb:NM 000880.1			ĺ
206700 s_at	0.019657	gb:NM 004653.1 /DEF=Homo	NM 004653		NP 00464
	0.0.000	sapiens SMC (mouse) homolog,			
		Y chromosome (SMCY), mRNA.			
		/FEA=mRNA /GEN=SMCY			
		•			
	1	/PROD=SMC (mouse) homolog,	ĺ		
	,	Y chromosome			
		/DB_XREF=gi:4759149			
		/UG=Hs.80358 SMC (mouse)			
		homolog, Y chromosome			1
		/FL=gb:U52191.1	:]
* *	1	gb:NM 004653.1			
		95tim_00			
206770 s at	0.034721	gb:NM_012243.1 /DEF=Homo	NM 012243		NP 03637
200770_3_at	0.034721		14141_012240		_00007
		sapiens solute carrier family 35		,	
		(UDP-N-acetylglucosamine (UDP-			
	1 .	GlcNAc) transporter), member 3	ł		· .
		(SLC35A3), mRNA. /FEA=mRNA			· ·
		/GEN=SLC35A3 /PROD=solute			
		carrier family 35(UDP-N-	,		-
•		acetylglucosamine (UDP-GlcNAc)			
		transporter), member3	1.0		
	Ì	/DB XREF=gi:6912667		}	
		/UG=Hs.159322 solute carrier	I .	1	
		family 35 (UDP-N-	1		
		· ` `			
I.		acetylglucosamine (UDP-GlcNAc)			
•		transporter), member 3			
•	Į.	/FL=gb:AB021981.1		1	1
		gb:NM_012243.1			
,	ŀ	1		1	i

Gene	p-value	ng to Figure 19 - Coronary Artery l Description	Gen	Unigene	Protein
Identifier	Talled		Acc ssion	Accession	Accession
identiniei			No.	No.	No.
206782 s at	0.036254	gb:NM 005528.1 /DEF=Homo	NM 005528	INO.	NP 005519
2007 92_3_at	0.000204	sapiens heat shock 40kD	11111_000020		_000010
-		protein 2 (HSPF2), mRNA.			
		/FEA=mRNA /GEN=HSPF2			
		/PROD=heat shock 40kD protein			
		2 /DB_XREF=gi:5031770		, ,	
		/UG=Hs.172847 DnaJ (Hsp40)			,
		homolog, subfamily C, member			
	ļ	4 /FL=gb:AF012106.1			
	100	gb:NM_005528.1			
•		gb.NM_005526.1	1.1	I_{i}	
	0.00000		NINA OAOCOA		ND OCCES
206914_at	0.028893	gb:NM_019604.1 /DEF=Homo	NM_019604		NP_062550
		sapiens class-I MHC-restricted T			
** - *	1	cell associated molecule	100		
100		(CRTAM), mRNA. /FEA=mRNA		* .	
		/GEN=CRTAM /PROD=class-I	et la		
•		MHC-restricted T cell			
	•	associatedmolecule			
•		/DB_XREF=gi:9624976			
		/UG=Hs.159523 class-I MHC-			
		restricted T cell associated			
		molecule /FL=gb:AF001622.1			
	ļ	gb:NM_019604.1	<u> </u>		
206958_s_at	0.034721	gb:AF318575.1 /DEF=Homo	AF318575		NP_542418
-		sapiens UPF3 (UPF3) mRNA,			
		complete cds. /FEA=mRNA			
	•	/GEN=UPF3 /PROD=UPF3			
		/DB_XREF=gi:12620405			•
		/UG=Hs.274412 similar to yeast			
•		Upf3, variant A		•	
		/FL=gb:AY013250.1			
_	· ·	gb:AF318575.1 gb:NM_023011.1			
206965_at	0.045316	gb:NM_016285.1 /DEF=Homo	NM_016285		NP_057369
		sapiens AP-2rep transcription			
		factor (LOC51717), mRNA.	*		
	· ·	/FEA=mRNA /GEN=LOC51717			
4		/PROD=AP-2rep transcription		1	
		factor /DB_XREF=gi:7706476			
		/UG=Hs.278998 AP-2rep		· .	
		transcription factor		```	
		/FL=gb:AF113122.1			
_		gb:AF161471.1 gb:NM_016285.1			

Gene	p-value	ng to Figure 19 - Coronary Artery ID scription	Gene	Unigene	Protein
Identifier	P 14.43		Accession	Accession	Accession
identifier	,		No.	No.	No.
207108_s_at	0 046749	gb:NM_015384.1 /DEF=Homo	NM_015384	NO.	NP 597677
201 100_3_at	0.040743	sapiens IDN3 protein (IDN3),	11111_010004		
		mRNA. /FEA=mRNA /GEN=IDN3	f		
	'	/PROD=IDN3 protein			
		/DB_XREF=gi:7661841			*
	<u>.</u>	/UG=Hs.225767 IDN3 protein			<u> </u>
		/FL=gb:AB019602:1			
**		gb:NM 015384.1		*.	
207186_s at	0.019022	gb:NM_004459.2 /DEF=Homo	NM 004459		NP_004450
207 100_S_at	0.010023		NNI_004459	· ·	INF_004450
• .		sapiens fetal Alzheimer antigen	i ,		
		(FALZ), mRNA. /FEA=mRNA	,		·
•		/GEN=FALZ /PROD=fetal			
		Alzheimer antigen	`\	1	ł.
		/DB_XREF=gi:6552329			
	1	/UG=Hs.99872 fetal Alzheimer			
		antigen /FL=gb:U05237.1	• • • • •	1.	
007004	0.005700	gb:NM_004459.2	NINA 000040		ND 000004
207234_at	0.035/63	gb:NM_002919.1 /DEF=Homo	NM_002919		NP_602304
		sapiens regulatory factor X, 3	, N		
		(influences HLA class II]		*.
		expression) (RFX3), mRNA.			
		/FEA=mRNA /GEN=RFX3			
		/PROD=regulatory factor X, 3			
	1	(influences HLA class			, i
	r	llexpression)	•		
. ,		/DB_XREF=gi:4506494			
		/UG=Hs.166019 regulatory factor			
	1.	X, 3 (influences HLA class II			
		expression) /FL=gb:NM_002919.1	l l		
					ļ
207351_s_at	0.040064	gb:NM_003975.1 /DEF=Homo	NM_003975		NP_003966
	ļ.	sapiens SH2 domain protein 2A			
* +*		(SH2D2A), mRNA. /FEA=mRNA			
r. La		/GEN=SH2D2A /PROD=SH2			
	,	domain protein 2A	1	1	
		/DB_XREF=gi:4503632			
		/UG=Hs.103527 SH2 domain			
		protein 2A /FL=gb:NM_003975.1			
		gb:AF097744.1		ļ. ·	
*.				i	

Gn		ng to Figure 19 - Coronary Artery I Description	Gen	Unigene	Protein
Identifier	b . m.c.	2000	Accession	Accession	Accession
identifici			No	No.	No.
207389_at	0.026013	gb:NM 000173.1 /DEF=Homo	NM_000173	NO.	NP_000164
207309_at	0.020013	sapiens_glycoprotein_lb_(platelet),	14141_000173		141 _000 104
		alpha polypeptide (GP1BA),			
, ,		mRNA. /FEA=mRNA			
	1.				
	• *	/GEN=GP1BA /PROD=platelet		7	
1		glycoprotein lb alpha			
		polypeptideprecursor			
		/DB_XREF=gi:4504070	· ·		· .
		/UG=Hs.1472 glycoprotein Ib		· .	22.1
		(platelet), alpha polypeptide			
ŀ		/FL=gb:J02940.1			
		gb:NM_000173.1	10		
207435_s_at	0.034721	,	NM_016333		NP_057417
		sapiens RNA binding protein; AT			
		rich element binding factor		8	
		(SRM300), mRNA. /FEA=mRNA			}
	·	/GEN=SRM300 /PROD=splicing			
		coactivator subunit SRm300	10.0		}
		/DB_XREF=gi:7706718			
		/UG=Hs.197114 RNA binding			j
		protein; AT-rich element binding	1		· .
]		factor /FL=gb:AF201422.1			:
		gb:NM 016333.1			
) .		
•				1	ł
207446_at	0.034721	gb:NM_006068.1 /DEF=Homo	NM_006068		NP_006059
		sapiens toll-like receptor 6			
		(TLR6), mRNA. /FEA=mRNA		·	
1		/GEN=TLR6 /PROD=toll-like	1] .	5.0
		receptor 6			1
	.	/DB_XREF=gi:5174720			
· :		/UG=Hs.227105 toll-like receptor			
		6 /FL=gb:AB020807.1			
1	[· ·	gb:NM 006068.1	1		

Gene	p-value	ng to Figure 19 - Coronary Artery Description	Gen	Unigene	Prot in
Identifier			Accession	Accession	Accession
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	İ		No.	No.	No.
207508_at	0.046749	gb:NM_001689.1 /DEF=Homo	NM 001689	ito.	NP_001680
		sapiens ATP synthase, H+		1	
		transporting, mitochondrial F0		1	
		complex, subunit c (subunit 9)			·
* .		isoform 3 (ATP5G3), mRNA.			
* .		/FEA=mRNA /GEN=ATP5G3			
	4	/PROD=ATP synthase, H+			
		transporting, mitochondrial			
	1.7	F0complex, subunit c (subunit 9)			
	'	isoform 3 /DB_XREF=gi:4502300			
		/UG=Hs.429 ATP synthase, H+			
17		transporting, mitochondrial F0			•
		complex, subunit c (subunit 9)			
	1	isoform 3 /FL=gb:U09813.1			
		gb:NM 001689.1		. ,	
		gb.14141_001009.1			
				7 7	
207509 s at	0.042466	gb:NM 002288.2 /DEF=Homo	NM 002288	-	NP 067154
201309_S_at	0.042400	sapiens leukocyte-associated lg-	NW_002200		1118_007134
		like receptor 2 (LAIR2),			
		transcript variant 1, mRNA.			•
		l control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont			
	ı	/FEA=mRNA /GEN=LAIR2			
		/PROD=leukocyte-associated Ig-	1		
		like receptor 2, isoforma			
*,		/DB_XREF=gi:10947100			
		/UG=Hs.43803 leukocyte-			1
		associated Ig-like receptor 2			-
007505	0.000570	/FL=gb:NM_002288.2	1114 005740	ļ	NE COSTO
207525_s_at	0.020576	gb:NM_005716.1 /DEF=Homo	NM_005716		NP_005707
		sapiens chromosome 19 open			٠.
·		reading frame 3 (C19ORF3),			
		mRNA. /FEA=mRNA		_	
		/GEN=C19ORF3 /PROD=GLUT1			
	¥+	C-terminal binding protein			
		/DB_XREF=gi:5031714	1		
		/UG=Hs.6454 chromosome 19	,		
		open reading frame 3			
		/FL=gb:AF089816.1		,	:
	1	gb:NM_005716.1		1	L .

		ng to Figure 19 - Coronary Artery I		22. 27	<u> </u>
Gen	p-value	Description	Gene	Unigene	Protein
ldentifier			Accession	Accession	Accession
			No	No.	No.
207549 x at	0.046749	gb:NM 002389.1 /DEF=Homo	NM_002389		NP 758871
	<u> </u>	sapiens membrane cofactor			, - ·
		protein (CD46, trophoblast-	- **		* * * *** ;
	·	lymphocyte cross-reactive	ĺ		1
]	antigen) (MCP), mRNA.	•	· .	}
		/FEA=mRNA /GEN=MCP			
	1	/PROD=membrane cofactor	1		
		protein (CD46,trophoblast-		1	
		lymphocyte cross-reactive		ļ	
	·	antigen) /DB_XREF=gi:11321566			
	,	/UG=Hs.83532 membrane			1
		cofactor protein (CD46,		,	ļ
		trophoblast-lymphocyte cross-	1 :		
		reactive antigen)	,	1.	1
0075541	0.000505	/FL=gb:NM_002389.1	NINA 004000	 	ND 0040E4
207554_x_at	0.038535	gb:NM_001060.1 /DEF=Homo	NM_001060		NP_001051
	ļ	sapiens thromboxane A2			1
		receptor (TBXA2R), mRNA.			
		/FEA=mRNA /GEN=TBXA2R	Ì		Ì
		/PROD=thromboxane A2 receptor	}		
		/DB_XREF=gi:4507380			
		/UG=Hs.89887 thromboxane A2	1.5		
		receptor /FL=gb:NM_001060.1			ł
·	ļ	gb:D38081.1 gb:U27325.1	<u> </u>		<u> </u>
207556_s_at	0.049425	gb:NM_003646.1 /DEF=Homo	NM_003646	·	NP_003637
• .	ľ	sapiens diacylglycerol kinase,			į
	ļ	zeta (104kD) (DGKZ), mRNA.			1
		/FEA=mRNA /GEN=DGKZ		,	
		/PROD=diacylglycerol kinase,			1
er .	1	zeta (104kD)	1		
	ļ	/DB_XREF=gi:4503316			J .
•		/UG≈Hs.89981 diacylglycerol			
		kinase, zeta (104kD)	1 .	ł	1
		/FL=gb:U51477.1			
	-	gb:NM_003646.1			
207651_at	0.034721		NM 013308		NP_037440
		sapiens platelet activating		1	_
		receptor homolog (H963),			
		mRNA. /FEA=mRNA /GEN=H963		į .	
•		/PROD=platelet activating	,	1	1.
		receptor homolog			
	1	//DB XREF=gi:7019400			
		, –	}		1
		/UG=Hs.159545 platelet	1]
		activating receptor homolog			
·		//FL=gb:AF002986.1	~		1
<u> </u>]	gb:NM_013308.1	<u> </u>	<u> </u>	1

		ng to Figure 19 - Coronary Artery I		1	
Gene Identifier	p-value	Description	Gene Accession No.	Unigene Accession No	Protein Accession No.
207665_at	0.034721	gb:NM_003813.1 /DEF=Homo	NM 003813		NP 003804
— • • • • - • • • •		sapiens a disintegrin and			
		metalloproteinase domain 21			
•		(ADAM21), mRNA. /FEA=mRNA			["
		/GEN=ADAM21 /PROD=a		£	
		disintegrin and metalloproteinase			1
·		domain 21preproprotein			
,		/DB_XREF=gi:11497039			
		/UG=Hs.178748 a disintegrin and	, ,		
		metalloproteinase domain 21			
		/FL=gb:NM 003813.1			
٠.					
207723_s at	0.027230	gb:NM 002261.1 /DEF=Homo	NM_002261		NP_031359
201125_3_at	0.027233	sapiens killer cell lectin-like	002201	200	100 1000
		receptor subfamily C, member 3			
		(KLRC3), transcript variant			
		NKG2-E, mRNA. /FEA=mRNA			
		/GEN=KLRC3 /PROD=killer cell			
			*		
š		lectin-like receptor subfamily C,member 3 isoform NKG2-E			
] -					
		//DB_XREF=gi:4504884			
		/UG=Hs.258850 killer cell lectin-			
		like receptor subfamily C,			
		member 3 /FL=gb:L14542.1	}	į	
007704	0.004704	gb:NM_002261.1	1111 044040		ND 055704
207724_s_at	0.034721	gb:NM_014946.2 /DEF=Homo	NM_014946		NP_055761
		sapiens spastic paraplegia 4			
		(autosomal dominant; spastin)	!		1
		(SPG4), mRNA. /FEA=mRNA			
		/GEN=SPG4 /PROD=spastin			
		/DB_XREF=gi:11875210	1		
· ·		/UG=Hs.26334 spastic paraplegia	· .	1	
		4 (autosomal dominant; spastin)	ì		
	· .	/FL=gb:NM_014946.2		,	
	<u> </u>				
207734_at	0.025284	gb:NM_017773.1 /DEF=Homo	NM_017773		NP_060243
		sapiens hypothetical protein	1		
		FLJ20340 (FLJ20340), mRNA.	1		1
		/FEA=mRNA /GEN=FLJ20340	. .	1	1
· ·		/PROD=hypothetical protein	1		
		FLJ20340 /DB_XREF=gi:8923315			
1		/UG=Hs.272794 hypothetical			
		protein FLJ20340		1	1
		/FL=gb:NM_017773.1			
	<u> </u>	<u> </u>			<u> </u>
					

		ng to Figure 19 - Coronary Artery		FATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE	
G ne	p-value	D scription	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
			No.	No.	No.
207760 s at	0.034721	gb:NM_006312.1 /DEF=Homo	NM_006312	-	NP_006303
		sapiens nuclear receptor co-			1.11 _000000
		repressor 2 (NCOR2), mRNA.	• • • • • •	in the second of the second	
		/FEA=mRNA /GEN=NCOR2	į.		
		/PROD=nuclear receptor co-			
	. ,	repressor 2			
the second		/DB_XREF=gi:5454073			
:		/UG=Hs.287994 nuclear receptor	<i>'</i>		
		co-repressor 2			
,		/FL=gb:AF113003.1			ν,
		gb:NM_006312.1			
207782_s at	0.018444	gb:NM 007319.1 /DEF=Homo	NM: 007319		NP_015558
	•	sapiens presenilin 1 (Alzheimer	[T		
		disease 3) (PSEN1), transcript			
		variant I-374., mRNA.			1
		/FEA=mRNA /GEN=PSEN1			ľ
		/PROD=presenilin 1 isoform I-			
		* *			ľ
		374 /DB_XREF=gi:7549814			
		/UG=Hs.3260 presenilin 1		! `	1
٩.	* .	(Alzheimer disease 3)			
		/FL=gb:U40380.1	[1	ļ
		gb:NM_007319.1			
207794_at	0.026842	gb:NM_000648.1 /DEF=Homo	NM_000648		NP_000639
		sapiens chemokine (C-C motif)			
·		receptor 2 (CCR2), mRNA.	{	· ·	[
		/FEA=mRNA /GEN=CCR2			1
		/PROD=chemokine (C-C motif)	[
	-	receptor 2			er i
		/DB_XREF=gi:4757937	[
	•	/UG=Hs.395 chemokine (C-C			
		motif) receptor 2	·		
·		/FL=gb:U03905.1			
				·	
2070504	0.004704	gb:NM_000648.1 gb:D29984.1	NIN 047054	20.	115 000 101
207856_s_at	0.034721	1 =	NM_017951		NP_060421
)	sapiens hypothetical protein			
	,	FLJ20297 (FLJ20297), mRNA.			
		/FEA=mRNA /GEN=FLJ20297] • •]	
		/PROD=hypothetical protein			
	·	FLJ20756	J]] .
•		/DB_XREF=gi:13443032			,
		/UG=Hs.94491 hypothetical]	
			1	I	
		protein FLJ20297	<u>.</u>	l.	7

		ng to Figur 19 - Coronary Artery I		42 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	<u> </u>
Gene	p-value	Description	G ne	Unigene	Protein
ldentifi r			Accession	Acc ssion	Accession
	1		No.	No.	No.
207892 at	0.023856	gb:NM_000074.1 /DEF=Homo	NM 000074		NP 000065
	0.02000	sapiens tumor necrosis factor			
	1	(ligand) superfamily, member 5	le e e e e e e e e e e e e e e		
	!	(hyper-IgM syndrome) (TNFSF5),	, ·		1.40
	1			<u>'</u>	
		mRNA /FEA=mRNA			
	l	/GEN=TNFSF5 /PROD=CD40		ĺ.	
	:	antigen ligand			
	, .	/DB_XREF=gi:4557432	, , ,		ĺ
	,	/UG=Hs.652 tumor necrosis			
e .		factor (ligand) superfamily,			
		member 5 (hyper-lgM syndrome)			4.
		/FL=gb:L07414.1			
		gb:NM 000074.1			
207979_s_at	0.019292	gb:NM 004931.1 /DEF=Homo	NM 004931		NP 757362
- 		sapiens CD8 antigen, beta			
		polypeptide 1 (p37) (CD8B1),	1	[
		mRNA. /FEA=mRNA			1 1
		/GEN=CD8B1 /PROD=CD8		1	
		antigen, beta polypeptide 1			
•					
		(p37) /DB_XREF=gi:4826666	19.2		· .
	-	/UG=Hs 2299 CD8 antigen, beta			
		polypeptide 1 (p37)			
	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	/FL=gb:NM_004931.1		·	
207992_s_at	0.018023	gb:NM_000480.1 /DEF=Homo	NM_000480	1	NP_000471
, .		sapiens adenosine	. "		
		monophosphate deaminase			ļ
	7.5	(isoform E) (AMPD3), mRNA.			ľ
	j	/FEA=mRNA /GEN=AMPD3			j
		/PROD=adenosine			
	1	monophosphate deaminase]-		}
		(isoform E)		i i	
•		/DB_XREF=gi:4502078	}	· **	j
	,	/UG=Hs.83918 adenosine			
]	monophosphate deaminase			
		(isoform E) /FL=gb:NM_000480.1			
	}	((SOIOITI E) // L-gb.(NIVI_000480.1		.	
208022 s at	0.022752	ab:NM 003671.1 /DEE=Uomo	NIM 003674		
200022_S_at	0.022/52	gb:NM_003671.1 /DEF=Homo	NM_003671		
•	ļ	sapiens CDC14 (cell division		-	
		cycle 14, S. cerevisiae) homolog			, .
		B (CDC14B), mRNA.			
		/FEA=mRNA /GEN=CDC14B			}
		/PROD=S. cerevisiae CDC14			
		homolog, gene B	1		
		/DB_XREF=gi:4502698			
] .	/FL=gb:NM_003671.1]		

		ng to Figure 19 - Coronary Artery	Disease		
Gene	p-value	Description	Gene	Unigene	Protein
Identifier		• ***	Accession	Accession	Accession
			No.	No.	No.
208024 s at	0.018444	gb:NM 005675.1 /DEF=Homo	NM 005675	110.	NP_005666
a(9.01011	sapiens DiGeorge syndrome			
		critical region gene 6 (DGCR6),]		
,		mRNA. /FEA=mRNA		* .	1
•		/GEN=DGCR6 /PROD=DiGeorge	,		
		syndrome critical region protein	ļ	ľ	
	. *	6 /DB_XREF=gi:5031662			
		/UG=Hs.153910 DiGeorge			
		syndrome critical region gene 6			
		/FL=gb:AF228707.1			\ .
		gb:NM_005675.1		. ,	
		gb.NW_003073.1			
208095 s_at	0.018023	gb:NM 001222.1 /DEF=Homo	NM 001222	 	NP 751913
200095_5_at	0.016023 	sapiens calciumcalmodulin-	[NINI_00 1222		NF_751913
		dependent protein kinase (CaM			
	, .	I	1	1	
		kinase) II gamma (CAMK2G), mRNA. /FEA=mRNA			*
·]
		/GEN=CAMK2G			
		/PROD=calciumcalmodulin-			
		dependent protein kinase			
1.		(CaMkinase) II gamma			
		/DB_XREF=gi:4502554			
• •		/UG=Hs.250857	,		
	ļ ·	calciumcalmodulin-dependent			
		protein kinase (CaM kinase) II			
		gamma /FL=gb:U81554.1			
		gb:NM_001222.1			
208116_s_at	0.046749	gb:NM_005907.1 /DEF=Homo	NM_005907	1	NP_005898
		sapiens mannosidase, alpha,			
E		class 1A, member 1 (MAN1A1),		,	
		mRNA. /FEA=mRNA			1
		/GEN=MAN1A1	ŀ	,	
		/PROD=mannosidase, alpha,			
		class 1A, member 1			
٠.	[.	/DB_XREF=gi:5174520			
		/UG=Hs.25253 mannosidase,		,	
		alpha, class 1A, member 1	1.0		
		/FL=gb:NM_005907.1			
208121_s_at	0.049425	gb:NM_002848.2 /DEF=Homo	NM_002848		NP_109596
		sapiens protein tyrosine	**		
		phosphatase, receptor type, O			. "
	,	(PTPRO), transcript variant 2,		``	
	1	mRNA. /FEA=mRNA			1
		/GEN=PTPRO /PROD=receptor-			1
		type protein tyrosine			·
		phosphatase O isoform b			
		precursor	i i		
		/DB_XREF=gi:13677212			
	,	/FL=gb:NM_002848.2		<u></u>	

Gene		ng to Figure 19 - Coronary Artery I Description	Gene	Unigene	Protein
Identifier	l raide		Accession	Accession	Accession
Identifici			No.	No.	No.
208151_x_at	0.010202	gb:NM_030881.1 /DEF=Homo	NM 030881	INO.	NP 112020
200151_X_at	0.019292		00000		NF_112020
		sapiens DEADH (Asp-Glu-Ala-			
		AspHis) box polypeptide 17			,
		(72kD) (DDX17), transcript] -
		variant 2, mRNA. /FEA=mRNA			
	\$.	/GEN=DDX17 /PROD=DEADH			
A second		(Asp-Glu-Ala-AspHis) box	• 1		·
		polypeptide 17 isoform 2			
		/DB_XREF=gi:13787203			
		/FL=gb:NM_030881.1	<u>. ب</u>		
208268_at	0.048741	gb:NM_021777.1 /DEF=Homo	NM_021777		NP_068548
	1	sapiens a disintegrin and			
		metalloproteinase domain 28		, ,	
		(ADAM28), transcript variant 3,			
		mRNA. /FEA=mRNA			
		/GEN=ADAM28 /PROD=a			
		disintegrin and metalloproteinase			
		domain 28,isoform 3			
r		preproprotein			
		/DB_XREF=gi:11496993	·		
	Ì	/UG=Hs.174030 a disintegrin and			
	,	metalloproteinase domain 28			
	1	/FL=gb:NM_021777.1		1	ř.
		gb:AF137335.1			
208304_at	0.046749	gb:NM_001837.1 /DEF=Homo	NM_001837		NP_847899
4		sapiens chemokine (C-C motif)			
		receptor 3 (CCR3), mRNA.	ľ		·
	j	/FEA=mRNA /GEN=CCR3	j		
		/PROD=chemokine (C-C motif)			
	,	receptor 3			
		/DB_XREF=gi:4502636			
		/UG=Hs.158324 chemokine (C-C	1		
		motif) receptor 3			
:	1	/FL=gb:U28694.1 gb:AF026535.1	1		
	,	gb:NM_001837.1			1,1

		ng to Figure 19 - Coronary Artery			la de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de
Gene	p-value	Description	Gene	Unigene	Prot in
Identifier			Accession	Accession	Acc ssion
			No.	No.	No.
208426_x_at	0.049425	gb:NM_002255.1 /DEF=Homo	NM_002255	7	NP_002246
7 A 78 78 1	e e é mande	sapiens killer cell	_		· -
		immunoglobulin-like receptor, two	÷, , , , , , , ,		
		domains, long cytoplasmic tail, 4		ł	1
67		(KIR2DL4), mRNA. /FEA=mRNA	,		, .
	. ,	` '			
	٠.	/GEN=KIR2DL4 /PROD=killer cell		·	∤
		immunoglobulin-like receptor,		J	j
	·	twodomains, long cytoplasmic		1	ļ
		tail, 4 /DB_XREF=gi:4504870	. *		
	1	/UG=Hs.166085 killer cell			* *,
		immunoglobulin-like receptor, two			1
7		domains, long cytoplasmic tail, 4	e ⁱ		ł
		/FL=gb:AF002981.1			,
		gb:NM_002255.1	}		1
		3	,		
208452_x_at	0.040064	gb:NM 004145.1 /DEF=Homo	NM 004145	 	NP 004136
200-102xat	0.040004	sapiens myosin IXB (MYO9B),	14141_004140		111 _00-100
•	ł	ImRNA /FEA=CDS	•		
	ļ		}		
·	}	/GEN=MYO9B /PROD=myosin	}		,
i	ł	IXB /DB_XREF=gi:4758749	ł ·	1	1
	j	/UG=Hs.159629 myosin IXB			
		/FL=gb:U42391.1			_
	·	gb:NM_004145.1	<u> </u>		L
208549_x_at	0.018023	gb:NM_016171.1 /DEF=Homo	NM_016171	1.	NP_057255
		sapiens prothymosin a14]		
	ł	(LOC51685), mRNA. /FEA=CDS			•
	}	/GEN=LOC51685			
	ļ	/PROD=prothymosin a14	}		
•		/DB_XREF=gi:7706414	1	1	
		/UG=Hs.247919 prothymosin a14	1	1	,
		/FL=gb:AF170294.1	\		Ì
ı.f	ì	(•			
200504	0.046740	gb:NM_016171.1	NA 000000	 	ND 000042
206591_S_at	0.046749	gb:NM_000922.1 /DEF=Homo	NM_000922		NP_000913
	1	sapiens phosphodiesterase 3B,	1.		1
	1 .	cGMP-inhibited (PDE3B), mRNA.	1.		1
	1	/FEA=CDS /GEN=PDE3B	1		1
	İ	/PROD=phosphodiesterase 3B,	1	ł	.
	1	cGMP-inhibited	1	1	
ı	} .	/DB_XREF=gi:4505660	ł	· ·	1
	1	/UG=Hs.326528	1	1	
	J	phosphodiesterase 3B, cGMP-			
	1	inhibited /FL=gb:NM 000922.1			

Gene	p-value	ng to Figure 19 - Coronary Artery I Description	Gene	Unigene	Protein
Identifier	p-value	beachphon	Accession	Accession	Accession
identillei			*		1
208611_s_at	0.019022	gb:U83867.1 /DEF≂Human alpha	No. U83867	No.	No. NP 003118
200011_S_at	0.016023		063607		NP_003116
		II spectrin mRNA, complete cds.		-	
		/FEA=mRNA /PROD=alpha II			
		spectrin /DB_XREF=gi:1805279			<u>{</u>
		/UG=Hs.77196 spectrin, alpha,	!		
		non-erythrocytic 1 (alpha-fodrin)			j
		/FL=gb:J05243.1 gb:U83867.1			
		gb:NM_003127.1			
·				<u> </u>	<u> </u>
208616_s_at	0.018023	gb:U48297.1 /DEF=Homo	U48297		NP_536317
		sapiens protein tyrosine			
		phosphatase PTPCAAX2		1	
		(hPTPCAAX2) mRNA, complete			•
**	,	cds. /FEA=mRNA			
		/GEN=hPTPCAAX2	•	'	
		/PROD=protein tyrosine		1	
· I		phosphatase PTPCAAX2			
		/DB_XREF=gi:1777756		4	·
		/UG=Hs.82911 protein tyrosine	,		,
		phosphatase type IVA, member			
		2 /FL=gb:U48297.1			
		gb:NM_003479.1 gb:AF208850.1			
208619_at	0.034721		L40326		NP 001914
		sapiens Hepatitis B virus X-			
		associated protein 1 mRNA,			,
	[complete cds. /FEA=mRNA			
,		/PROD=X-associated protein 1			
		/DB_XREF=gi:695361		}	
		/UG=Hs.108327 damage-specific			j.
		DNA binding protein 1 (127kD)			1 .
				1	1
		/FL=gb:U18299.1 gb:U32986.1			1
146		gb:NM_001923.2 gb:L40326.1		Į	, ,
2020221	0.040740	 - - 05004.4 /DEE	105004		ND 000070
208623_s_at	0.046749	gb:J05021.1 /DEF=Human	J05021		NP_003370
	1	cytovillin 2 (VIL2) mRNA,	{		}
	}	complete cds. /FEA=mRNA	}		1
		/GEN=VIL2 /DB_XREF=gi:340216	<u>'</u>	•]
		/UG=Hs.155191 villin 2 (ezrin)			
		/FL=gb:J05021.1 gb:AL162086.1	Ì		1
		gb:NM_003379.2			1
			1	1	1

Gene List Co	rrespondir	ng to Figure 19 - Coronary Artery I	Disease		
Gene Identifier		Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
208634 s at	0.018023	gb:AB029290.1 /DEF=Homo	AB029290		NP_149033
 .		sapiens mRNA for actin binding			-
		protein ABP620, complete cds.			
		/FEA=mRNA /GEN=abp620			ł
	* 1.	/PROD=actin binding protein			
		ABP620 /DB_XREF=gi:5821433	•		·
		/UG=Hs.108258 actin binding			
]	protein; macrophin (microfilament			
		and actin filament cross-linker		1	
	[protein) /FL=gb:AB029290.1	. *		
		protein // E-gb./\bozozozoc.			
	[
208644 at	0.025284	gb:M32721.1 /DEF=Human	M32721		NP_001609
200044_al	0.020204	(poly(ADP-ribose) polymerase	14102721	,	_001003
		mRNA, complete cds.	1		
		//FEA=mRNA /GEN=PPOL	, , , , , ,		
		1)		}
		/DB_XREF=gi:190266]		}
		/UG=Hs.177766 ADP-			
		ribosyltransferase (NAD+; poly			
		(ADP-ribose) polymerase)			
	}	/FL=gb:NM_001618.2			
	ł	gb:M18112.1 gb:M32721.1			
		gb:J03473.1			<u> </u>
208653_s_at	0.034721	Consensus includes	AF299343		NP_006007
		gb:AF263279.1 /DEF=Homo	1		,
		sapiens CD164 mRNA, complete	1	Ì	
	,	cds. /FEA=CDS /PROD=CD164	1		
		/DB_XREF=gi:9230740		1 1	
		/UG=Hs.43910 CD164 antigen,			
		sialomucin /FL=gb:AF299341.1			,
		gb:AF299343.1 gb:AF263279.1	1		1
	ſ .				
208657 s at	0.018222	gb:AF142408.1 /DEF=Homo	AF142408		NP_006631
		sapiens cell division control		,	-
[j ·	protein septin D1 mRNA,			
		complete cds. /FEA=mRNA	}		,
		/PROD=cell division control			
		protein septin D1	1)	, ,
}		//DB_XREF=gi:11055010		· ·	
* + * * * * * * * * * * * * * * * * * *		//UG=Hs.181002 MLL septin-like	*		
	}	fusion /FL=gb:AF142408.1	100		<u></u>
					ļ ·
L	<u> </u>	gb:AF142569.1	L	<u> </u>	

G ne	p-value	ng to Figure 19 - Coronary Artery I Description	Gene	Unigene	Protein
	p-value	Description	l :	Accession	
ldentifier	1		Accession	1	Accession
200050 -4	0.004704	-b-DC000405 4 /DEE-Home	No.	No.	No.
208658_at	0.034721	gb:BC000425.1 /DEF=Homo	BC000425		NP_004902
		sapiens, protein disulfide			
	1	isomerase related protein			1
	}	(calcium-binding protein,	1		1
•		intestinal-related), clone			
	1	MGC:8346, mRNA, complete			
×		cds. /FEA=mRNA /PROD=protein		1	
	1	disulfide isomerase related		1	ł
	1	protein(calcium-binding protein,	,	1	ļ
		intestinal-related)			
**		/DB_XREF=gi:12653312			i .
1 · · · · · · · · · · · · · · · · · · ·	1	/UG=Hs 93659 protein disulfide	}	1 2 2 2	1
	1	isomerase related protein			1
	-	(calcium-binding protein,			
4 * ·	1	intestinal-related)			
	1	/FL=gb:BC000425.1	ĺ	·	
		gb:BC001928.1			}
٠,		30,000	* -	1.	.)
208663 s at	0.018693	Consensus includes gb:Al652848	D84294	· · · · · · · · · · · · · · · · · · ·	NP 003307
		/FEA=EST			
		/DB_XREF=gi:4736827			1
	1.	/DB XREF=est:wb40a04.x1	1	A 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
		/CLONE=IMAGE:2308110		} '	ļ
		/UG=Hs.118174 tetratricopeptide			
		repeat domain 3		1.	1
		//FL=gb:D84294.1	1. 1.		
208690 s at	0.034721	gb:BC000915.1 /DEF≈Homo	BC000915	 	NP 066272
200090_S_ai	0.034721	1~	BC000913	1	NF_000272
		sapiens, Similar to LIM protein,	1.		
		clone MGC:5344, mRNA,			1
		complete cds. /FEA=mRNA	* * *		1
•	.,	/PROD=Similar to LIM protein		,	1
1		//DB_XREF=gi:12654194		1.	
	ſ	/UG=Hs.75807 PDZ and LIM			1 .
	ł	domain 1 (elfin)		1	
		/FL=gb:BC000915.1			
	<u> </u>		<u> </u>		<u> </u>
208702_x_at	0.025284	Consensus includes gb:Al525212	BC000373	·	NP_001633
		/FEA=EST		1	1
		/DB_XREF=gi:4439347			
` .		/DB_XREF=est:pt1.1-2.A08.r			
•		/UG=Hs.279518 amyloid beta			
		(A4) precursor-like protein 2	İ		1
	* ·	/FL=gb:BC000373.1		1	ŀ

		ng to Figure 19 - Coronary Artery I	Dis ase	 	
Gene	p-value	Description	Gen	Unigene	Protein
Identifier	,		Accession	Accession	Accession
,	}		No.	No.	No.
208714 at	0.034721	gb:AF092131.1 /DEF=Homo	AF092131	110	NP_009034
200; 14_at	0.00-1121	sapiens 51kDa subunit of NADH	002101		000004
i I	•	dehydrogenase mRNA, complete			
]
		cds. /FEA=mRNA /PROD=51kDa			
		subunit of NADH dehydrogenase			
	}	/DB_XREF=gi:5138911	1		
-	ļ.	/UG≈Hs.7744 NADH		1	·
	1	dehydrogenase (ubiquinone)			
		flavoprotein 1 (51kD)		1	
	ł	/FL=gb:AF053070.1			
		gb:AF092131.1 gb:NM_007103.1		1	ŀ
208722 s at	0.018023	gb:BC001081.1 /DEF=Homo	BC001081	· · · · · · · · · · · · · · · · · · ·	NP 057321
— — — — — — — — — — — — — — — — — — —		sapiens, anaphase-promoting]		J55. 52.
		complex subunit 5, clone			
		MGC:2750, mRNA, complete			1
· ·	ŀ	cds. /FEA=mRNA			1.
		I			
	{	/PROD=anaphase-promoting			<u> </u>
} ·:		complex subunit 5			}
		/DB_XREF=gi:12654502			
) ·	/UG=Hs.7101 anaphase-			
	} ·	promoting complex subunit 5	1)	* ·
		/FL=gb:BC001081.1	j	,	
		gb:BC001950.1 gb:AF191339.1			· ·
		gb:NM_016237.1			
208723_at	0.018693	gb:BC000350:1 /DEF=Homo	BC000350		NP 004642
-	1	sapiens, ubiquitin specific	1		
	1	protease 11, clone MGC:8620,	+4.	1	
· ·	· `	mRNA, complete cds.	ì		· .
		/FEA=mRNA /PROD=ubiquitin			ł
					_
	•	specific protease 11	1 1		
]		/DB_XREF=gi:12653164			
]) .	/UG=Hs.171501 ubiquitin specific]	}.	}
		protease 11 /FL=gb:BC000350.1		ļ .	,
	1.	gb:U44839.1 gb:NM_004651.1			
[. :	<u> </u>		<u> </u>		<u> </u>
208727_s_at	0.046749	gb:BC002711.1 /DEF=Homo	BC002711		NP_426359
		sapiens, cell division cycle 42			1
		(GTP-binding protein, 25kD),	1	1	1
1	1	clone MGC:3497, mRNA,		1	1
1	}	complete cds. /FEA=mRNA			1
	}	/PROD=cell division cycle 42	1		ł .
1		(GTP-binding protein,25kD)	1 .		
Ì]	/DB_XREF=gi:12803746	1		,
		, – -		}	<u> </u>
		/UG=Hs.146409 cell division	[]
\	1	cycle 42 (GTP-binding protein,	1		1
1	ŀ	25kD) /FL=gb:BC002711.1	**		
1	1	gb:BC003682.1 gb:M57298.1	1		İ
		gb:NM_001791-1			//

Gene List Co	rrespondir	ng to Figure 19 - Coronary Artery	Disease		a, transmitted
Gene ld ntifier	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
208735_s_at	0.046749	gb:AF022231.1 /DEF=Homo sapiens unknown protein mRNA, complete cds. /FEA=mRNA /PROD=unknown protein /DB_XREF=gi:4103319 /UG=Hs.180669 conserved gene amplified in osteosarcoma /FL=gb:AF000152.1 gb:AF022231.1	AF022231		NP_005721
200755 v. ot	0.024724	LI2 history of family 20	DE242224	11- 404007	ND 000000
208755_x_at 208758_at		H3 histone, family 3A gb:D89976.1 /DEF=Homo sapiens mRNA for 5-	BF312331 D89976	Hs 181307	NP_002098 NP_004035
		aminoimidazole-4-carboxamide ribonucleotide transformylase, complete cds. /FEA=mRNA /PROD=5-aminoimidazole-4-			
		carboxamide ribonucleotidetransformylase /DB_XREF=gi:2317691 /UG=Hs.90280 5-aminoimidazole-			
		4-carboxamide ribonucleotide formyltransferaseIMP cyclohydrolase /FL=gb:U37436.1 gb:D82348.1 gb:D89976.1			
		gb:NM_004044.1			
208835_s_at	0.018023	cisplatin resistance-associated overexpressed protein	AW089673	Hs.3688	NP_057508
208853_s_at	0.046749	gb:L18887.1 /DEF=Human calnexin mRNA, complete cds. /FEA=mRNA /PROD=calnexin	L18887		NP_001737
		/DB_XREF=gi:306480 /UG=Hs.155560 calnexin /FL=gb:NM_001746.1 gb:BC003552.1 gb:M94859.1 gb:M98452.1 gb:L10284.1 gb:L18887.1			
208875_s_at	0.025284	Consensus includes gb:BF796470 /FEA=EST /DB_XREF=gi:12101524 /DB_XREF=est:602259926F1 /CLONE=IMAGE:4342999	AF092132		
		/UG=Hs.284275 Homo sapiens PAK2 mRNA, complete cds /FL=gb.AF092132.1			· .

Gene List Co	rrespondir	ng to Figure 19 - Coronary Artery [Disease		
Gene	p-value	Description	Gene	Unigene	Protein
ldentifier			Accession	Accession	Accession
			No.	No.	No.
208876 s at	0.046749	Consensus includes gb:Al076186			
Tarakar a rani.		/FEA=EST			
		/DB_XREF=gi:3405364		·	
		/DB_XREF=est:oz01g01.x1		,	
		/CLONE=IMAGE:1674096		-	
. ,		/UG=Hs.284275 Homo sapiens	1		
		PAK2 mRNA, complete cds			
*				·	Ì
200040	0.005004	/FL=gb:AF092132.1	L04636	·, · · · · · · · · · · · · · · · · · ·	NP 001203
208910_s_at	0.025284	gb:L04636.1 /DEF=Homo	LU4030	,	NP_001203
		sapiens pre-mRNA splicing			
	[factor 2 p32 subunit (SF2p32)			
		mRNA, complete cds.	1.0		
	i .	/FEA=mRNA /PROD=splicing			
		factor /DB_XREF=gi:338044		1. 1	٠.
•		/UG=Hs.78614 complement			
		component 1, q subcomponent			
	ĺ	binding protein		,	
•	}	/FL=gb:NM_001212.2	ļ	j	
	•	gb:BC000435.1 gb:L04636.1			·
208927 at	0.034721	speckle-type POZ protein	BF673888	Hs.129951	NP 003554
208934_s_at		gb:AF342815.1 /DEF=Homo	AF342815		NP 006490
	}	sapiens colorectal carcinoma-	, ,, , , , , , ,		
		derived galectin-8 variant I		<i>J</i>	
	ļ	mRNA, complete cds.			
	-	/FEA=mRNA /PROD=colorectal			
		•			
		carcinoma-derived galectin-8		,	. *
		variantl /DB_XREF=gi:13249298	ļ ·		
		/UG=Hs.4082 lectin, galactoside-	•	, i	
		binding, soluble, 8 (galectin 8)			ļ
		/FL=gb:AF342815.1 gb:L78132.1			
		gb:AF074000.1 gb:NM_006499.1			
					1
208965_s_at	0.036254	interferon, gamma-inducible	BG256677	Hs.155530	NP_005522
		protein 16			
208997_s_at	0.034721	gb:U82819.1 /DEF=Homo	U82819		NP_003346
		sapiens UCP2 mRNA, complete			
	ł.	cds. /FEA=mRNA /PROD=UCP2		ł.	
		/DB_XREF=gi:1877473			
	{	/UG=Hs.80658 uncoupling protein	1	}	ŀ
		2 (mitochondrial, proton carrier)			
		/FL=gb:NM 003355.2		1	1
Ì		gb:U76367.1 gb:U82819.1			
		gb:U94592.1		ľ	1
1		You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You You	1		
200050 2 24	0.010022	ral quanina nucleatida discociation	A1421550	Hs.396157	ND ODGOET
209050_s_at	0.010023	ral guanine nucleotide dissociation	MI42 1998	101060.01	NP_006257
L	<u> </u>	stimulator	<u> </u>	L	<u> </u>

Gene	p-value	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
idonanioi .			No.	No.	No.
209057 x_at	0.034721	gb:AB007892.1 /DEF=Homo	AB007892	1	1
		sapiens KIAA0432 mRNA			
		complete cds. /FEA=mRNA			
		/GEN=KIAA0432	i		
! !		/DB XREF=gi:2887434			1
		/UG=Hs.155174 CDC5 (cell	` `		
	·	division cycle 5, S. pombe,			
		homolog)-like	}		1
	,	/FL=gb:NM_001253.1			· 1
		gb:U86753.1 gb:AB007892.1			
209092_s_at	0.018023	gb:AF061730.1 /DEF=Homo	AF061730		NP_057164
		sapiens clone 016b03 My027	{	}	
		protein mRNA, complete cds.			1
		/FEA=mRNA /PROD=My027	Ì	.	
	Ì	protein /DB_XREF=gi:12001995			
		/UG=Hs.279061 CGI-150 protein	·	į	,
٠.	, i	/FL=gb:AF061730.1			
		gb:AF151908.1 gb:NM_016080.1			<u> </u>
209128_s_at	0.025284	gb:D63879.1 /DEF=Human	D63879		NP_055521
		mRNA for KIAA0156 gene,	ļ	1	
	-	complete cds. /FEA=mRNA	1		
		/GEN=KIAA0156			1
		/DB_XREF=gi:961449		1	1
• •		/UG=Hs.116875 KIAA0156 gene	Ì		1
		product /FL=gb:AB020880.1			ľ
	İ	gb:NM_014706.1 gb:D63879.1	1	İ	
					
		ubiquitin specific protease 10	BG390445	Hs.78829	NP_005144
209143_s_at	0.046749	gb:AF005422.1 /DEF=Homo	AF005422		NP_001284
Ì		sapiens reticulocyte plCln			1
,		mRNA, complete cds.	1	1	
<u>,</u> *		/FEA=mRNA /PROD=reticulocyte		1	1
		pICln /DB_XREF=gi:2209234			ł
	1	/UG=Hs.84974 chloride channel,		1	}
		nucleotide-sensitive, 1A		1	1
	1	/FL=gb:U53454.1 gb:AF005422.1			1
		gb:AF026003.1 gb:NM_001293.1		1	
		gb:U17899.1		1	1
	100000	 	10000000	11. 00000	115 600
209146_at	0.025284	sterol-C4-methyl oxidase-like	AV704962	Hs.239926	_NP_006736

		ng to Figure 19 - Coronary Artery I			
Gen Identifier	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
-			No.	No.	No.
209177_at	0.034721	gb:BC002873.1 /DEF=Homo	BC002873		
		sapiens, Similar to nuclear		-	***
v		protein E3-3 orf1, clone			•
		MGC:10527, mRNA, complete			
* *		cds. /FEA=mRNA /PROD=Similar			
	-	to nuclear protein E3-3 orf1		1	
-		/DB_XREF=gi:12804040	* 4		
		/UG=Hs.31387 DKFZP564J0123			:
		protein /FL=gb:BC002873.1			* * * * * * * * * * * * * * * * * * * *
	,				
209197_at		synaptotagmin XI	AA626780	Hs.380439	NP_689493
209198_s_at	0.018023	gb:BC004291.1 /DEF=Homo	BC004291		NP_689493
		sapiens, Similar to			٠.
9 (4)		synaptotagmin 11, clone			
		MGC:10881, mRNA, complete	•		
31 21	7	cds. /FEA=mRNA /PROD=Similar	:		i di di di di di di di di di di di di di
		to synaptotagmin 11			
		/DB_XREF=gi:13279139 /UG=Hs.74554 KIAA0080 protein			
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		/FL=gb:BC004291.1			
209258 s at	0.049425	Consensus includes gb:Al373676	NM 005445		NP 005436
200200_3_at	0.045425	/FEA=EST	14141_000443		1005450
		/DB_XREF=gi:4153542		!-	
		/DB_XREF=est:qz53h11.x1			
		/CLONE=IMAGE:2030661	, ,		
·		/UG=Hs.24485 chondroitin sulfate			
		proteoglycan 6 (bamacan)			1.5
		/FL=gb:AF020043.1			
• :		gb:NM_005445.1_gb:AF067163.1			
209263_x_at	0.034721	gb:BC000389.1 /DEF=Homo	BC000389	1	NP 003262
		sapiens, transmembrane 4			
•		superfamily member 7, clone		:	
		MGC:8437, mRNA, complete			-
		cds. /FEA=mRNA			
		/PROD=transmembrane 4			
		superfamily member 7			
		/DB_XREF=gi:12653240	*.		
		/UG=Hs.26518 transmembrane 4			
		superfamily member 7			
		/FL=gb:BC000389.1			
5		gb:AF022813.1 gb:AF054841.1			
	1	gb:NM_003271.1	,		I

Gene	p-value	Description	Gene	Unigene	Protein
ldentifier		•	Accession	Accession	Accession
	}	,	No.	No.	No.
209274 s at	0.046749	gb:BC002675.1 /DEF=Homo	BC002675		NP 112202
		sapiens, Similar to CG8198			- ·
		gene product, clone MGC:4276,			
		mRNA, complete cds.	l .		4
		/FEA=mRNA /PROD=Similar to			ļ
	V.	CG8198 gene product			1
		/DB XREF=gi:12803678			
* * * * * * * * * * * * * * * * * * *		/UG=Hs.177776 hypothetical		·	
		protein MGC4276 similar to			
		CG8198 /FL=gb:AF284752.1			
		gb:BC002675.1			
		gb.D0002070.7			[.
209275 s at	0 049425	gb:AF015593.1 /DEF=Homo	AF015593	· · · · · · · · · · · · · · · · · · ·	NP 000077
200270_3_ac	0.043423	sapiens CLN3 protein (CLN3)	7 10000		141 _000077
		mRNA, complete cds.			
		/FEA=mRNA /GEN=CLN3	•		
		I/PROD=CLN3 protein			1
		//DB_XREF=gi:4102728			
		//UG=Hs.194660 ceroid-		,	
		lipofuscinosis, neuronal 3,			
		jiporuscinosis, neuronai 3, juvenile (Batten, Spielmeyer-Vogt			
	,	disease /FL=gb:U32680.1			
				}	
		gb:BC002394.1 gb:BC004433.1			
	,	gb:AF015593.1 gb:NM_000086.1		4	
		gb:AF078169.1 gb:AF077956.1			1.5
		gb:AF077957.1 gb:AF077958.1			1.31
		gb:AF077959.1 gb:AF077961.1			
		gb:AF077962.1 gb:AF077966.1			1
000040	0.004704	gb:AF077971.1	070400	<u> </u>	ND 000400
209340_at	0.034721	gb:S73498.1 /DEF=Homo	S73498		NP_003106
		sapiens AgX-1 antigen mRNA,]	
		complete cds. /FEA=mRNA			
		/PROD=AgX-1 antigen		1	
		/DB_XREF=gi:688010	<u>'</u>		
	}	/UG=Hs.21293 UDP-N-	} .		1
	,	acteylglucosamine			
	}	pyrophosphorylase 1		1	
		/FL=gb:AB011004.1			
	<u> </u>	gb:NM_003115.1 gb:S73498.1	·	<u> </u>	<u> </u>

Gen	p-value	Description	Gene	Unigene	Prot in
Identifier			Accession	Accession	Acc ssion
			N	No.	No.
209358_at	0.046749	gb:AF118094.1 /DEF=Homo	AF118094		NP_005634
		sapiens PRO2134 mRNA,			
		complete cds. /FEA=mRNA	}		1.
		/PROD=PRO2134		1	1
		/DB_XREF=gi:6650833	, ·	1	
	•	/UG=Hs.83126 TATA box			
		binding protein (TBP)-associated			
		factor, RNA polymerase II, I,			[
	٠.	28kD /FL=gb:D63705.1			1
		gb:NM_005643.1 gb:AF118094.1		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
		ga., titl_0000 to 1 ga., ti 1 1000 titl			
209379_s_at	0.034721	gb:AF241785.1 /DEF=Homo	AF241785		NP 061872
	0.00 .,	sapiens NPD012 (NPD012)			111 _001012
		mRNA, complete cds.]		
		/FEA=mRNA /GEN=NPD012			
	,	/PROD=NPD012			
a di cara	ŀ	/DB_XREF=gi:12005486			
· ·		/UG=Hs.81897 KIAA1128 protein			1
		/FL=gb:AF241785.1			
209389_x_at	0.034721		M15887		NP_065438
		endozepine (putative ligand of			
	a.	benzodiazepine receptor) mRNA,		}	
		complete cds. /FEA=mRNA			
		/DB_XREF=gi:181960			
	-	/UG=Hs.78888 diazepam binding			
		inhibitor (GABA receptor	ļ		
		modulator, acyl-Coenzyme A			1
2	·	binding protein) /FL=gb:M15887.1	1		· · · · · · · · · · · · · · · · · · ·
•		1	1		
	**		1		
209430_at	0.046749	Consensus includes	AJ001017		NP_003963
		gb:AJ001017.2 /DEF=Homo			<u> </u>
17		sapiens partial mRNA for TBP-) .		1
		associated factor 170] .]
		(TAFII170). /FEA=mRNA			
•		/GEN=TAFII170 /PROD=TBP	1		
		associated factor			
,		/DB_XREF=gi:7018281		,	
	}	/UG=Hs.180930 TBP-associated	1		
	ļ	factor 172 /FL=gb:AF038362.1	ļ	j	1

		ng to Figure 19 - Coronary Artery			
G ne	p-valu	Description	Gene	Unigene	Protein
ld ntifi r		,	Accession	Accession	Accession
			No.	No.	No.
209434_s_at	0.023856	gb:U00238.1 /DEF=Homo	U00238		NP_002694
]- -	sapiens glutamine PRPP	1		
	•	amidotransferase (GPAT) mRNA,	1		
		complete cds. /FEA=mRNA	·		
	1	/GEN=GPAT /PROD=glutamine			
		PRPP amidotransferase			
	- 1	/DB XREF=gi:404860			
	1	/UG=Hs.311 phosphoribosyl			
		pyrophosphate amidotransferase	1	,	
		/FL=gb:U00238.1		,	
		// L-gb.000200.1			
209436_at	0.049425	Consensus includes	AB018305		NP_006099
200400_u	0.043420	gb:AB018305.1 /DEF=Homo	AB0 10303		
*		sapiens mRNA for KIAA0762			
•		protein, partial cds. /FEA=mRNA			
		/GEN=KIAA0762			.*
					\$
		/PROD=KIAA0762 protein			
4 .		/DB_XREF=gi:3882244			
		/UG=Hs.5378 spondin 1, (f-	•		2 -
· .		spondin) extracellular matrix		,	
		protein /FL=gb:AB051390.1		 	
209447_at	0.046749	gb:AF043290.1 /DEF=Homo	AF043290		NP_598411
		sapiens lymphocyte membrane			
		associated protein (8B7) mRNA,	1		ł
		complete cds. /FEA=mRNA			
		/GEN=8B7 /PROD=lymphocyte			
		membrane associated protein			
•		/DB_XREF=gi:2895592	: *		
	•	/UG=Hs.8182 synaptic nuclei			*
	ľ	expressed gene 1b			
		/FL=gb:AF043290.1			
209457_at	0.018023	gb:U16996.1 /DEF=Human	U16996	- W1	NP 004410
.		protein tyrosine phosphatase			,=
		mRNA, complete cds.			
		/FEA=mRNA /PROD=protein	,		
	,	tyrosine phosphatase			
		/DB_XREF=gi:642012			
		/UG=Hs.2128 dual specificity	1		
		phosphatase 5		. ,	
		/FL=gb:NM 004419.2	1	j	,
		gb:U16996.1 gb:U15932.2	1 1		
	<u> </u>	190.0 10000.1 gb.0 10002.2	1	1	<u>L</u>

		ng to Figure 19 - Coronary Art ry			
Gene Identifier	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
		•	No.	No.	No.
209477 at	0.018444	gb:BC000738.1 /DEF=Homo	BC000738		NP 000108
· · · · · · · · · · · · · · · · · · ·		sapiens, emerin (Emery-Dreifuss			
**		muscular dystrophy), clone	· :	·	
	1	MGC:2126, mRNA, complete		-	
		cds. /FEA=mRNA /PROD=emerin		,	
•		(Emery-Dreifuss muscular			-
		(dystrophy)	·	•	
		/DB_XREF=gi:12653890			
		/UG=Hs.2985 emerin (Emery-			
		Dreifuss muscular dystrophy)			
		/FL=gb:BC000738.1			
000.100	0.04000	gb:NM_000117.1	1105015		
209489_at	0.018023	CUG triplet repeat, RNA binding	N25915	Hs.81248	NP_006551
		protein 1		,	
209503_s_at	0.038017	gb:AF035309.1 /DEF=Homo	AF035309		
		sapiens clone 23598 mRNA,			
		complete cds. /FEA=mRNA			
		/DB_XREF=gi:2661070			
		/UG=Hs.79387 proteasome			
		(prosome, macropain) 26S			
	.]	subunit, ATPase, 5	1		
		/FL=gb:AF035309.1			
209534_x_at	0.025284	A kinase (PRKA) anchor protein 13	BF222823	Hs.301946	NP_658913
209535_s_at	0.036254	gb:AF127481.1 /DEF=Homo	AF127481		NP 658913
	• • •	sapiens non-ocogenic Rho			- -
		GTPase-specific GTP exchange			:
		factor (proto-LBC) mRNA,			
		complete cds. /FEA=mRNA			
	-	/GEN=proto-LBC /PROD=non-			
·	:	ocogenic Rho GTPase-specific			
		GTP exchangefactor			
,	'	/DB XREF=gi:5199315	,		!
٠,					
	,	/UG=Hs.301946 lymphoid blast			
		crisis oncogene			
200594+	0.040000	/FL=gb:AF127481.1	A E 1 C E E C C		ND OCCOO
209584_x_at	0.018023	gb:AF165520.1 /DEF=Homo	AF165520		NP_055323
		sapiens phorbolin I protein (PBI)			
		mRNA, complete cds.			
		/FEA=mRNA /GEN=PBI			
		/PROD=phorbolin I protein			
		/DB_XREF=gi:9294746		1	
,		/UG=Hs.8583 similar to			
*		APOBEC1 /FL=gb:AF165520.1			

Gene List Co	rr spondir	ig to Figure 19 - Coronary Artery I	Disease		
Gene	p-value	Description	Gene	Unigene	Protein
ld ntifier			Accession	Accession	Accession
,			No.	No.	No.
209586 s at	0.046749	gb:AF123539.1 /DEF=Homo	AF123539	1.10.	NP 067045
		sapiens clone 143 prune protein			
	•	mRNA, complete cds.,		1	
	1	alternatively spliced. /FEA=mRNA			
		/PROD=prune protein		1 .	ľ
9		/DB XREF=gi:12655791	}		
		/UG=Hs.78524 TcD37 homolog	ŀ		
		/FL=gb:AF123539.1		1	l
209608 s at	0.018023	gb:BC000408.1 /DEF=Homo	BC000408		NP_005882
209000_S_at	0.016023	1	BC000406	1	INF_003662
		sapiens, acetyl-Coenzyme A			
	İ	acetyltransferase 2 (acetoacetyl	ł ·		
		Coenzyme A thiolase), clone			
		MGC:8573, mRNA, complete	1		
		cds. /FEA=mRNA /PROD=acetyl-		,	. , !
	· .	Coenzyme A acetyltransferase	[
		2(acetoacetyl Coenzyme A			
	i .	thiolase) /DB_XREF=gi:12653278			[
	. *	/UG=Hs.278544 acetyl-Coenzyme	1		
		A acetyltransferase 2			[·
		(acetoacetyl Coenzyme A		. :	
,		thiolase) /FL=gb:BC000408.1			•
j]		1	
209626_s_at	0.036254	oxysterol binding protein-like 3	Al202969	Hs.197955	NP_663164
209627_s_at	0.034317	gb:AY008372.1 /DEF=Homo	AY008372		NP_663164
		sapiens oxysterol binding protein			- '
	1 .	related protein 3 (ORP3) mRNA,	1		· .
		complete cds. /FEA=mRNA	<u> </u>	· ·	1
		/GEN=ORP3 /PROD=oxysterol			
	ļ <u>"</u>	binding protein-related protein 3		}	
		/DB_XREF=gi:10880972	· '	1	
		/UG=Hs.197955 KIAA0704			
1	1.	protein /FL=gb:AY008372.1	1	1	
•		protein // E-gb./(10000/2.1			
209705_at	0.026013	Consensus includes	AF073293	 	NP_031384
200700_at	0.020013	gb:BG033764 /FEA=EST	77 07 3230		_001004
	ľ	/DB_XREF=gi:12426228	Í	1	·
		//DB_XREF=est:602302025F1			
		//CLONE=IMAGE:4403238	1	İ	
, · · ·	ĺ	/UG=Hs.31016 putative DNA			
	l	binding protein			
000744	0.004704	/FL=gb:AF073293.1	AE440044	 	ND 005004
209741_x_at	0.034721	gb:AF119814.1 /DEF=Homo	AF119814	j	NP_065894
		sapiens MSTP063 mRNA,			
	ļ	complete cds. /FEA=mRNA		1	
l		/PROD=MSTP063			
1		/DB_XREF=gi:12056567		1	
		1/1/C-U- 205040 VIA A 1/6/	1	Ī	Ī
!	1	/UG=Hs.285848 KIAA1454 protein /FL=gb:AF119814.1	,		

		ng to Figure 19 - Coronary Artery		11-1-	Ducto:
Gen Identifi r	p-value	Description	Gene Accession	Unig ne Accession	Protein
identiii r			· · · · · · · · · · · · · · · · · · ·	1	Accession
200780 at	0.024724	gb:AL136883.1 /DEF=Homo	No. AL136883	No.	No.
209780_at	0.034721	•	AL 130883		NP_065165
1 4		sapiens mRNA; cDNA]
		DKFZp434D166 (from clone		1,	
	*	DKFZp434D166); complete cds.		* * *	
		/FEA=mRNA		· · · .	
e ·		/GEN=DKFZp434D166			*
		/PROD=hypothetical protein			
		/DB_XREF=gi:12053266			
		/UG=Hs.128653 hypothetical			
		protein DKFZp564F013	*		
		/FL=gb:AL136883.1			
209791_at	0.034721	Consensus includes	AL049569		
	1	gb:AL049569 /DEF=Human DNA	:		a se
		sequence from clone RP1-		* *	
		37C10 on chromosome 1p35.2-			·
· · · · · · · · · · · · · · · · · · ·		35.21. Contains the gene for		* **	
	1	the ortholog of mouse and rat			
		PDI (protein-arginine deiminase			
	1	(KIAA0994, EC 3.5.3.15,			
		peptidylarginine deiminase)), the]		
	**	SDHB gene for succinate			
	·	dehydrogenase /FEA=mRNA_4	,	*	
	٠.	/DB_XREF=gi:5263031			
		/UG=Hs.33455 peptidyl arginine			
		deiminase, type II			
٠.		/FL=gb:AB030176.1			•
	. t.	/			
209815 at	0.018444	Consensus includes	U43148	· · · · · · · · · · · · · · · · · · ·	NP_000255
>		gb:BG054916 /FEA=EST	0,10,110		000200
	·.	/DB_XREF=gi:12512119			
		/DB_XREF=est:nac92b02.x1			*
		/CLONE=IMAGE:3441723			
		/UG=Hs.159526 patched		, , , , , , , , , , , , , , , , , , ,	
. •		(Drosophila) homolog			
		/FL=gb:U43148.1			
209824_s_at	0.034721		AB000812		NP_001169
203024_S_at	0.054721	sapiens mRNA for BMAL1b,	AB000012		NF_00116
	de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la				
		complete cds. /FEA=mRNA			
		/PROD=BMAL1b			
÷.		/DB_XREF=gi:2094734			[\cup
	,	/UG=Hs.74515 aryl hydrocarbon		1	
		receptor nuclear translocator-like			<i>.</i> *
		/FL=gb:AB000812.1			
		gb:AF044288.1	1	·	

		ng to Figure 19 - Coronary Artery		ļ	
Gene	p-value	Description	Gene	Unigene	Protein
ldentifi r			Acc ssion	Accession	Accession
			No	No.	No.
209835_x_at	0.034721	gb:BC004372.1 /DEF=Homo	BC004372		NP 000601
· · · · · · · · · · · · · · · · · · ·		sapiens, Similar to CD44			 -
•		antigen (homing function and			
-		Indian blood group system),	[
	-	clone MGC:10468, mRNA,			
		complete cds. /FEA=mRNA	e i	·	
		/PROD=Similar to CD44 antigen			1
		(homing function andIndian blood			!
		group system)			
•		/DB_XREF=gi:13325117			
		/UG=Hs.169610 CD44 antigen			
		(homing function and Indian			
		blood group system)			ļ
		/FL=gb:BC004372.1		e Silver	
209839_at	0.034721	gb:AL136712.1 /DEF=Homo	AL136712	 	NP_056384
	0.00 ,721	sapiens mRNA; cDNA	1/12/90/ 12		_000004
		DKFZp566K013 (from clone	! .		
		DKFZp566K013); complete cds.	1. (. *
		/FEA=mRNA			
		/GEN=DKFZp566K013		· .	
		/PROD=hypothetical protein			-
		/DB_XREF=gi:12052943	· · ·		
· ·					
		/UG=Hs.33578 KIAA0820 protein			
209862 s at	0.046749	/FL=gb:AL136712.1	BC001233	 	ND OFFICE
209002_S_at	0.040749	gb:BC001233.1 /DEF=Homo sapiens, Similar to KIAA0092	BC001233		NP_055494
i.					
	,	gene product, clone MGC:4896,			
		mRNA, complete cds.			
	.	/FEA=mRNA /PROD=Similar to	,		
		KIAA0092 gene product		1	
*	*	/DB_XREF=gi:12654780			
		/UG=Hs.134158 Homo sapiens,			
		Similar to KIAA0092 gene		1	
		product, clone MGC:4896,			
<u>;</u>		mRNA, complete cds		1	<u>'</u>
		/FL=gb:BC001233.1			
200004	0.02002	-h-AE02000E4 /DEE-11	A E00000E	<u> </u>	ND OFFOOD
209881_s_at	0.03002	gb:AF036905.1 /DEF=Homo	AF036905		NP_055202
1		sapiens linker for activation of T			J [*]
		cells (LAT) mRNA, complete		1	
		cds. /FEA=mRNA /GEN=LAT			
		/PROD=LAT			
		/DB_XREF=gi:2828023	1	1 .	(
		/UG=Hs.83496 linker for	j	J	J ·
		activation of T cells			
		/FL=gb:AF036905.1	L	<u> </u>	L

		ng to Figure 19 - Coronary Artery		1	
Gene	p-value	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
			No.	No.	No.
209892_at	0.02008	Consensus includes	AF305083	1	NP_002024
	–	gb:AF305083.1 /DEF=Homo	-,		
		sapiens alpha(1,3)-			*.
		fucosyltransferase IV (FUTIV)			
		gene, 3 UTR. /FEA=mRNA			
		/DB_XREF=gi:11096240			
		/UG=Hs.2173 fucosyltransferase			
*		4 (alpha (1,3) fucosyltransferase,			·
		myeloid-specific)	• • •		
		/FL=gb:M58596.1 gb:M58597.1			
		gb:NM_002033.1			1
209903 s at	0.034721	gb:U49844.1 /DEF=Human FRAP	U49844	.:	NP 001175
		related protein (FRP1) mRNA,			
		complete cds. /FEA=mRNA			
•		/GEN=FRP1 /PROD=FRAP-			• .
		related protein			
		/DB_XREF=gi:1235901		-	
		/UG=Hs.77613 ataxia			
		telangiectasia and Rad3 related			
	•	/FL=gb:U49844.1 gb:U76308.1			,
200000	0.040000	gb:NM_001184.1	DC000704		ND C44074
209969_s_at	0.016023	gb:BC002704.1 /DEF=Homo	BC002704		NP_644671
*1 *		sapiens, Similar to signal			
		transducer and activator of			
		transcription 1, 91kD, clone		;	
		MGC:3493, mRNA, complete			
		cds: /FEA=mRNA /PROD=Similar	4.		
	٠	to signal transducer and			
		activator oftranscription 1, 91kD			
		/DB_XREF=gi:12803734			
		/UG=Hs.21486 signal transducer	- 1		
		and activator of transcription 1,		·	
		91kD /FL=gb:BC002704.1			
-					
210007_s_at	0.045316	gb:U36310.1 /DEF=Human	U36310		NP_000399
		glycerol-3-phosphate			
		dehydrogenase mRNA, nuclear			_
		gene encoding mitochondrial		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	·
	e e	protein, complete cds.	1		·
		/FEA=mRNA /PROD=glycerol-3-			
	,	phosphate dehydrogenase			
4 .		/DB_XREF=gi:1020314			·
		/UG=Hs.93201 glycerol-3-			
		phosphate dehydrogenase 2			
		(mitochondrial) /FL=gb:U36310.1		1	1

		ng to Figure 19 - Coronary Art ry I			
Gene	p-value	D scription	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
	i .		No.	No.	No.
210038 at	0.018693	Consensus includes	AL137145		
-		gb:AL137145 /DEF=Human DNA		.]	
>		sequence from clone RP11-			
		563J2 on chromosome 10			
4		Contains ESTs, STSs, GSSs			100
. •		and a CpG island. Contains a		1	.
		novel pseudogene and the 3			
		part of the PRKCQ gene for		,	
		protein kinase C theta		i.	Ç.
		/FEA=mRNA			1
		/DB_XREF=gi:9581557			1
; ·		/UG=Hs.211593 protein kinase			
					14 X 1
	(C, theta /FL=gb:L07032.1	-	1	1
0400404	0.040000	gb:NM_006257.1 gb:L01087.1	1050444		
210046_s_at	0.018023	gb:U52144.1 /DEF=Human	U52144		
		isocitrate dehydrogenase mRNA,			
%	i -	complete cds. /FEA=mRNA			**
	.	/PROD=isocitrate dehydrogenase] ' '		
		/DB_XREF=gi:1277202			
-		/UG=Hs.5337 isocitrate			ļ
		dehydrogenase 2 (NADP+),			
-	•	mitochondrial /FL=gb:U52144.1			
210057_at	0.038017	gb:U32581.2 /DEF=Homo	U32581] , –	NP_055907
		sapiens lambdaiota protein			_
*	i	kinase C-interacting protein			
,	-	mRNA, complete cds.			
		/FEA=mRNA /PROD=lambdaiota			1
		protein kinase C-			1
		interactingprotein		}	}
	, '	/DB_XREF=gi:5542015		,	
		/UG=Hs.168052 KIAA0421			
		protein /FL=gb:U32581.2	ļ		
210105_s_at	0.025284	gb:M14333.1 /DEF=Homo	M14333	 	NP_694593
a.	0.02020	sapiens c-syn protooncogene	1411-000		141 _054555
-	[mRNA, complete cds.	ĺ		(
	:	/FEA=mRNA	:		
÷		· ·	,		
, T		/DB_XREF=gi:181171	J]	
		/UG=Hs.169370 FYN oncogene			
		related to SRC, FGR, YES			
	1	/FL=gb:M14333.1 gb:M14676.1			
		gb:NM_002037.1			L ··

Gen	p-value	Description	Gene	Unigene	Protein
	p-value	pėscubuon	1 *	-	
ld ntifier	,		Accession	Accession	Accession
040440	0.00054		No.	No.	No.
210116_at	0.036254	gb:AF072930.1 /DEF=Homo	AF072930		NP_002342
		sapiens clone 14 T cell signal		· · · · · · · · · · · · · · · · · · ·	
•	·	transduction molecule SAP		, ,	
		mRNA, complete cds.			
		/FEA=mRNA /PROD=T cell		-	,
		signal transduction molecule			
		SAP /DB_XREF=gi:3695068	.,	. "	,
		/UG=Hs.151544 SH2 domain			
	,	protein 1A, Duncans disease		•	
44	ļ :	(lymphoproliferative syndrome)			**
		/FL=gb:AF072930.1			
• •		1			
		gb:AF073019.1 gb:AF100541.1			1
		gb:NM_002351.1	00001000		NID 004046
210137_s_at	0.018023	gb:BC001286.1, /DEF=Homo	BC001286	i i	NP_001912
		sapiens, Similar to dCMP			
		deaminase, clone MGC:5160,			1
		mRNA, complete cds.			` .
	-	/FEA=mRNA /PROD=Similar to		*	
4.	i	dCMP deaminase			
1		/DB_XREF=gi:12654884			
	i	/UG=Hs.76894 dCMP deaminase			
• •		/FL=gb:BC001286.1			
210148_at	0.025284	gb:AF305239.1 /DEF=Homo	AF305239	 	NP 005725
210140_at	0.020204	sapiens Fas-interacting	7.11 000200		111,_000720
	· ·	serinethreonine kinase 3 (FIST3)	(·		[
					*
		mRNA, complete cds.	1.0	1	1
		/FEA=mRNA /GEN=FIST3		,	
		/PROD=Fas-interacting			
		serinethreonine kinase 3	4		
		/DB_XREF=gi:10998781	[•	·
	<u> </u>	/UG=Hs.30148 homeodomain-			
1 -		interacting protein kinase 3	1.0		
		/FL=gb:AF305239.1			
210193_at	0.034317	gb:D28114.1 /DEF=Human	D28114		NP 006492
		mRNA for MOBP (myelin-			
	i	associated oligodendrocytic basic	[1	1
		protein), complete cds, clone			
		hOPRP2. /FEA=mRNA		1.	
		· ·			,
		/PROD=MOBP			
		/DB_XREF=gi:662277			
Ĺ		/UG=Hs.169309 myelin-			1.
·	· ·	associated oligodendrocyte basic			1
	l .	protein /FL=gb:D28114.1			

G ne		ng to Figure 19 - Coronary Artery Description	Gene	llning	Protein
	p-value	Describrion		Unigene	
ldentifier			Accession	Accession	Accession
040005	0.040405	L HOOGAE'A IDEE H	No.	No.	No.
210235_s_at	0.049425	gb:U22815.1 /DEF=Human LAR-	U22815		NP_803172
	-	interacting protein 1a mRNA,			
		complete cds. /FEA=mRNA			_
	•	/PROD=LAR-interacting protein			
	ļ. -	1a /DB_XREF=gi:930340			,
•	·	/UG=Hs.183648 protein tyrosine			
	ļ. ·	phosphatase, receptor type, f			
		polypeptide (PTPRF), interacting			,
		protein (liprin), alpha 1			
		/FL=gb:U22815.1			
210257_x_at	0.018023	gb:AF212995.1 /DEF=Homo	AF212995	· · · · · · · · · · · · · · · · · · ·	NP_003579
210207_x_at	0.010020	sapiens cullin CUL4B (CUL4B)	A 2 12333		141 _003373
		mRNA, complete cds.			
		/FEA=mRNA /GEN=CUL4B		İ	
		/PROD=cullin CUL4B			•
		/DB_XREF=gi:13259126			
		/UG=Hs,155976 cullin 4B			
		/FL=gb:AF212995.1		·	* * * * * * * * * * * * * * * * * * * *
210266_s_at	0.025284	gb:AF220137.1 /DEF=Homo	AF220137		NP_148980
		sapiens tripartite motif protein			
		TRIM33 beta mRNA, complete			•
		cds; alternatively spliced.			
		/FEA=mRNA /PROD=tripartite		-	
		motif protein TRIM33 beta			
,		/DB_XREF=gi:12407442			
** **	-	/UG=Hs 287414 transcriptional			
		intermediary factor 1 gamma		i	
•					
210276	0.046740	/FL=gb:AF220137.1 gb:AF281030.1 /DEF=Homo	AE004000		ND C40500
210276_s_at	0.046749	1 -	AF281030	1.	NP_619538
		sapiens Tara mRNA, complete			·
		cds. /FEA=mRNA /PROD=Tara			
•		/DB_XREF=gi:12006357			
		/UG=Hs.40342 putative nuclear			
		protein /FL=gb:AF281030.1			
		gb:BC003618.1			
210279_at	0.018023	gb:AF261135.1 /DEF=Homo	AF261135	1 3	NP_005283
		sapiens GPR18-iso mRNA,		1	· -
	, ,	complete cds. /FEA=mRNA			
]	/PROD=GPR18-iso		1	
		/DB_XREF=gi:12005919			
		/UG=Hs.88269 Homo sapiens	,	1	
		clone IMAGE:1837189, mRNA			
		sequence /FL=gb:AF261135.1	L	1	l

		ng t Figur 19 - Coronary Artery	T	<u> </u>	
Gene	p-value	Description	G ne	Unigene	Protein
Identifier		1	Acc ssion	Accession	Accession
	2		No.	No.	No.
210285 x at	0.034721	gb:BC000383.1 /DEF=Homo	BC000383		NP_690597
		sapiens, Wilms tumour 1-			
		associating protein, clone			
		MGC:8419, mRNA, complete			
	•.	cds. /FEA=mRNA /PROD=Wilms			*
					• • •
		tumour 1-associating protein			
		/DB_XREF=gi:12653228			·
		/UG=Hs.119 Wilms tumour 1-	4		
		associating protein	•		
		/FL=gb:BC000383.1			
		gb:BC004432.1			\$.
210321_at	0.045316	gb:M36118.1 /DEF=Human	M36118		
 ·.	·	cytotoxin serine protease-C			
		mRNA, complete cds			<u>l</u> .
:		/FEA=mRNA			
*		/DB_XREF=gi:181163		1 2	
		/UG=Hs.1051 granzyme B		·	
		(granzyme 2, cytotoxic T-			
***	-				
•		lymphocyte-associated serine			-
6.100=1	0.010000	esterase 1) /FL=gb:M36118.1			1.12
210354_at	0.018222	gb:M29383.1 /DEF=Human	M29383		NP_000610
		interferon-gamma (HuIFN-			2.5
.90		gamma) mRNA, complete cds.			-
* 1		/FEA=mRNA			
•		/DB_XREF=gi:186514			
	•	/UG=Hs.856 interferon, gamma			
	,	/FL=gb:NM_000619.1	t ·		
	· .	gb:M29383.1			
210357_s_at	0.020576	gb:BC000669.1 /DEF=Homo	BC000669		NP 787036
		sapiens, Similar to hypothetical			
•		protein, clone MGC:1010,			*
		mRNA, complete cds.			- + 6
		/FEA=mRNA /PROD=Similar to			
					,
- 1		hypothetical protein			
		/DB_XREF=gi:12653766			
		/UG=Hs.92374 hypothetical			
		protein /FL=gb:BC000669.1			
210389_x_at	0.034721	gb:BC000258.1 /DEF=Homo	BC000258		NP_057345
		sapiens, Similar to delta-tubulin,	. C		
	,	clone MGC:2619, mRNA,	, v ¹		
		complete cds. /FEA=mRNA			
		/PROD=Similar to delta-tubulin			
		/DB_XREF=gi:12652994			
		/UG=Hs.270847 delta-tubulin			
		/FL=gb:BC000258.1		. 2	
		## L=UD.DCUUUZJO.I	1.3		ī.

		ng to Figure 19 - Coronary Artery			
Gen	p-value	Description	Gene	Unigene	Protein
ldentifier			Acc ssion	Accession	Accession
			No.	No.	No. /
210396_s_at	0.034721	gb:AF271775.1 /DEF=Homo	AF271775		
		sapiens DC49 mRNA, complete			
	N	cds. /FEA=mRNA /PROD=DC49			
		/DB_XREF=gi:12006206			
		/UG=Hs.307093 Homo sapiens			
	-	DC49 mRNA, complete cds		2	
'		/FL=gb:AF271775.1			
					· ·
210438 x at	0.018023	gb:M25077.1 /DEF=Human SS-	M25077		NP_004591
	0.0.00=0	ARo ribonucleoprotein			
		autoantigen 60 kd subunit			
•		mRNA, complete cds.			
		/FEA=mRNA			[·
		/DB_XREF=gi:387656			
					A.
]	/UG=Hs.554 Sjogren syndrome			
4.1		antigen A2 (60kD,			
		ribonucleoprotein autoantigen SS-		,	
0404404	0.004704	ARo) /FL=gb:M25077.1	1140000		
210448_s_at	0.031704	gb:U49396.1 /DEF=Human	U49396		NP_778256
•		ionotropic ATP receptor P2X5b			
		mRNA, complete cds.			
		/FEA=mRNA /PROD=P2X5b	1	1.5	
14.		/DB_XREF=gi:1552523		,	
		/UG=Hs.77807 purinergic			
		receptor P2X, ligand-gated ion			
÷		channel, 5 /FL=gb:U49396.1		•	
		gb:AF070573.1			**
210449_x_at	0.027792	gb:AF100544.1 /DEF=Homo	AF100544		NP_620583
		sapiens stress-activated protein			
. *		kinase 2a (CSBP) mRNA,		:	
		complete cds. /FEA=mRNA			
. 1		/GEN=CSBP /PROD=stress-			
*		activated protein kinase 2a	,		
*		/DB XREF=gi:7109716		· · · · · ·	
		/UG=Hs.79107 mitogen-activated			
		protein kinase 14			1
		/FL=gb:BC000092.1 gb:L35264.1			
	5.	gb:AF100544.1			
210466_s_at	0.046749	gb:BC002488.1 /DEF=Homo	BC002488		NP_056455
210100_0_4	0.010110	sapiens, Similar to	10002400		000400
		DKFZP564M2423 protein, clone			
		MGC:1357, mRNA, complete		1	
		icds. /FEA=mRNA /PROD=Similar			1
				1	1
		to DKFZP564M2423 protein			l .
		/DB_XREF=gi:12803338			1
		/UG=Hs 165998 PAI-1 mRNA-			
	,	binding protein		1	
		/FL=gb:BC002488.1	1		1
			l'		

Gene	p-value	ng to Figure 19 - Coronary Artery Description	Gene	Unia n	Prot in
	p-value	Description		Unig n	1
ldentifier	-		Acc ssion	Accession	Accession
	0.000125		No.	No.	No.
210502_s_at	0.021165	gb:AF042386.1 /DEF=Homo	AF042386		NP_006103
		sapiens cyclophilin-33B (CYP-33)			
•		mRNA, complete cds.	,		
		/FEA=mRNA /GEN=CYP-33			
		/PROD=cyclophilin-33B			
		/DB_XREF=gi:2828150		; *	
		/UG=Hs.33251 peptidylprolyl			
		isomerase E (cyclophilin E)			
		/FL=gb:AF042386.1			
210513_s_at	0.018023	gb:AF091352.1 /DEF=Homo	AF091352		NP_003367
		sapiens vascular permeability		1	
*		factor 148 mRNA, complete cds.	·		
	·	/FEA=mRNA /PROD=vascular			
		permeability factor 148	1.0		
• .		/DB_XREF=gi:5901560		<u>'</u>	
		/UG=Hs.73793 vascular			
3		endothelial growth factor			
		/FL=gb:M32977.1 gb:AF022375.1			
	1	gb:NM_003376.1 gb:AB021221.1	1		. *
		gb:AF091352.1		•	
		9-11-11-11-11-11-11-11-11-11-11-11-11-11			
210514 x at	0.049425	gb:AF226990.2 /DEF=Homo	AF226990	-	NP_002118
		sapiens MHC class I antigen			
		(HLA-G) mRNA, HLA-G1 allele,			
		complete cds. /FEA=mRNA	·		
		/GEN=HLA-G /PROD=MHC class			
•		I antigen /DB XREF=gi:7245285			
4. *		/UG=Hs.73885 HLA-G			
1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -		histocompatibility antigen, class			
, ,	ļ	I, G /FL=gb:M90683.1			\
		• · · · · · · · · · · · · · · · · · · ·			-
		gb:M32800.1 gb:NM_002127.1			
		gb:AF226990.2		*	
210527 2 24	0.010000	ab 1 11645 1 /DEE-Homo	1 11645		ND 504575
210527_x_at	0.0,10222	gb:L11645.1 /DEF=Homo	L11645	'	NP_524575
	l. 	sapiens alpha-tubulin mRNA,	1		
		complete cds. /FEA=mRNA			
		/PROD=alpha-tubulin			1.
		/DB_XREF=gi:306450			
• •		/UG=Hs.98102 tubulin, alpha 2			
	1	/FL=gb:L11645.1		I .	

Gene	p-value	ng to Figure 19 - Coronary Artery Description	Gene	Unicono	Droto
	h-vaine	nescubtion	I 1	Unigene	Protein
ldentifier			Accession	Accession	Accession
040506	0.001155	1	No.	No.	No.
210528_at	0.021165	gb:AF010447.1 /DEF=Homo	AF010447		NP_001522
		sapiens MHC class I related			
		protein 1 isoform C (MR1C)			
		mRNA, complete cds.			
۲.		/FEA=mRNA /GEN=MR1C			
		/PROD=MHC class I related			1
•		protein 1 isoform C		·	
-		/DB_XREF=gi:4102223			
	.**	/UG=Hs.101840 major			
		histocompatibility complex, class	•		
		I-like sequence			
		/FL=gb:AF010447.1		1 1 1	
210574_s_at	0.046749	gb:AF241788.1 /DEF=Homo	AF241788		NP_006591
		sapiens NPD011 (NPD011)			-
		mRNA, complete cds.		F	
		/FEA=mRNA /GEN=NPD011			† .
	·	/PROD=NPD011			
		/DB_XREF=gi:12005492			·
		/UG=Hs.263812 nuclear			
		distribution gene C (A.nidulans)			
		homolog /FL=gb:AF241788.1		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	,
210580_x_at	0.025284	gb:L25275.1 /DEF=Human	L25275		NP 808220
,		estrogen sulfotransferase mRNA,			
	11.5	complete cds. /FEA=mRNA			
		/PROD=estrogen sulfotransferase			
		/DB_XREF=gi:463124		-	
		/UG=Hs 274614 sulfotransferase			1
		family, cytosolic, 1A, phenol-			
		preferring, member 3			£
		/FL=gb:L25275.1			
	r r				
210705 s at	0.046749	gb:AF220028.1 /DEF=Homo	AF220028		NP 149084
210100 <u>-</u> 0_at	0.040740	sapiens tripartite motif protein	71 220020	<i>;</i>	1400
	- "	TRIM5 isoform delta (TRIM5)		· .	
		mRNA, complete cds;			
		alternatively spliced. /FEA=mRNA]		
		/GEN=TRIM5 /PROD=tripartite			
		motif protein TRIM5 isoform	-		
		delta /DB_XREF=gi:12407386			,
		/UG=Hs.30445 Homo sapiens			
		tripartite motif protein TRIM5			
		• ·			
		isoform epsilon (TRIM5) mRNA,			
	i .	complete cds; alternatively		l	1
	i	spliced /FL=gb:AF220028.1	1	i	J

		ng to Figur 19 - Coronary Artery I	201 A 101 11 11 1	1	
Gene	p-value	D scription	Gene	Unigen	Protein
Identifier			Accession No.	Accession	Accession
210715 s at	0.034734	gb:AF027205.1 /DEF=Homo	AF027205	No.	No. NP 066925
210/15_S_at	0.034721	1=	AF027203		NP_000925
4 · **		sapiens Kunitz-type protease			*
		inhibitor (kop) mRNA, complete			
		cds. /FEA=mRNA /GEN=kop			
		/PROD=Kunitz-type protease	1,	·	
	*	inhibitor /DB_XREF=gi:2598967			
		/UG=Hs.31439 serine protease			
	·	inhibitor, Kunitz type, 2		•	
040740	0.000054	/FL=gb:AF027205.1	DOGGETO		ND 00000
210719_s_at	0.036254	gb:BC002552.1 /DEF=Homo	BC002552		NP_006330
		sapiens, high-mobility group 20B,			
		clone MGC:1965, mRNA,			1.
**	1	complete cds. /FEA=mRNA			
		/PROD=high-mobility group 20B			
		/DB_XREF=gi:12803454			
		/UG=Hs.32317 high-mobility	•		
		group 20B /FL=gb:BC002552.1	 		<u> </u>
210731_s_at	0.046749	Consensus includes	AL136105		
		gb:AL136105 /DEF=Human DNA			-
		sequence from clone RP4-		,	
	• "	670F13 on chromosome 1q42.2-		,	•
	ar"	43. Contains an enolase 1,		,	•
	1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min 1 min	(alpha) (ENO1) pseudogene, the	~ ~		
		gene for Po66 carbohydrate ,			
		binding protein similar to soluble	-		
		galactoside-binding lectin 8			
		(galectin 8, LGALS8), the 3 end	•		
. 1		of /FEA=mRNA_3			
•	, ·	/DB_XREF=gi:9801288			
		/UG=Hs.4082 lectin, galactoside-	1 2		.
**	! .	binding, soluble, 8 (galectin 8)		-	
		/FL=gb:AF342816.1			7
		gb:AF074001.1			,
210778_s_at	0.034317	gb:BC002713.1 /DEF=Homo	BC002713		NP_006445
*		sapiens, Similar to Mad4	1		
		homolog, clone MGC:3542,			1
		mRNA, complete cds.			
		/FEA=mRNA /PROD=Similar to			
		Mad4 homolog	1	1.	***
	1	/DB_XREF=gi:12803750			
,		/UG=Hs.102402 Mad4 homolog	1		
		/FL=gb:BC002713.1		1	· [. *

Gene List Co		ng to Figure 19 - Coronary Artery l	Disease		
Gene Identifier	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
	· ·		No.	No.	No.
210840 s at	0.046749	gb:D29640.1 /DEF=Human	D29640	1.10.	NP_003861
		mRNA for KIAA0051 gene,			(1, 1) (1, 2 1 3, 1 1
	ļ	complete cds. /FEA=mRNA			
		/GEN=KIAA0051			
		/DB XREF=gi:473930			'
l		/UG=Hs.1742 IQ motif containing			· ·
		GTPase activating protein 1	1 ·	ĺ	
i i		/FL=gb:D29640.1			ļ
210865_at	0.018222	gb:D38122.1 /DEF=Human	D38122		NP 000630
2,000 <u>0_</u> at	0.010222	mRNA for Fas ligand, complete	500.22		
•		cds. /FEA=mRNA /PROD=Fas			
		ligand /DB_XREF=gi:601892		·	
! * 		/UG=Hs.2007 tumor necrosis			* .
		factor (ligand) superfamily,			
		member 6 /FL=gb:NM_000639.1	1		1
		gb:U11821.1 gb:D38122.1		5	
		lgb:U08137.1	ĺ	1	
		90.000137.1 			
		1.00			
210879 s at	0.036254	gb:AF334812.1 /DEF=Homo	AF334812	-	NP_056285
2100/9_5_at	0.030234	sapiens Rab11 interacting	AF334612		NP_056265
		protein Rip11a mRNA, complete			
,		cds: /FEA=mRNA /PROD=Rab11	1		
		· · · · · · · · · · · · · · · · · · ·			
		interacting protein Rip11a			·
		//DB_XREF=gi:13377896			·
	,	/UG=Hs.24557 KIAA0857 protein			
*		/FL=gb:AF334812.1			
210016	0.040740	ph. A F000044 4 //DEF-11	A E000044	 	
210916_s_at	0.046749	gb:AF098641.1 /DEF=Homo	AF098641		•
		sapiens CD44 isoform RC			
	1	(CD44) mRNA, complete cds.			ę.
•		/FEA=mRNA /GEN=CD44			
		/PROD=CD44 isoform RC			}
		/DB_XREF=gi:3832517			
•		/UG=Hs.306278 Homo sapiens]		
	}	CD44 isoform RC (CD44)			\
		mRNA, complete cds	,		
040000	0.040000	/FL=gb:AF098641.1		 	<u> </u>
210926_at	0.018023	gb:AY014272.1 /DEF=Homo	AY014272		ļ
		sapiens FKSG30 (FKSG30)			
	}	mRNA, complete cds.	}		· ·
	[/FEA=mRNA /GEN=FKSG30	l		ĺ
		/PROD=FKSG30			
	}	/DB_XREF=gi:12408251	ļ ·		ļ
		/UG=Hs.315492 Homo sapiens			
		FKSG30 (FKSG30) mRNA,	j	ì	
		complete cds	1		. 4
	L	/FL=gb:AY014272.1	L	<u> </u>	<u> </u>

		ng to Figure 19 - Coronary Artery			<u> </u>
Gen	p-value	Description	Gene	Unigene	Protein
ldentifi r	+ 4		Accession	Accession	Accession
			No.	No.	No.
211034 s at	0.036254	gb:BC006270.1 /DEF=Homo	BC006270	1	110.
		sapiens, clone MGC:11291,			
		mRNA, complete cds.			
		/FEA=mRNA /PROD=Unknown			
					Α
		(protein for MGC:11291)			· · · · · · · · · · · · · · · · · · ·
		/DB_XREF=gi:13623331			
044074	0.004704	/FL=gb:BC006270.1			
211074_at	0.034721	gb:AF000381.1 /DEF=Homo	AF000381		
*	:	sapiens non-functional folate			4.5
•		binding protein mRNA, complete			
	•	cds. /FEA=mRNA /PROD=non-			
		functional folate binding protein			
		/DB_XREF=gi:2565195			
		/FL=gb:AF000381.1			1
	•		,		
211102_s at	0.049425	gb:U82277.1 /DEF=Human	U82277		NP 006857
		immunoglobulin-like transcript 1b			
		mRNA, complete cds.		•	,
		/FEA=mRNA			
•		I .	*:		· .
		/PROD=immunoglobulin-like	*		
		transcript 1b			
		/DB_XREF=gi:1907320			
		/UG=Hs.94498 leukocyte		. '	,
	4*	immunoglobulin-like receptor,			
		subfamily A (with TM domain),			
		member 2 /FL=gb:U82277.1			
211106_at	0.02008	gb:AF064804.1 /DEF=Homo	AF064804		
		sapiens transcription factor			
		SUPT3H (SUPT3H) mRNA,			
		complete cds. /FEA=mRNA		•	
		/GEN=SUPT3H		ŧ	
		/PROD=transcription factor			
		SUPT3H /DB_XREF=gi:3283361			
		/UG=Hs.96757 suppressor of Ty			
		, , ,			
÷		(S.cerevisiae) 3 homolog		1.	
2444001	0.004704	/FL=gb:AF064804.1	A E 0 E 4 0 4 0		ND COOPE
211189_x_at	บ.บ31/04	gb:AF054816.1 /DEF=Homo	AF054816		NP_003865
٠		sapiens leukocyte differentiation		[· · · · .	-
		antigen CD84 isoform CD84a	4		* *
		(CD84) mRNA, complete cds.			
*		/FEA=mRNA /GEN=CD84		1	
		/PROD=leukocyte differentiation			
		antigen CD84 isoformCD84a			
		/DB_XREF=gi:6650107		* *	
		/UG=Hs.137548 CD84 antigen		1	
		(leukocyte antigen)	1		
·	*				

		ng to Figure 19 - Coronary Artery I		h	<u> </u>
Gene	p-value	Description	Gene	Unigene	Protein
ldentifier			Accession	Accession	Accession
	,		No.	No.	No.
211251_x at	0.026013	gb:U78774.1 /DEF=Human NFY-			NP_055038
		C mRNA, complete cds.		ļ.,	[· · · - · · · · · ·
		/FEA=mRNA /PROD=NFY-C			
100	.*				
		/DB_XREF=gi:2327008		l .	
• •		/UG=Hs.168157 nuclear		V.	
		transcription factor Y, gamma			
		/FL=gb:U78774.1			
211296_x_at	0.025284	gb:AB009010.1 /DEF=Homo	AB009010		NP_06628
· · · · · · · · · · · · · · · · · · ·		sapiens mRNA for polyubiquitin		•	_
		UbC, complete cds. /FEA=mRNA			1
	,	/GEN=UbC1 /PROD=polyubiquitin			
	,				;
- # · · · · ·		UbC /DB_XREF=gi:2647407			
	1.	/UG=Hs.183704 ubiquitin C]].
		/FL=gb:BC000449.1			ŀ
		gb:AB009010.1			<u> </u>
211372 s at	0.046749	gb:U64094.1 /DEF=Human	U64094		
#: ———————————————————————————————		soluble type II interleukin-1		*	
	}	receptor mRNA, complete cds.	\	\	1
					,
		/FEA=mRNA /PROD=soluble			
		type II interleukin-1 receptor			* .
		/DB_XREF=gi:1488065			
		/UG=Hs.25333 interleukin 1			
		receptor, type II			
•		/FL=gb:U64094.1			
211665_s at	0.046749	gb:L20686.1 /DEF=Homo	L20686		
211000_0_a	0.010740	sapiens guanine nucleotide		1.0	
• •		releasing factor (SOS2) mRNA,			
1		complete cds. /FEA=mRNA		ļ	
	-	/GEN=SOS2 /PROD=guanine		, .	
		nucleotide releasing factor			
		/DB_XREF=gi:1220367	1		
		/FL=gb:L20686.1			
211685_s at	0.026013	gb:AF251061.1 /DEF=Homo	AF251061		NP 11443
<u></u>		sapiens neurocalcin mRNA,	-3.331	1	
		1 · ·]]
-		complete cds. /FEA=mRNA			
	[·	/PROD=neurocalcin		*	1
		/DB_XREF=gi:13625183			
		/FL=gb:AF251061.1			
211749_s_at	0.046749	gb:BC005941.1 /DEF=Homo	BC005941		NP_00477
· — —	\	sapiens, Similar to vesicle-	•	1	
		associated membrane protein 3,	1		
•		clone MGC:14563, mRNA,			
		complete cds. /FEA=mRNA			
	1	/PROD=Similar to vesicle-			
	Ţ	associated membrane protein3	<u>, </u>	ļ	1
		/DB_XREF=gi:13543573			1
	1	/FL=gb:BC005941.1	1	1	1

Gene List Co		ng to Figur 19 - Coronary Artery			2.0000000000000000000000000000000000000
Gene	p-valu	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
	·		No.	No.	No.
211771 s at	0.03002	gb:BC006101.1 /DEF=Homo	BC006101	NO.	NP_002689
211//1_5_al	0.03002	1 4	1		NF_002009
] .	sapiens, Similar to POU domain,			٠.
	ł	class 2, transcription factor 2,			
		clone MGC:12814, mRNA,			
	'	complete cds. /FEA=mRNA			
		/PROD=Similar to POU domain,			,
		class 2, transcriptionfactor 2			
	i .	/DB_XREF=gi:13543912	·	·	
		/FL=gb:BC006101.1	1		
		// L-gb.bC000101.1			4
044700	0.010000	 	D0000477		115 00 1000
211783_s_at	0.018023	gb:BC006177.1 /DEF=Homo	BC006177		NP_004680
	· ·	sapiens, Similar to metastasis	. 1		
	1	associated 1, clone MGC:13258,		ŀ	• ,
		mRNA, complete cds.			
	,	/FEA=mRNA /PROD=Similar to			
• `	ŀ	metastasis associated 1			
•		/DB XREF=gi:13544097			
	l	/FL=gb:BC006177.1	Ta *	ļ.	
	<u> </u>				
211825_s_at	0.049425	gb:AF327066.1 /DEF=Homo	AF327066		
		sapiens Ewings sarcoma EWS-			
		Fli1 (type 1) oncogene mRNA,	1		,
		complete cds. /FEA=CDS			
		/PROD=Ewings sarcoma EWS-			
		<u> </u>		1	
		Fli1 (type 1) oncogene	1	•	
The second second		/DB_XREF=gi:12963354			
		/UG=Hs.129953 Ewing sarcoma			
		breakpoint region 1	·		
		/FL=gb:AF327066.1		-	
211883_x_at	0.034721		M76742		NP 001703
		sapiens alternatively spliced			
. *		biliary glycoprotein (BGPa)			
		1 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			-
		mRNA, complete cds.			1
		/FEA=CDS /GEN=BGPa			
		/PROD=biliary glycoprotein			
٠.		/DB_XREF=gi:179480			
		/UG=Hs.50964 carcinoembryonic	. '		
	1	antigen-related cell adhesion			
		molecule 1 (biliary glycoprotein)			
	1	/FL=gb:M76742.1			
04400	0.04000	1 150 105 11 1 15 15 1	1 = 10=1	ļ	100 000
211921_x_at	J 0.018023	gb:AF348514.1 /DEF=Homo	AF348514	*	NP_002814
	1	sapiens fetal thymus	I .	·	1
,	1	prothymosin alpha mRNA,			1
		complete cds. /FEA=CDS			•
	· [·	/PROD=prothymosin alpha			
	1	1	1		
	1 .	/DB_XREF=gi:13560658			1
	Į.	/FL=gb:AF348514.1	1	1	1

		ng to Figure 19 - Coronary Artery			
G ne	p-value	Description	Gene	Unig n	Protein
ld ntifier	:		Accession	Accession	Acc ssion
			No.	No.	No.
211922_s_at	0.025284	gb:AY028632.1 /DEF=Homo	AY028632		NP_001743
		sapiens catalase (CAT) mRNA,			1
A. C.		complete cds. /FEA=CDS	4		-
-		/GEN=CAT /PROD=catalase			
		/DB_XREF=gi:13562131			
		/FL=gb:AY028632.1		Lis et	
211932_at	0.034721	Homo sapiens BX1 mRNA, partial	BE867771	Hs.249247	
		cds			
211941_s_at		prostatic binding protein	BF686267	Hs.80423	NP_002558
211943_x_at	0.046749	tumor protein, translationally-	AL565449	Hs.279860	T. *
		controlled 1	* :	is en	
211948_x_at	0.026013	Consensus includes	AL096857	7-1	NP_055987
	14	gb:BG261071 /FEA=EST		Sp. J. Sec. 1	
		/DB_XREF=gi:12770887			
		/DB_XREF=est:602372693F1			
		/CLONE=IMAGE:4480631			
		/UG=Hs.69559 KIAA1096 protein		,	
			* **	.*	**************************************
211969_at	0.034721	Consensus includes	NM_005348		NP 005339
		gb:BG420237 /FEA=EST	'		
		/DB_XREF=gi:13326743			
		/DB_XREF=est:602448244F1	(
•		/CLONE=IMAGE:4586914			
		/UG=Hs.289088 heat shock		n de	
		90kD protein 1, alpha		*	•*
¥ .		/FL=gb:NM_005348.1			*
211986_at	0.018023	Homo sapiens cDNA FLJ33834 fis,	BG287862	Hs.378738	
		clone CTONG2004264,			*
		moderately similar to			
		NEUROBLAST			
	1.0	DIFFERENTIATION			
	71	ASSOCIATED PROTEIN AHNAK			•
211996_s_at	0.046749	KIAA0220 protein	BG256504	Hs.110613	
212001_at		Consensus includes	AB002363	X:	
-		gb:AV738039 /FEA=EST			
		/DB_XREF=gi:10855620		1	
		/DB_XREF=est:AV738039	•		
		/CLONE=CBFBDH07			
		/UG=Hs.190452 KIAA0365 gene			1
	1	product	1	I a second	i

Gene List Co	rrespondii	ng to Figure 19 - Coronary Artery	Disease		· = -
Gene	p-valu	D scription	Gene	Unigene	Protein
Identifier	-		Accession	Accession	Accession
	٠.		No.	No.	No.
212004 at	0.036254	Consensus includes	AL050028	INO.	NP 056424
212004_at	0.030234		AL030020	. <u>.</u>	INP_050424
	· .	gb:AL050028.1 /DEF=Homo			
		sapiens mRNA; cDNA		• .	1.
		DKFZp566C0424 (from clone		. ,	, `
	·	DKFZp566C0424); partial cds.	. * *		
		/FEA=mRNA			
**		/GEN=DKFZp566C0424			
		/PROD=hypothetical protein			
		/DB_XREF=gi:4884267			
	,	/UG=Hs.226770			
		DKFZP566C0424 protein	<u> </u>	,	
212030_at	0.025284	Homo sapiens cDNA: FLJ22454	BE466128	Hs.409075	
		fis, clone HRC09703		,	<u></u> _
212034_s_at	0.046749	likely ortholog of mouse exocyst	BE646386	Hs.325530	NP 056034
		component protein 70 kDa			-
	·	homolog (S. cerevisiae) Exo70:			
*	,	exocyst component protein 70 kDa	6 · · · · · · · · · · · · · · · · · · ·	t	
**		homolog (S. cerevisiae)	٠		
242027 04	0.024704		1400700		ND 000070
212037_at	0.034721	Consensus includes	Y09703	•	NP_002678
		gb:BF508848 /FEA=EST			
		/DB_XREF=gi:11592146	,		
		/DB_XREF=est:UI-H-BI4-aor-e-06-			
* .		0-UI.s1 /CLONE=IMAGE:3085907			
4.	ľ	/UG=Hs.44499 pinin, desmosome			+ - k - 1
		associated protein		·	
		lassociated protein			9
212056 at	0.024724	Concensus includes shipsoned d	D00004	,	
212036_at	0.034721	Consensus includes gb:D80004.1	D80004		•
•		/DEF=Human mRNA for	-		
		KIAA0182 gene, partial cds.			
		/FEA=mRNA /GEN=KIAA0182	٠,,		
		/DB_XREF=gi:1136423	· .	1.	
		/UG=Hs.75909 KIAA0182 protein			
· .					
			1,	,	
212061 at	0.040425	Consensus includes	AB002330		
212001_at	0.049425	· ·	AB002330		
4.		gb:AB002330.1 /DEF=Human		. 4	
		mRNA for KIAA0332 gene,		,	
		partial cds. /FEA=mRNA			
		/GEN=KIAA0332		÷	* *
		/DB XREF=gi:2224604			.
		/UG=Hs.7976 KIAA0332 protein			
		Consensus includes	AB011087		<u> </u>
212069 s at	0.033533	ICONSCISUS IIICIIOES			
212069_s_at	0.033533	•	1,001,1007		
212069_s_at	0.033533	gb:AK026025.1 /DEF=Homo	1,0011007		
212069_s_at	0.033533	gb:AK026025.1 /DEF=Homo sapiens cDNA: FLJ22372 fis,	1,100,1100,1		
212069_s_at	0.033533	gb:AK026025.1 /DEF=Homo sapiens cDNA: FLJ22372 fis, clone HRC06695. /FEA=mRNA	7.007		
212069_s_at	0.033533	gb:AK026025.1 /DEF=Homo sapiens cDNA: FLJ22372 fis, clone HRC06695. /FEA=mRNA /DB_XREF=gi:10438733	7.5077007		
212069_s_at	0.033533	gb:AK026025.1 /DEF=Homo sapiens cDNA: FLJ22372 fis, clone HRC06695. /FEA=mRNA	7.0011007		

	rrespondir	ng to Figure 19 - Coronary Artery	Dis ase		
Gene Identifier	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
212078 s at	0.019657	Consensus includes	NM 005933	NO.	NP 005924
		gb:AA704766 /FEA=EST		la de la companya de la companya de la companya de la companya de la companya de la companya de la companya de	
		/DB_XREF=gi:2714684			
		/DB_XREF=est:zj34h05.s1			
		/CLONE=IMAGE:452217			
		/UG=Hs.199160 myeloidlymphoid	•	Ì	1
		or mixed-lineage leukemia		1.	
		(trithorax (Drosophila) homolog)			
		/FL=gb:L04284.1			
		gb:NM_005933.1			
			T-12	· · · · · · · · · · · · · · · · · · ·	
212080_at	0.036254	Consensus includes	NM_005933		NP_005924
		gb:AV714029 /FEA=EST]	· ·	Ì
		/DB_XREF=gi:10795546			
		/DB_XREF=est:AV714029			
		/CLONE=DCBCDA03	100		ļ
		/UG=Hs.199160 myeloidlymphoid		-	
		or mixed-lineage leukemia (trithorax (Drosophila) homolog)			
		(//FL=qb:L04284.1			
,		gb:NM_005933.1			
	*	gb:NM_003933.1			
212087 s at	0.034721	Era G-protein-like 1 (E. coli)	AL562733	Hs.3426	NP 005693
212096_s_at		Consensus includes	AL096842		NP_065800
		gb:AL096842.1 /DEF=Homo			
		sapiens mRNA; cDNA			<u>;</u>
	1	DKFZp586D1519 (from clone			
		DKFZp586D1519). /FEA=mRNA			
		/DB_XREF=gi:5524930			
040404	0.00==00	/UG=Hs.7946 KIAA1288 protein	1111		ND 000446
212101_at	0.027792	Consensus includes	NM_012316		NP_036448
		gb:AU154321 /FEA=EST			
		/DB_XREF=gi:11015842	,		
	<u> </u>	/DB_XREF=est:AU154321 /CLONE=NT2RP4000774			
		/UG=Hs.301553 karyopherin			
		alpha 6 (importin alpha 7)			(
		/FL=gb:AF060543.1		•	
		gb:NM_012316.1			
212139_at	0.036254	Consensus includes gb:D86973.1	D86973		<u> </u>
		/DEF=Human mRNA for			
ĺ		KIAA0219 gene, partial cds.			
,		/FEA=mRNA /GEN=KIAA0219			
		/DB_XREF=gi:1504019			· ·
		/UG=Hs.75354 GCN1 (general			,
1		control of amino-acid synthesis			
		1, yeast)-like 1			
	1		1		

		ng to Figure 19 - Coronary Artery	Disease		
G ne Identifi r	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession
212144 at	0.034721	Consensus includes	AL021707	INO.	No.
212144_at	0.034721	gb:AL021707 /DEF=Human DNA	ALOZ 1707		
		19			
		sequence from clone RP3-	4 - 4		
		508I15 on chromosome 22q12-			
		13 Contains the gene for			
		GTPBP1 (GTP binding protein			
		1), two novel genes KIAA0063	_	ļ. ·	and the second
		and KIAA0668, a novel gene	-		
		based on ESTs and cDNA, a	1.0		
		pseudogene similar to AOP1		20 A	
		(antioxidant protein 1)			-
* .		/FEA=mRNA_3			
	, ,	/DB_XREF=gi:4582132	\		
		/UG=Hs.5898 KIAA0668 protein			
212155_at	0.046749	Homo sapiens, clone	AA085748	Hs.381076	
i 	•	IMAGE:3453993, mRNA, partial			
	·	cds	1 1 1		
212167_s_at	0.018023	Consensus includes	AK021419		NP_003064
	0.010020	gb:AK021419.1 /DEF=Homo	1.10		
		sapiens cDNA FLJ11357 fis,			
		clone HEMBA1000201, highly			
	* .				
		similar to Homo sapiens mRNA			
		for integrase interactor 1b		. '	
	1	protein (INI1B). /FEA=mRNA			
		/DB_XREF=gi:10432598			
		/UG=Hs 159971 SWISNF related,			
# · ·		matrix associated, actin	·		
	•	dependent regulator of			
		chromatin, subfamily b, member		-	
,]1			
			· ·		
212177_at	0.046749	Consensus includes	AL080186		NP_116259
		gb:AW081113 /FEA=EST		l .	
		/DB_XREF=gi:6036265			
		/DB_XREF=est:xc29c08.x1			Ţ
		/CLONE=IMAGE:2585678			
		/UG=Hs.18368 DKFZP564B0769	and the second		,
		protein			
212196_at	0.034721	Consensus includes	AL049265		
- 12 100_at	0.004721	gb:AW242916 /FEA=EST	7.5043203	, ,	
		1 -			
		/DB_XREF=gi:6576686			
		/DB_XREF=est:xn27f03.x1			
		/CLONE=IMAGE:2694941			
		/UG=Hs.71968 Homo sapiens			
		mRNA; cDNA DKFZp564F053			
	l	(from clone DKFZp564F053)		1	

		ng to Figur 19 - Coronary Artery I			
Gene	p-value	Description	Gen	Unigene	Prot in
ldentifier	. *	•	Accession	Accession	Accession
			No.	No.	No.
212202 s at	0.046749	Consensus includes	AF132733		NP_056312
		gb:BG493972 /FEA=EST	· · · · · · · · · · · · · · · · · · ·		
		/DB_XREF=gi:13455486	,		
		/DB XREF=est:602542252F1			
		/CLONE=IMAGE:4673316			
		/UG=Hs.16492 DKFZP564G2022			
	·	protein			
212221 et	0.046740	Consensus includes	AK001699		NP_296373
212231_at	0.046749		14001099		INF_29037
		gb:AB020682.1 /DEF=Homo	•		
		sapiens mRNA for KIAA0875			
		protein, partial cds. /FEA=mRNA	•		
1		/GEN=KIAA0875	* .		
1 - 1 - 1 - 1		/PROD=KIAA0875 protein	\$47	· ·	
		/DB_XREF=gi:4240238			
		/UG=Hs.184227 F-box only	·		1
<u> </u>		protein 21 /FL=gb:AF174601.1			
212237_at	0.034721	Consensus includes gb:N64780	AL117518		NP_05615
<u> </u>		/FEA=EST		, ,	
		/DB_XREF=gi:1212609	1		1
•		/DB_XREF=est:yz30f08.s1	ن د		
		/CLONE=IMAGE:284583			
	· . `	/UG=Hs.3686 KIAA0978 protein			l .
212251 at	0.018023	Homo sapiens LYRIC mRNA,	AI972475	Hs.395896	 - : - : - : - : - : - : - : - : - : -
212251_at	0.010023	complete cds	N372473	113.555555	·
212274 at	0.041705	Consensus includes	D80010		NP 66373
212214_al	0.041795				INF_005/3
		gb:AV705559 /FEA=EST		•	
		/DB_XREF=gi:10722858			,
		/DB_XREF=est:AV705559			
	l .	/CLONE=ADBAPE04			
<u> </u>	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	/UG=Hs.81412 lipin 1		 	ļ. <u>.</u>
212276_at	0.046749	Consensus includes gb:D80010.1	D80010		NP_66373
		/DEF=Human mRNA for			1
*		KIAA0188 gene, partial cds.			1
	1	/FEA=mRNA /GEN=KIAA0188			1
1.		/DB_XREF=gi:1136435	1	,	ļ
		/UG=Hs.81412 lipin 1	, ,		
				, `	
212291 at	0.028893	Consensus includes gb:Al393355	AB014530		NP_68990
		/FEA=EST	,		
*		/DB XREF=gi:4222902		,	
	1	/DB XREF=est:tg44d05.x1	1.	}	1.
	:	/CLONE=IMAGE:2111625			
		/UG=Hs.12259 KIAA0630 protein	. ^ `		
		1 13.12203 KIA KOOSO PIOLEIII		1	
21220F a at	0.019022	Homo sapiens, clone MGC:18288	ΔΙΛΙΑΕΩΕΩΩ	Hs.409092	+
212295_s_at	0.010023	· · · · · · · · · · · · · · · · · · ·	AW452623	1 19.409092	
	\	IMAGE:4179238, mRNA, complete	1	}	1
	1	cds		L	l

Gen	p-value	ng to Figure 19 - Coronary Artery Description	Gene	Unig ne	Protein
ldentifier	p-value	Description	Accession	Accession	Accession
lucillilei	•				
212206 at	0.046740	Consonalia includos	No. NM 005805	No.	No. NP 005796
212296_at	0.046749	Consensus includes	LIVINI_OOSOOS		NP_005/96
•		gb:NM_005805.1 /DEF=Homo			
		sapiens 26S proteasome-	. *		
		associated pad1 homolog			
		(POH1), mRNA. /FEA=CDS			
	•	/GEN=POH1 /PROD=26S			
		proteasome-associated pad1			
and "		homolog /DB_XREF=gi:5031980			
		/UG=Hs.178761 26S proteasome-			
		associated pad1 homolog			
		/FL=gb:U86782.1		-	
		gb:NM_005805.1		* · · · · · · · · · · · · · · · · · · ·	
212303 x at	0.018973	KH-type splicing regulatory protein	BG255575	Hs.91142	NP_003676
-		(FUSE binding protein 2)			
212314_at	0.025284	Consensus includes	AB018289	1	
	0.020201	gb:AB018289.1 /DEF=Homo	7 10200		
	, .	sapiens mRNA for KIAA0746			
		protein, partial cds. /FEA=mRNA		<i>√</i> ′	
40.0		/GEN=KIAA0746	10.5	}	
•		/PROD=KIAA0746 protein		1, 1	
	,	/DB_XREF=gi:3882212			
		/UG=Hs.49500 KIAA0746 protein			
0.100.10	0.040=40			-	
212318_at	0.046749	Consensus includes	NM_012470		NP_036602
		gb:NM_012470.1 _/ /DEF=Homo		<u>'</u>	1. 1
	·	sapiens transportin-SR (TRN-		,	
	• •	SR), mRNA. /FEA=CDS			
	,	/GEN=TRN-SR			
		/PROD=transportin-SR			
		/DB_XREF=gi:6912733]]	
				1	
•		I/UG=Hs.69235 transportin-SR	1	1.	
		/UG=Hs.69235 transportin-SR /FL=qb:NM 012470.1			
212351 at	0.018023	/FL=gb:NM_012470.1	U23028		
212351_at	0.018023	/FL=gb:NM_012470.1 Consensus includes gb:U23028.1			,
212351_at	0.018023	/FL=gb:NM_012470.1 Consensus includes gb:U23028.1 /DEF=Human eukaryotic initiation			
212351_at	0.018023	/FL=gb:NM_012470.1 Consensus includes gb:U23028.1 /DEF=Human eukaryotic initiation factor 2B-epsilon mRNA, partial			,
212351_at	0.018023	/FL=gb:NM_012470.1 Consensus includes gb:U23028.1 /DEF=Human eukaryotic initiation factor 2B-epsilon mRNA, partial cds. /FEA=mRNA /PROD=eIF-			,
212351_at	0.018023	/FL=gb:NM_012470.1 Consensus includes gb:U23028.1 /DEF=Human eukaryotic initiation factor 2B-epsilon mRNA, partial cds. /FEA=mRNA /PROD=eIF-2Bepsilon /DB_XREF=gi:806853			
212351_at	0.018023	/FL=gb:NM_012470.1 Consensus includes gb:U23028.1 /DEF=Human eukaryotic initiation factor 2B-epsilon mRNA, partial cds. /FEA=mRNA /PROD=eIF- 2Bepsilon /DB_XREF=gi:806853 /UG=Hs.2437 eukaryotic			
212351_at	0.018023	/FL=gb:NM_012470.1 Consensus includes gb:U23028.1 /DEF=Human eukaryotic initiation factor 2B-epsilon mRNA, partial cds. /FEA=mRNA /PROD=eIF-2Bepsilon /DB_XREF=gi:806853			

	rrespondir	ng to Figur 19 - Coronary Artery I	Disease		
G ne Identifier	p-value	D scription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
212372_at	0.020576	Consensus includes	AK026977	And And Andrew	-
		gb:AK026977.1 /DEF=Homo sapiens cDNA: FLJ23324 fis, clone HEP12482, highly similar to HUMMYOHCB Human			
		nonmuscle myosin heavy chain-B (MYH10) mRNA. /FEA=mRNA /DB_XREF=gi:10439970 /UG=Hs.296842 Homo sapiens, clone IMAGE:3357927, mRNA, partial cds			
212376_s_at	0.023856	E1A binding protein p400	BE880591	Hs.306094	NP 056224
212380_at	0.026013	Consensus includes gb:D43949.1 /DEF=Human mRNA for KIAA0082 gene, partial cds. /FEA=mRNA /GEN=KIAA0082 /DB_XREF=gi:603952 /UG=Hs.154045 KIAA0082 protein	D43949		NP_055865
212398_at	0.025284	Consensus includes gb:Al057093 /FEA=EST /DB_XREF=gi:3330969 /DB_XREF=est:oz23e12.x1 /CLONE=IMAGE:1676206 /UG=Hs.263671 Homo sapiens mRNA; cDNA DKFZp434I0812 (from clone DKFZp434I0812); partial cds	AL137751		
212399_s_at	0.018023	Consensus includes gb:D50911.2 /DEF=Homo sapiens mRNA for KIAA0121 protein, partial cds. /FEA=mRNA /GEN=KIAA0121 /PROD=KIAA0121 protein /DB_XREF=gi:6633996 /UG=Hs.155584 KIAA0121 gene product	D50911		
212426_s_at		tyrosine 3- monooxygenase/tryptophan 5- monooxygenase activation protein, theta polypeptide	BF033313	Hs.74405	NP_006817
212454_x_at	0.046749	heterogeneous nuclear ribonucleoprotein D-like	AI762552	Hs.170311	NP_112740

Gene List Co	rrespondir	ng to Figure 19 - Coronary Artery I	Diseas	T	
Gene Id ntifier		Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
212456_at	0.045316	Consensus includes gb:AB014564.1 /DEF=Homo sapiens mRNA for KIAA0664	AB014564		NP_056044
		protein, partial cds. /FEA=mRNA /GEN=KIAA0664 /PROD=KIAA0664 protein /DB_XREF=gi:3327141 /UG=Hs.22616 KIAA0664 protein			
212486 s_at	0.018023	ESTs	N20923	Hs.388309	
212503_s_at	0.034721	KIAA0934 protein	N31807	Hs.227716	
212514_x_at		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3	R60068	Hs.380774	NP_076829
212520_s_at	0.028893	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	Al684141	Hs.78202	NP_003063
212534_at	0.034721	Homo sapiens OVN6-2 mRNA, partial cds	AU144066	Hs.285519	
212538 at	0.034721		AL576253	Hs.8021	NP 056111
212539 at	0.034721	hypothetical protein FLJ22530	Al422099	Hs.14570	NP 078844
212546_s_at		Consensus includes gb:Al126634 /FEA=EST /DB_XREF=gi:3595148 /DB_XREF=est:qd83b10.x1 /CLONE=IMAGE:1736059 /UG=Hs.169600 KIAA0826 protein	AB020633		
212589_at	0.019292	related RAS viral (r-ras) oncogene homolog 2	BG168858	Hs.206097	NP_036382
212602_at	0.046749	ALFY	AI806395	Hs.198135	NP_848700
212607_at		Consensus includes gb:N32526 /FEA=EST /DB_XREF=gi:1152925 /DB_XREF=est:yy11f04.s1 /CLONE=IMAGE:270943 /UG=Hs.300642 serologically defined colon cancer antigen 8	U79271		NP_006633
212616_at	0.046749	Consensus includes gb:BF668950 /FEA=EST /DB_XREF=gi:11942845 /DB_XREF=est:602123069F1 /CLONE=IMAGE:4280153 /UG=Hs:10351 KIAA0308 protein	AB002306		NP_525127

		ng to Figure 19 - Coronary Artery		+	D-4-1
Gene	p-value	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
			No.	No.	No.
212622_at	0.034721	Consensus includes gb:N64760	D26067		
		/FEA=EST			
		/DB_XREF=gi:1212589	İ		
		/DB_XREF=est:yz30c06.s1		1	
		/CLONE=IMAGE:284554			
		/UG=Hs.174905 KIAA0033	e e		,
		protein			
212646 at	0.034721	Consensus includes gb:D42043.1	D42043		
	1	/DEF=Human mRNA for			
		KIAA0084 gene, partial cds.			,
		/FEA=mRNA /GEN=KIAA0084			
		/DB_XREF=gi:577298			
	Į.	/UG=Hs.79123 KIAA0084 protein			ļ. ·
			1		
. %	2. P				
040000 -+	0.046740	141A A 0220 in the	A1705000	11- 0700	ND 050400
212660_at		KIAA0239 protein	AI735639	Hs.9729	NP_056103
212674_s_at	0.034721	Consensus includes	AK002076		NP_619520
	.	gb:AK002076.1 /DEF=Homo		,	
	-	sapiens cDNA FLJ11214 fis,			
•		clone PLACE1007990.			
		/FEA=mRNA	1 :		
•		/DB_XREF=gi:7023738			
		/UG=Hs.281616 Homo sapiens			İ
	1	cDNA FLJ11214 fis, clone			
		PLACE1007990			
212690_at	0.018023	Consensus includes	AB018268		
		gb:AB018268.1 /DEF=Homo		•	· ·
	· .	sapiens mRNA for KIAA0725		,	
		protein, partial cds. /FEA=mRNA) .	
	Í	/GEN=KIAA0725			Ì
		/PROD=KIAA0725 protein			1.
		/DB_XREF=gi:3882170			
		/UG=Hs.26450 KIAA0725 protein		'	
-		7.00 110.20400 11.70 0720 protein		,	l
212692 s at	0.034721	LPS-responsive vesicle trafficking,	W60686	Hs.62354	NP_006717
2 12002_3_at	0.054721	beach and anchor containing	14400000	113.02334	_000717
		beach and anchor containing	1 .		
212693 at	0.040064	MDN1 midgein hamalas (ias = 1)	DE670000	Un 76720	ND 055400
		MDN1, midasin homolog (yeast)	BE670928	Hs.76730	NP_055426
212696 s at		ring finger protein 4	BF968633	Hs.66394	NP_002929
212704_at		KIAA0191 protein	AI049962	Hs.394825	
212720_at	0.034/21	poly(A) polymerase alpha	BG110231	Hs.49007	NP_116021

Gene		ng to Figure 19 - Coronary Artery I Description	Gene	Unigene	Protein
Identifier	p value		Accession	Accession	Accession
idelitillei			No.	No.	No.
212772 s at	0.034721	Consensus includes	AL162060	INO.	NP_001597
212112_5_at	0.034721	gb:AL162060.1 /DEF=Homo	AL 102000		NF_001397
•		•			
		sapiens mRNA; cDNA		. `	
		DKFZp547P193 (from clone			<u> </u>
		DKFZp547P193); partial cds.		,	
	7.3	/FEA=mRNA			
		/GEN=DKFZp547P193			*
	* .	/PROD=hypothetical protein			Į.
		/DB_XREF=gi:7328110			
		/UG=Hs.94806 KIAA1062 protein			
			,	,	1
212777_at	0.034721	Consensus includes gb:L13857.1	L13857		NP 005624
	*	/DEF=Human guanine nucleotide			
•		exchange factor mRNA,			
		complete cds. /FEA=CDS			
	. 7	/PROD=guanine nucleotide			
	7.			. *	
		exchange factor			
A Table		/DB_XREF=gi:306777	1.		
		/UG=Hs.326392 son of			
r		sevenless (Drosophila) homolog			
·		1 /FL=gb:L13857.1		1.	
212791_at		hypothetical protein FLJ38984	AL042729	Hs.112023	NP_689587
212798_s_at	0.018222	Consensus includes	AK001389		NP_064715
		gb:AK001389.1 /DEF=Homo			
		sapiens cDNA FLJ10527 fis,			
		clone NT2RP2000932, highly			
		similar to Homo sapiens mRNA;			
	7 · *	cDNA DKFZp564O043.			to a constant
		/FEA=mRNA			٠,
t Williams	· .	/DB_XREF=gi:7022618			1
ć .,	٠.	/UG=Hs.15144 hypothetical		1	1
		protein DKFZp564O043			
212804 s. at	0.025284	Consensus includes gb:Al797397	AK023841	+	100
212004_3_at	0.020204	/FEA=EST	/XIXU23041		
					4
		/DB_XREF=gi:5362869	1		
		/DB_XREF=est:we87f12.x1		1 .	
	,	/CLONE=IMAGE:2348111	4 ·		1
3		/UG=Hs.172069 DKFZP434C212			
-		protein		·	
212842_x_at	0.046749	RAN binding protein 2	AL043571	Hs.179825	NP_115636
212869_x_at		tumor protein, translationally-	AI721229	Hs.279860	NP_003286

		ng to Figure 19 - Coronary Artery			
Gene	p-value	Description	Gene	Unigene	Protein
ld ntifier		· '	Accession	Accession	Accession
	·		No.	No.	No.
212886 at	0.034721	Consensus includes	AL080169		NP 056436
·		gb:AL080169.1 /DEF=Homo			
<u> </u>		sapiens mRNA; cDNA	:		*
	*	DKFZp434C171 (from clone			•
	. •	DKFZp434C171); partial cds.			
		I/FEA=mRNA		<u> </u>	
		/GEN=DKFZp434C171			
		•			
		/PROD=hypothetical protein			
		/DB_XREF=gi:5262637			
		/UG=Hs.209100 DKFZP434C171			
		protein	<u> </u>		
212902_at		GTP-binding protein Sara	BE645231	Hs.279582	
212918_at	0.034721	RecQ protein-like (DNA helicase	BF219234	Hs.235069	NP_079130
		Q1-like)			
212927_at	0.034721	Consensus includes	AB011166	*	NP_055925
•		gb:AB011166.1 /DEF=Homo			
* · · ·		sapiens mRNA for KIAA0594			
- 1		protein, partial cds. /FEA=mRNA		4	
		/GEN=KIAA0594			
		/PROD=KIAA0594 protein		13°	[
		/DB_XREF=gi:3043711			1.
		/UG=Hs.103283 KIAA0594			
		protein			
212932_at	0.026013	Consensus includes	AK022494		-
2 12002_at	0.020010	gb:AK022494.1 /DEF=Homo	/ 11 (022-13-1		
		sapiens cDNA FLJ12432 fis,			
		clone NT2RM1000018, highly			
		similar to Human mRNA for			
		KIAA0066 gene. /FEA=mRNA			
		/DB_XREF=gi:10433912			* * *
	ļ	/UG=Hs.227881 RAB3 GTPase-			
		ACTIVATING PROTEIN			
	0.018222		BE543527	Hs.16411	
213006_at	0.034721	CCAAT/enhancer binding protein	AV655640	Hs.76722	NP_005186
	<u> </u>	(C/EBP), delta			
213018_at	0.034721	ocular development-associated	Al337901	Hs.21145	NP_066990
		gene			
213022 s at	0.046749	Consensus includes	NM 007124		NP 009055
- (-, -		gb:NM_007124.1 /DEF=Homo	\		i –
		sapiens utrophin (homologous to		,	
٠ . ن	1	dystrophin) (UTRN), mRNA.		1	1
		/FEA=CDS /GEN=UTRN		1	*
		/PROD=utrophin	}		
		//DB_XREF=gi:6005937		1	
		/UG=Hs.251967 utrophin			1
			20		
•	· ·	(homologous to dystrophin)	1	1]
	L	/FL=gb:NM_007124.1	L	<u></u>	

		ig to Figure 19 - Coronary Artery I		3 2 1 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
Gene	p-value	Description	G n	Unigene	Protein
ldentifier			Accession	Accession	Accession
	·	<u></u>	No.	No.	No.
213041_s_at	0.046749	ATP synthase, H+ transporting,	BE798517	Hs:89761	NP_001678
		mitochondrial F1 complex, delta			
		subunit			٠.
213079_at	0.025284	hypothetical protein DT1P1A10	AA223871	Hs.178207	NP_477511
213088_s_at	0.025284	DnaJ (Hsp40) homolog, subfamily	BF240590	Hs.44131	
		C, member 9			.*
213089_at	0.019657	ESTs, Highly similar to T17212	AU158490	Hs.356638	
		hypothetical protein			
		DKFZp434P211.1 - human		1,000	
		(fragments) [H.sapiens]			
213104_at	0.025284	Consensus includes gb:Al799802	AL031709		
		/FEA=EST			
1.5	<u> </u>	/DB_XREF=gi:5365274	,		
		/DB_XREF=est:wc43d09.x1			*
	. * *	/CLONE=IMAGE:2321393			
		/UG=Hs.134846 Human DNA	p.		
		sequence from clone 316G12			
		on chromosome 16. Contains			
		the gene for C2 domain protein		1	}
•		KIAA0734, the gene for a novel		-	•
		protein similar to predicted			
		yeast, worm and archae-bacterial			
	· .	proteins, a novel gene and the			
	l i	3 part of the gene for a novel		ļ	\ .
		prot			
213134 x at	0.025284	BTG family, member 3	AI765445	Hs.77311	NP_006797
213156 at		Consensus includes	AL049423		
- · · - · · - · · · · · · · · · · · · ·		gb:BG251521 /FEA=EST			
	2.1	/DB_XREF=gi:12761337			1
	<u>'</u>	/DB_XREF=est:602363985F1	\		ì.
		/CLONE=IMAGE:4472180			
		/UG=Hs 16193 Homo sapiens		:	,
		mRNA; cDNA DKFZp586B211		'	
		(from clone DKFZp586B211)			
213164 at	0.034721	ESTs, Weakly similar to A43932	AI867198	Hs.389698	NP_008864
	0.004,21	mucin 2 precursor, intestinal -			
	·	human (fragments) [H.sapiens]			
213187 x at	0.046749	ferritin, light polypeptide	BG538564	Hs.111334	
. 10 101 _ X_at_	10.040148	herrigh, iight polypeptide	1000004	1113.111334	l

Gene List Co	rrespondir	ng to Figure 19 - Coronary Artery I	Disease		
Gene	p-value	Description	Gene	Unigene	Protein
Identifier	·		Accession	Accession	Accession
, , , , , , , , , , , , , , , , , , , ,		·	No.	No.	No.
213213 at	0.025284	Consensus includes	AL035669		
	Lantara.	gb:AL035669 /DEF=Human DNA			
		sequence from clone RP5-885L7			
		on chromosome 20q13.2-13.33			
		Contains ESTs, STSs, GSSs			
		and eight CpG islands. Contains	,		
	· ·	the 3 end of the NTSR1 gene			
	·	for high affinity neurotensin		1	
		receptor 1, a putative novel			
		gene, a novel gene similar to a			• .
		f /FEA=mRNA 3		1.	· ·
* *	+ 1	/DB_XREF=gi:8979786			
			ļ		ļ ·
	·	/UG=Hs.155313 death associated			
		transcription factor 1			
040000	0.040740		4 4 40000 4	17 400000	NE 004005
213233_s_at		KIAA1354 protein	AA460694	Hs.106283	NP_061335
213262_at	0.025284	spastic ataxia of Charlevoix-	Al932370	Hs 159492	NP_055178
	01040000	Saguenay (sacsin)			
213274_s_at		cathepsin B	BE875786	Hs.297939	NP_680093
213280_at	0.025284	Consensus includes	AK000478	1	
		gb:AK000478.1 /DEF=Homo			
		sapiens cDNA FLJ20471 fis,			
	}	clone KAT06974. /FEA=mRNA			·
1		/DB_XREF=gi:7020593	/		
i		/UG=Hs.301552 KIAA1039	· .		
		protein			
213331_s_at	0.027792	Consensus includes	AL050385	* -	
		gb:AV700007 /FEA=EST		ļ ·	1 1
	-	/DB_XREF=gi:10301978			
		/DB_XREF=est:AV700007			
·		/CLONE=GKCBQC12			
		/UG=Hs.48332 NIMA (never in			
		mitosis gene a)-related kinase 1			
213333_at	0.023856	malate dehydrogenase 2, NAD	AL520774	Hs.343521	NP_005909
		(mitochondrial)			
213353_at	0.018023	ATP-binding cassette, sub-family A	BF693921	Hs.180513	NP_758424
		(ABC1), member 5	<u> </u>	<u></u>	<u></u>
213355_at	0.031704	Consensus includes gb:Al989567	AK001922		NP_006091
		/FEA=EST		,	
		/DB_XREF=gi:5836448			
		/DB_XREF=est:ws34e03.x1		-	
		/CLONE=IMAGE:2499100			
		/UG=Hs.34578 alpha2,3-			*4
,		sialyltransferase	l	Į.	

		ng to Figure 19 - Coronary Artery I	Diseas	<u> </u>	
Gene	p-value	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
			No.	No.	No.
213434_at	0.019657	ESTs, Weakly similar to cytokine	H95263	Hs.408811	
		receptor-like factor 2; cytokine		lang en de de	
* 1		receptor CRL2 precusor [Homo			•
		sapiens] [H.sapiens]			
213448_at	0.018222		Al693193	Hs.247551	NP 002446
213475_s_at	0.025284	Consensus includes	AC002310		
— —		gb:AC002310 /DEF=Human		ĺ	
	·	Chromosome 16 BAC clone			
		CIT987SK-A-635H12			
		/FEA=mRNA 2			
	-	/DB_XREF=gi:2576342			
		/UG=Hs.174103 integrin, alpha L			
		(antigen CD11A (p180),			
		lymphocyte function-associated			
1.		antigen 1; alpha polypeptide)			
213483 at	0.018023	Consensus includes	AK025679		NP_056157
210400_at	0.010023	gb:AK025679.1 /DEF=Homo	A11023079		NF_030137
		sapiens cDNA: FLJ22026 fis,		1.1	1 1 1
		clone HEP08537. /FEA=mRNA			Ì
		/DB_XREF=gi:10438273	•		
P2		/UG=Hs.1191 KIAA0073 protein			
213494 s at	0.027702	YY1 transcription factor	AA748649	Hs.97496	NP_003394
213504_at		COP9 subunit 6 (MOV34 homolog,	W63732	Hs.15591	
213504_at	0.049425	34 kD)	VVQ3/32	Ins. 15591	NP_006824
213521_at	0.025284		ANALEZEOZO	11- 050450	
			AW575379	Hs.356456	ND 050500
213524_s_at	0.036254	Consensus includes	NM_015714	1.5	NP_056529
	i	gb:NM_015714.1 /DEF=Homo			
		sapiens putative lymphocyte			
	ļ	G0G1 switch gene (G0S2),			ļ.
	-	mRNA. /FEA=CDS /GEN=G0S2			
		/PROD=putative lymphocyte			ŀ
		G0G1 switch gene	· .		· ·
		/DB_XREF=gi:7657103			l .
•		/UG=Hs.95910 putative			
		lymphocyte G0G1 switch gene	\		
···		/FL=gb:NM_015714.1			
213527_s_at	0.048741	similar to hypothetical protein	Al350500	Hs.301463	NP_660314
		MGC13138			

	rrespondii	ng to Figure 19 - Coronary Artery	Disease		<u> </u>
Gene	p-value	Description	Gene	Unigene	Protein
ldentifier	[• • • •	Accession	Accession	Accession
	1		No.	No.	No.
213546 at	0.046749	Consensus includes	AL050378	110.	NP_689960
	0.0 107 10	gb:AL050378.1 /DEF=Homo	1.12000010		_009900
		sapiens mRNA; cDNA			1.
		DKFZp586I1420 (from clone			
				1	
	}	DKFZp586I1420); partial cds.	}	,	1 .
		/FEA=mRNA			
		/GEN=DKFZp586I1420			
		/PROD=hypothetical protein		·	
-	·	/DB_XREF=gi:4914581			
		/UG=Hs.112423 Homo sapiens		1	1.
		mRNA; cDNA DKFZp586l1420		·	
		(from clone DKFZp586I1420);			
		partial cds	i		
213551_x_at	0.019292	zinc finger protein 144 (Mel-18)	Al744229	Hs.184669	
213587 s at	0.018023	vacuolar proton-ATPase subunit	AI884867	Hs.351612	
213605_s_at		Consensus includes	AL049987		
		gb:AL049987.1 /DEF=Homo		1	•
		sapiens mRNA; cDNA		`.	1.
		DKFZp564F112 (from clone	100		1
		DKFZp564F112). /FEA=mRNA			
	Ì	/DB_XREF=gi:4884238		Ì	
		/UG=Hs.166361 Homo sapiens		-	
	Į.	mRNA; cDNA DKFZp564F112			
040000	0.000010	(from clone DKFZp564F112)	1 1 100-00		
213620_s_at		intercellular adhesion molecule 2	AA126728	Hs.347326	<u> </u>
213639_s_at	0.035763	Consensus includes gb:Al871396	AB011129		1
	l,	/FEA=EST		1	
		/DB_XREF=gi:5545445			
		/DB_XREF=est:wl81f07.x1		}	
		/CLONE=IMAGE:2431333			
		/UG=Hs.101414 KIAA0557			
		protein	1		
213677_s_at	0.018222	PMS1 postmeiotic segregation	BG434893	Hs.111749	NP_000525
- -		increased 1 (S. cerevisiae)			-
213686 at	0.034721		Al186145	Hs.404749	
213698 at		zinc finger protein 258	AI805560	Hs.301637	NP_660353
213703_at		Homo sapiens cDNA FLJ33034 fis,		Hs.349607	NP 787049
, oo_a.	0,0200.0	clone THYMU2000236	1133043	113.545,007	- 7 0 7 0 4 3
213704 at	0.046749	Rab geranylgeranyltransferase,	AA129753	Hs.78948	NP 004573
219704_at	0.040743	beta subunit	A 129733	115,70540	JNF_004573
213742 at	0.010202		0101044750	Ho 11100	ND 004750
213/42_at	0.019292	splicing factor, arginine/serine-rich	AW241752	Hs.11482	NP_004759
040005	0.040745	[11]	NIGOS (S S	11. 65555	ļ., <u>s</u>
213805_at	U.046749	ESTs, Weakly similar to neuronal	Al692428	Hs.392055	NP_057090
		thread protein [Homo sapiens]		1	1
	<u> </u>	[H.sapiens]			<u> </u>
213830_at	I N NAR741	immunoglobulin heavy constant	AW007751	Hs.300697	
213030_at	[0.070771	minumograpumi nadvy constant	1,	113.000007	1

		ng to Figure 19 - Cor nary Artery I			
Gene	p-value	Description	G ne	Unigene	Protein
ldentifier			Accession	Accession	Accession
			No.	No.	No.
213843 x at	0.038535	solute carrier family 6	AW276522	Hs.187958	NP 005620
	\	(neurotransmitter transporter,		'	
		creatine), member 8			
213849 s at	0.018023	protein phosphatase 2 (formerly	AA974416	Hs.7688	NP 004567
- -		2A), regulatory subunit B (PR 52),			_
	ļ. ·	beta isoform	`		<u> </u>
213867 x at	0.046749	actin, beta	AA809056	Hs.288061	NP 001092
213872 at		hypothetical protein FLJ12619	BE465032	Hs.7779	NP_112201
213876_x_at		U2 small nuclear ribonucleoprotein	AW089584	Hs.171909	V 14
		auxiliary factor, small subunit 2			
213878 at	0.025284	RecQ protein-like (DNA helicase	Al685944	Hs.235069	NP_079130
		Q1-like)			
213892 s at	0.034721	adenine phosphoribosyltransferase	AA927724	Hs.28914	NP_000476
	1.				
213906 at	0.025284	v-myb myeloblastosis viral	AW592266	Hs.300592	
		oncogene homolog (avian)-like 1	7.7		
213915 at	0.025284	Consensus includes	NM_005601	<u> </u>	NP_005592
	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gb.NM_005601.1 /DEF=Homo			
	, "	sapiens natural killer cell group			
	· ·	7 sequence (NKG7), mRNA.	•		
	;	/FEA=CDS /GEN=NKG7			
		/PROD=natural killer cell group			
•		7 sequence		,	
-		/DB_XREF=gi:5031948		4 1	
•	,	/UG=Hs.10306 natural killer cell			
		group 7 sequence			
		/FL=gb:NM_005601.1	· .		
213931_at	0.018023	inhibitor of DNA binding 2,	AI819238	Hs.180919	NP 002157
		dominant negative helix-loop-helix			
		protein			l
213932_x_at	0.018023	major histocompatibility complex,	Al923492	Hs.77961	NP_002107
	0.0100,20	class I, C	1		
213936 x at	0.049425	ESTs, Moderately similar to	AW276646	Hs.355462	
		hypothetical protein FLJ20294		\	,
		[Homo sapiens] [H.sapiens]			
213947 s at	0.031704	nucleoporin 210	AI867102	Hs.56966	NP_079199
213971_s_at		joined to JAZF1	Al924660	Hs.197803	NP 056170
213982 s_at		KIAA0471 gene product	BG107203	Hs.242271	NP_055672
213988 s_at		spermidine/spermine N1-	BE971383	Hs.396709	NP_002961
2 10000_5_ac	0.040140	acetyltransferase	15207 1000	115.5557.55	141 _002001
214032 at	0.036254	ESTs, Highly similar to	AI817942	Hs.406272	
217002_at	0.030234	ZA70_HUMAN Tyrosine-protein	17.1017.342	1113.400272	
7		kinase ZAP-70 (70 kDa zeta-			
	1				
	,	associated protein) (Syk-related			
214054: 54	0.040000	tyrosine kinase) [H.sapiens]	A1929020	Ho 74045	ND COROS
214054_at		docking protein 2, 56kDa	AI828929	Hs.71215	NP_003965
214055_x_at	T 0.018222	KIAA1096 protein	AW238632	Hs.69559	NP_055987

		ng to Figure 19 - Coronary Artery	4.7	Uning	B-4-
Gene	p-value	Description	Gene	Unigene	Protein
ldentifier			Accession	Accession	Accession
011000			No.	No.	No.
214059_at	0.042466	Fc fragment of IgG, low affinity Ilb,	BE049439	Hs.82316	NP_006408
		receptor for (CD32)			<u> </u>
214061_at		unknown MGC21654 product	AI017564	Hs.392896	NP_663622
214131_at	0.021876	Consensus includes	AL049280		NP_115965
		gb:AL049280.1 /DEF=Homo			
		sapiens mRNA; cDNA		·	
	4	DKFZp564K143 (from clone			ţ
		DKFZp564K143). /FEA=mRNA	,		
	1	/DB_XREF=gi:4500037			
		/UG=Hs.155397 Homo sapiens			Y
•		mRNA; cDNA DKFZp564K143			
•		(from clone DKFZp564K143)		· .	
214163 at	0.018222	HSPCO34 protein	AV700696	Hs.46967	
214241 at		NADH dehydrogenase	AA723057	Hs.198273	NP 00499
		(ubiquinone) 1 beta subcomplex, 8,	'	110.100270	1.00,000
	•	19kDa			ŀ .
214246 x at	0.034721	Misshapen/NIK-related kinase	AI859060	Hs.112028	NP 00007
214240_x_at 214257_s_at		SEC22 vesicle trafficking protein-	AA890010	Hs.50785	NP_00488
214201_5_al	0.010023	1	1777090010	[HS.50765	INF_00400
214200 1/104	0.010022	like 1 (S. cerevisiae)	AL568374	IJ- 00000	ND 66500
214298_x_at				Hs.90998	NP_66580
214308_s_at	0.027239	homogentisate 1,2-dioxygenase	Al478172	Hs.15113	NP_00017
044044	0.040405	(homogentisate oxidase)	DE400047	11- 450000	
214314_s_at		translation initiation factor IF2	BE138647	Hs.158688	100 00400
214315_x_at		calreticulin	Al348935	Hs.16488	NP_00433
214327_x_at	0.018023	tumor protein, translationally-	AI888178	Hs.279860	NP_00328
 		controlled 1			<u> </u>
214339_s_at	0.018222	mitogen-activated protein kinase	AA744529	Hs.86575	NP_00911
	·	kinase kinase 1			<u> </u>
214435_x_at	0.046749	Consensus includes	NM_005402		NP_00539
		gb:NM_005402.1 /DEF=Homo			
i. 1		sapiens v-ral simian leukemia			* .
		viral oncogene homolog A (ras	-		İ
		related) (RALA), mRNA.			1
		/FEA=CDS /GEN=RALA			
	ļ ·	/PROD=v-ral simian leukemia		.E	
		viral oncogene homolog A(ras			
		related) /DB_XREF=gi:4885568			
		/UG=Hs.288757 v-ral simian			
		leukemia viral oncogene			
		homolog A (ras related)	1		
	ļ	//FL=gb:M29893.1	1		}

		ng to Figure 19 - Coronary Artery I			
Gene	p-value	Description	Gen	Unigene	Protein
Identifier	•		Accession	Accession	Accession
**			No.	No.	No.
214455 at	0.034721	Consensus includes	NM_003526		NP 003517
And Tall is		gb:NM_003526.1 /DEF=Homo			
ta ta ta ta t		sapiens H2B histone family,			J.
		member L (H2BFL); mRNA.	A Company		
		, · · · · ·	,		, i
		/FEA=CDS /GEN=H2BFL	. :	1	
		/PROD=H2B histone family,			
		member L	٠.		
*		/DB_XREF=gi:4504272			
	,	/UG=Hs.239884 H2B histone			·
		family, member L		•.	
		/FL=gb:NM 003526.1		l	
214459_x_at	0.034721	Consensus includes gb:M12679.1	M12679		
		/DEF=Human Cw1 antigen	\		\
		mRNA, complete cds.	· ·		· ·
		/FEA=mRNA /GEN=HLA-C			1
		/DB XREF=gi:187911			
				ļ.	
		/UG=Hs.274485 Cw1 antigen	**		
		/FL=gb:M12679.1			
214483_s_at	0.046749	Consensus includes	AF124489	•	NP_055262
		gb:AF124489.1 /DEF=Homo			
•		sapiens arfaptin-1b mRNA,			
		alternatively spliced, complete			•
		cds. /FEA=CDS /PROD=arfaptin-			
		1b /DB_XREF=gi:4761515		}	\ .
		/UG=Hs.301064 arfaptin 1			
		/FL=gb:AF124489.1			
*		// L gb./ (124400.1			
214513 s at	0.036254	Consensus includes gb:M34356.1	M3/356		NP 604391
2 145 15_5_at	0.030234	/DEF=Human active transcription	10134330		141 _004591
	ļ		ļ.	1	·
·		factor CREB mRNA, complete			
	1	cds. /FEA=CDS		1	
		/DB_XREF=gi:181042	. :		
		/UG=Hs.79194 cAMP responsive			[]
		element binding protein 1		-	
		/FL=gb:M34356.1		1	
				<u> </u>	
214525_x at	0.038017	Consensus includes	AB039667		NP_055196
		gb:AB039667.1 /DEF=Homo	I		
•	ŀ	sapiens mRNA for DNA			
		mismatch repair protein MLH3,			
	1	complete cds. /FEA=CDS	1		1
		1 7 "			
		/GEN=MLH3 /PROD=DNA	· .		4.
,		mismatch repair protein MLH3			
		/DB_XREF=gi:7209865			
		/UG=Hs.279843 mutL (E. coli)			
		homolog 3 /FL=gb:AB039667.1		<u> </u>	1
214657_s_at	0.018023	Human clone 137308 mRNA,	AU134977	Hs.408944	, , , , , , , , , , , , , , , , , , ,
	Ī	partial cds	1	1	1

Gene List Co		ng to Figure 19 - Coronary Artery I			
Gene	p-value	Description	G ne	Unigene	Protein
Identifier			Accession	Accession	Accession
	ļ		No.	No.	No.
214661_s at	0.040064	gene near HD on 4p16.3 with	R06783	Hs.117487	140.
2 1400 1_3_at	0.040004	homology to hypothetical S. pombe		1113.117407	
1 1					,
	<u> </u>	gene			
214688_at	0.046749	transducin-like enhancer of split 4	BF217301	Hs.83958	+-
·	<u> </u>	(E(sp1) homolog, Drosophila)			<u> </u>
214697_s_at	0.034721	ROD1 regulator of differentiation 1	AW190873	Hs.145078	NP_005147
. , – .		(S. pombe)			
214721 x at	0.025284	Consensus includes	AL162074	Bertin Strain	NP_036253
- · · · · - · <u>-</u> · · <u>-</u> · · ·		gb:AL162074.1 /DEF=Homo			
		sapiens mRNA; cDNA			
	1 '				
	1	DKFZp762L106 (from clone	1	1	<u></u>
,		DKFZp762L106); partial cds.			
<u>.</u>	, ,	/FEA=mRNA			
	ļ	/GEN=DKFZp762L106	į		
		/PROD=hypothetical protein			'
•		/DB XREF=gi:7328153			
		/UG=Hs.3903 Cdc42 effector			
		protein 4; binder of Rho			
	1	17.7			
<u> </u>	<u> </u>	GTPases 4		 	
214730_s_at	0.046749	Consensus includes	AK025457		NP_036333
		gb:AK025457.1 /DEF=Homo			
	1	sapiens cDNA: FLJ21804 fis,			
		clone HEP00746, highly similar			
	1	to HSU64791 Human Golgi	•		,
'		membrane sialoglycoprotein	1: .	-1	, .
ì	1	MG160 (GLG1) mRNA.		1 1	
			1		,
		/FEA=mRNA]		
	ļ:	/DB_XREF=gi:10437977	ļ	<u> </u>	
·		/UG=Hs.78979 Golgi apparatus			
		protein 1	1		
214739 at	0.025284	hypothetical protein MGC4126	AI357539	Hs.289038	NP 116162
214741 at		zinc finger protein 131 (clone pHZ-	AW968301	Hs.78743	
		(10)	,	1	
214749_s_at	0.046740	Consensus includes	AK000818	 	NP_061880
2 14/45_5_al	0.040749		AK000010		NF_00100C
		gb:AK000818.1 /DEF=Homo			
	1	sapiens cDNA FLJ20811 fis,	ļ	ļ	
		clone ADSE01435. /FEA=mRNA	1		ŀ
		/DB_XREF=gi:7021128			
		/UG=Hs.83530 hypothetical			
1	1	protein			
		le, arail,			
214752 4 =4	0.019000	filomin A sinho (actin hinding	AIGOEFEO	Un 220270	ND 00144
214752_x_at	0.018023	filamin A, alpha (actin binding	Al625550	Hs.328270	NP_001447
I		protein 280)		1	ľ

Gene List Co	rrespondir	ng to Figure 19 - Coronary Artery I	Disease		
Gene	p-valu	Description	Gene	Unigene	Protein
Identifier	,	,	Accession	Accession	Accession
idonani,		•	No.	No.	No.
214765 s at	0.026013	Consensus includes	AK024677	NO.	NP 055250
217705_3_at	0.020013	gb:AK024677.1 /DEF=Homo	/\.\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	-	141 _055250
				·	
.0		sapiens cDNA: FLJ21024 fis,			
	* *	clone CAE06651, highly similar			
		to HUMPLT Human LTR mRNA.			
	i i	/FEA=mRNA			'
	,	/DB_XREF=gi:10437016			
	٠ .	/UG=Hs.264330 N-	:		
		acylsphingosine amidohydrolase			
		(acid ceramidase)-like			
214785 at	0.046749	Consensus includes	AB023203		NP_150648
· -		gb:AB023203.1 /DEF=Homo			
i de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya della companya della companya de la companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya dell		sapiens mRNA for KIAA0986			
		protein, partial cds. /FEA=mRNA		, t	
•		/GEN=KIAA0986	!		
•		/PROD=KIAA0986 protein			
				200	* 1
	. "	/DB_XREF=gi:4589615			
		/UG=Hs.53542 KIAA0986 protein			
214791_at	0.025284	Consensus includes	AK023116		NP_612411
•		gb:AK023116.1 /DEF=Homo			
	-	sapiens cDNA FLJ13054 fis,			
		clone NT2RP3001527, highly			
	}	similar to Human Sp140 protein			
	•	(Sp140) mRNA /FEA=mRNA			.*
		/DB_XREF=gi:10434889			
		/UG=Hs.158761 Homo sapiens			
		cDNA FLJ13054 fis, clone			
		NT2RP3001527, highly similar to			
		Human Sp140 protein (Sp140)			1
		mRNA],		
		IIIKNA			
044700 -4	0.000047	KIAA0702	A14/004 CC4	1)- 0400	
214798_at		KIAA0703 gene product	AW291664	Hs.6168	
214869_x_at	0.018023	Consensus includes	AK021533		·
		gb:AK021533.1 /DEF=Homo		i .	
		sapiens cDNA FLJ11471 fis,		1	, .
4 *		clone HEMBA1001675, weakly			
:		similar to VACUOLAR PROTEIN			
	* 4	SORTING-ASSOCIATED			
		PROTEIN VPS9. /FEA=mRNA			
		/DB_XREF=gi:10432733			
		/UG=Hs.306601 Homo sapiens	٠,	1	
	· ·	cDNA FLJ11471 fis, clone			
•		HEMBA1001675, weakly similar			• •
		to VACUOLAR PROTEIN	٠.		
				· ·	
]	SORTING-ASSOCIATED]	
		PROTEIN VPS9		1	
L	<u> </u>	I	1	<u></u>	L

Gene	p-valu	ng to Figure 19 - Coronary Artery l Description	Gene	Unigene	Protein
ld ntifier	الم ترسي		Accession	Accession	Accession
id illiloi		*	No.	No.	No.
214895_s_at	0.046749	a disintegrin and metalloproteinase		Hs.172028	NP_001101
2 14000_3_4	0.040743	domain 10	100 100 10-		
214946_x_at	0.046740	hypothetical protein FLJ10824	AV728658	Hs.13273	
214948_s_at		Consensus includes	AL050136	115.13213	
2 14940_5_at	0.040749	gb:AL050136.1 /DEF=Homo	AL030130		,
		sapiens mRNA; cDNA		,	
	*				
		DKFZp586L141 (from clone			
		DKFZp586L141). /FEA=mRNA			
		/DB_XREF=gi:4884346			
•	, .	/UG=Hs.140945 Homo sapiens	*		1.
		mRNA; cDNA DKFZp586L141			
11111111111		(from clone DKFZp586L141)			<u> </u>
214974_x_at	0.034721	Consensus includes	AK026546		NP_002985
		gb:AK026546.1 /DEF=Homo			
		sapiens cDNA: FLJ22893 fis,			
		clone KAT04792. /FEA=mRNA	ļ.		
		/DB_XREF=gi:10439427			
		/UG=Hs.287716 Homo sapiens			
		cDNA: FLJ22893 fis, clone			
· ·	ľ	KAT04792	•		
215012_at	0.036254	coactivator for steroid receptors	AU144775	Hs.172329	NP_056370
215040_at	0.021876	Consensus includes	AL049218	4 447	
		gb:AL049218.1 /DEF=Homo			
		sapiens mRNA; cDNA			
		DKFZp564I1916 (from clone			
		DKFZp564I1916). /FEA=mRNA			3.,
ı		/DB XREF=gi:4499947		,	¥
	1	/UG=Hs.306291 Homo sapiens	i .		
~	1	mRNA; cDNA DKFZp564I1916			
1		(from clone DKFZp564I1916)		4	
215075_s_at	0.025284	Consensus includes gb:L29511.1	L29511	 	NP_002077
2 10070_3_ac	0.020204	/DEF=Human GRB2 isoform	L29311	·	_002077
		mRNA /FEA=mRNA			
		/PROD=growth factor receptor-			
	[l .		
		bound protein 3			
•		/DB_XREF=gi:460667			
		/UG=Hs.296381 growth factor			
		receptor-bound protein 2	·	l .	1

Gene	p-value	Description	Gene	Unigene	Protein
Identifier	Ī		Accession	Accession	Accession
1 -	· ·		No.	No.	No.
215078 at	0.019292	Consensus includes	AL050388	1101	NP_000627
		gb:AL050388.1 /DEF=Homo			
		sapiens mRNA; cDNA			
		DKFZp564M2422 (from clone]	1
	1.	DKFZp564M2422); partial cds.			\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
•		/FEA=mRNA			
		/GEN=DKFZp564M2422		1. 1.	1
•		/PROD=hypothetical protein	· · ·		
	·	/DB_XREF=gi:4914612			
, 1		/UG=Hs.306320 Homo sapiens		\$	
٠		mRNA; cDNA DKFZp564M2422	1		
+ 1		(from clone DKFZp564M2422);			
		partial cds	•	1	
215111_s_at	0.034721	Consensus includes	AK027071		NP_006013
		gb:AK027071.1 /DEF=Homo			
	٠,	sapiens cDNA: FLJ23418 fis,		Territoria,	
		clone HEP21245, highly similar			
	•	to HSU35048 Human TSC-22		• •	
		protein mRNA. /FEA=mRNA			
		/DB_XREF=gi:10440100			
		/UG=Hs.114360 transforming			
	1	growth factor beta-stimulated			
•	1.5	protein TSC-22			
215114_at	0.035763	Consensus includes	AK000923		NP_056485
		gb:AK000923.1 /DEF=Homo	, (0.0 0.20		-000 100
		sapiens cDNA FLJ10061 fis,			
	٠,	clone HEMBA1001413.		,	
		/FEA=mRNA			1
		/DB_XREF=gi:7021892			
· . •		/UG=Hs.118926 sentrinSUMO-			Ì
* .*		specific protease 3		',	,
215118 s at	0.018444	Homo sapiens translocation	AW519168	Hs.367852	
	0.0.0	associated fusion protein	7	110.007.002	
		IRTA1/IGA1 (IRTA1/IGHA1)			
		mRNA, complete cds			
215148_s_at	0.025284		Al141541	Hs.17528	NP_004877
		protein-binding, family A, member		1.0.17.020	
	,	3 (X11-like 2)			
215157_x_at	0.025284	poly(A) binding protein,	AI734929	Hs.172182	NP_002559
	1 2.020207	IE-17 A SURVING STORM	1 0-1020	1.10.112.102	1.41 _002000

		ng to Figure 19 - Coronary Artery	A 100 101 1011 100		
Gene	p-valu	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
			No.	No.	No.
215193 x at	0.025284	Consensus includes	AJ297586		NP_002115
		gb:AJ297586.1 /DEF=Homo] -
* *		sapiens mRNA for MHC class II	,		,
1		antigen (HLA-DRB1 gene),			
		DRB1*0402 allele /FEA=CDS			
		/GEN=HLA-DRB1 /PROD=MHC			
		class II antigen			
		/DB_XREF=gi:10185079	- '		
		/UG=Hs.279930 major			
	-	histocompatibility complex, class			
•		II, DR beta 3			
215204_at	0.046740	ESTs, Weakly similar to 2109260A	A11147205	Hs.288575	
2 13204_at	0.040749		AU 147295	INS.200373	
		B cell growth factor [Homo			
045000 -4	0.00000	sapiens] [H.sapiens]	A1K0054.40		
215206_at	0.028893	Consensus includes	AK025143		
		gb:AK025143.1 /DEF=Homo			
	,	sapiens cDNA: FLJ21490 fis,			.
		clone COL05464. /FEA=mRNA		,	}
		/DB_XREF=gi:10437602			
		/UG=Hs.288700 Homo sapiens			
100		cDNA: FLJ21490 fis, clone			
		COL05464			
215235_at	0.046749	Consensus includes	AL110273		NP_003118
·		gb:AL110273.1 /DEF=Homo			1.
		sapiens mRNA; cDNA			
		DKFZp564P0562 (from clone	-		
		DKFZp564P0562); partial cds.	, i		
		/FEA=mRNA			* * * * * * * * * * * * * * * * * * *
	· · · · · · · · · · · · · · · · ·	/GEN=DKFZp564P0562			· ·
		/PROD=hypothetical protein	· -		
	Ì	/DB_XREF=gi:5817091			1:
	, •	/UG=Hs.77196 spectrin, alpha,			
		non-erythrocytic 1 (alpha-fodrin)			
215236 s at	0.038017	ubiquitin carboxyl-terminal	AV721177	Hs.114765	NP_665801
2 10200_3_at	0.030017	esterase L1 (ubiquitin	AV12,1111	1115.114703	147 _003001
		thiolesterase)	•		, i
215287 at	0.046740	Homo sapiens ELISC-1 mRNA,	AA975427	Up 120124	<u> </u>
215261_at	0.040749		AA9/542/	Hs.128434	
245242	0.040466	partial cds	A D040400		<u> </u>
215342_s_at	0.042400	Consensus includes	AB019490		
		gb:AB019490.1 /DEF=Homo		,	
		sapiens IDN4-GGTR7 mRNA,		1	
:		partial cds. /FEA=mRNA			
		/GEN=IDN4-GGTR7			1 1
		/DB_XREF=gi:4760540	-		
		/UG=Hs.242271 KIAA0471 gene			
	\	product	1		1 :

Gene	p-value	ng to Figur 19 - Coronary Artery Description	Gene	Unigene	Protein
	p-value	Description	1		
Identifier			Acc ssion	Accession	Accession
			No.	No.	No.
215483_at	0.018973	Consensus includes	AK000270		NP_671714
		gb:AK000270.1 /DEF=Homo			
	ļ	sapiens cDNA FLJ20263 fis,	·	1	
		clone COLF7804, highly similar			
		to AJ131693 Homo sapiens			
1 .]	mRNA for AKAP450 protein.] .	
				_	
		/FEA=mRNA			
•		/DB_XREF=gi:7020239			
	1	/UG=Hs.164036 Homo sapiens			
. '		AKAP350C mRNA sequence,			
		alternatively spliced			
215525_at	0.046749	Consensus includes	AL050185	,, ,,	y
	1	gb:AL050185.1 /DEF=Homo			1
		sapiens mRNA; cDNA		•	
		I T	•		
		DKFZp586A0423 (from clone		ľ	
	1.0	DKFZp586A0423). /FEA=mRNA			
		/DB_XREF=gi:4884400	· '	, .	
	. '	/UG=Hs.225988 Homo sapiens			
	-	mRNA; cDNA DKFZp586A0423			
	<u> </u>	(from clone DKFZp586A0423)			
215577 at	0.046749		AU146791	Hs.287474	\$ · · · · · · · · · · · · · · · · · · ·
215737 x at		Consensus includes gb:X90824.1		1.0.20	NP_003358
	0.010020	/DEF=H.sapiens mRNA for			-000000
	\	USF2a & USF2b, clone P9DH.			
• .					
:		/FEA=mRNA /GEN=USF2			1.
		/PROD=USF2a, USF2b protein			
		/DB_XREF=gi:1279506			1.
,		/UG=Hs 93649 upstream			•
		transcription factor 2, c-fos			
		interacting			
1					-
215758 v at	0.018023	HTF34-like ZNF gene, Homo	AC007204		
2 10/00_x_at	0.010023		AC007204	14	1
		sapiens chromosome 19, BAC	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		
1	1	273239 (CIT-B-320G13), complete	1		
		sequence.	<u> </u>		
215760_s_at	0.040064	Consensus includes	AC005390		
		gb:AC005390 /DEF=Homo			
	İ	sapiens chromosome 19, cosmid		1	
) ·	R31180 /FEA=CDS_1			
		/DB_XREF=gi:3399675			
				· ·	
	•	/UG=Hs.251410 Homo sapiens	1		
	}	chromosome 19, cosmid R31180	1		1

		ng to Figure 19 - Coronary Artery		100.500	Direction :
G ne Identifier	p-value	Description	Gen Accession	Unigene Acc ssion	Protein Accession
245000+	0.040740	O	No.	No.	No.
215806_x_at	0.046749	Consensus includes gb:M13231.1	IVI 1323 		
		/DEF=Human T-cell receptor	•**		
		aberrantly rearranged gamma-			'
		chain mRNA from cell line HPB-			
	ļ .	MLT. /FEA=mRNA			
]	/DB_XREF=gi:339168			
		/UG=Hs.274509 T cell receptor			,
		gamma constant 2		, .	
				1	
215909 x_at	0.018023	Consensus includes	AL157418	 	
210909_X_at	0.010023		AL 13/410		
		gb:AL157418.1 /DEF=Homo			1
		sapiens mRNA; cDNA			
•		DKFZp761K18121 (from clone			1.5
		DKFZp761K18121). /FEA=mRNA		1 .	
		/DB_XREF=gi:7018439			
	ļi i	/UG=Hs.112028 MisshapenNIK-			1.00
		related kinase			
				1	ļ. `
215966 x at	0.049425	glycerol kinase	AA292874	Hs.1466	NP 00015
216033 s at		Consensus includes gb:S74774.1	S74774	1113.1400	NP 69459
210033_s_at	0.010023		3/4//4		101-09459
	e e	/DEF=p59fyn(T)=OKT3-induced			
		calcium influx regulator human,			
	1	Jurkat J6 T cell line, mRNA	,		1
		Partial, 1605 nt. /FEA=CDS			
		/PROD=tyrosine kinase p59fyn(T)		*	
		/DB_XREF=gi:802050			
		/UG=Hs.169370 FYN oncogene			l
		related to SRC, FGR, YES			
216159_s_at	0.025284	Consensus includes	AK023757	•	
210109_5_at	0.023204		AR023737	.	
		gb:AK023757.1 /DEF=Homo			1
•		sapiens cDNA FLJ13695 fis,			
		clone PLACE2000124.			
•		/FEA=mRNA			·
		/DB_XREF=gi:10435786			1.
	:	/UG=Hs 306658 Homo sapiens			
	,	cDNA FLJ13695 fis, clone			
		PLACE2000124	į		
216170_at	0.021165	Consensus includes	AK025271	1	†
<u></u> _ac	0.021100	gb:AK025271.1 /DEF=Homo	1.1102027		
		1 T 1	1		
tut.	2	sapiens cDNA: FLJ21618 fis,			
	1	clone COL07487. /FEA=mRNA	1		ĺ
•		/DB_XREF=gi:10437753			
		/UG=Hs.306790 Homo sapiens			
		cDNA: FLJ21618 fis, clone		,	
	1	COL07487	Į.	l .	1

Gene List Co		ng to Figure 19 - Coronary Artery			
Gen Identifier	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
			No	No.	No.
216173 at	0.041795	Consensus includes	AK025360		1.0.
		gb:AK025360.1 /DEF=Homo			ľ
		sapiens cDNA: FLJ21707 fis,			
,		clone COL09953. /FEA=mRNA] .		
	,	/DB_XREF=gi:10437861			
		/UG=Hs.306806 Homo sapiens			
		cDNA: FLJ21707 fis, clone			
		COL09953			
216211 at	0.018603	Consensus includes	AL049233	77.7.7.40	
2102 1_at	0.0 10093	gb:AL049233.1 /DEF=Homo	ALU49233		
	,	sapiens mRNA, cDNA			
	1.5				1
.3		DKFZp564A023 (from clone	1	1	}
· · · · · · · · · · · · · · · · · · ·	,	DKFZp564A023). /FEA=mRNA			
		/DB_XREF=gi:4499967			
		/UG=Hs.42244 Homo sapiens			
		mRNA; cDNA DKFZp564A023	1		
		(from clone DKFZp564A023)		<u> </u>	<u> </u>
216231_s_at		beta-2-microglobulin	AW188940	Hs.75415	NP_004039
216318_at	0.018444	Consensus includes gb:S55735.1	S55735		
		/DEF=Homo sapiens	i .	1.	
		immunoglobulin A1-A2 lambda			
		hybrid GAU heavy chain mRNA,		<u>'</u>	
		partial cds. /FEA=mRNA			
75.]	/PROD=immunoglobulin A1-A2			
*	•	lambda hybrid GAU heavychain			
]	/DB_XREF=gi:265703			.
		/UG=Hs.293441 VPS28 protein			
		<u> </u>			
216384_x_at	0.018023	Homo sapiens prothymosin alpha	AF257099		,
		(PTMA) gene, complete cds.	,	,n ' .	<u> </u>
216396 s_at	0.046749	Consensus includes	AF131850		NP_004870
		gb:AF131850.1 /DEF=Homo		•	\ \ \ \ \ \ .
	1 -	sapiens clone 24988 mRNA	1		
		sequence. /FEA=mRNA			
	}	/DB_XREF=gi:4406694	<u>}</u>		}
		/UG=Hs.286027 etoposide-			
		induced mRNA			1
216444 at	0.042057		AK024138		1
,		gb:AK024138.1 /DEF=Homo			.
		sapiens cDNA FLJ14076 fis,			
] .	Iclone HEMBB1001925.]
		/FEA=mRNA		1	
		//DB_XREF=gi:10436445]
		/UG=Hs.306667 Homo sapiens			
		cDNA FLJ14076 fis, clone			1
		■			1
	<u></u>	HEMBB1001925	<u> </u>	<u> </u>	<u> </u>

		ng to Figure 19 - Coronary Artery	1.00	 	<u> </u>
Gene	p-value	Description	Gene	Unigene	Protein
ldentifier			Accession	Accession	Accession
··			No.	No.	No.
216526_x_at	0.034721	Consensus includes	AK024836		NP_002108
		gb:AK024836.1 /DEF=Homo			<u> </u>
		sapiens cDNA: FLJ21183 fis,		1	
٠.		clone CAS11634, highly similar		•	1
		to HSHLACW07 Homo sapiens	1		ŀ
		mRNA for human leukocyte		}	}
				1	
•		antigen C alpha chain.		4	ļ
		/FEA=mRNA			1
		/DB_XREF=gi:10437242			Į.
		/UG=Hs.277477 major			
•		histocompatibility complex, class			
•		II, C	1	1	1.
216591_s_at	0.049425	integral membrane protein subunit	AF080579		-
		of complex II; no evidence for			
	}	translation; putative pseudogene;			1
		Homo sapiens integral membrane		,	
	'	protein subunit of complex II (CII-	-		ļ
	<i>(</i>				
		3) pseudogene, complete	Į.		Į
		sequence.			· ·
. 12 <u>-1</u> 1-1	2 2 2 2 2 2 2 2 3 3 3				<u> </u>
216730_at	0.048741	Consensus includes	AK024561	ĺ	
		gb:AK024561.1 /DEF=Homo			
	1	sapiens cDNA: FLJ20908 fis,			
	,	clone ADSE00417. /FEA=mRNA		· .	}
	,	/DB_XREF=gi:10436870			{
		/UG=Hs.306689 Homo sapiens			
		cDNA: FLJ20908 fis, clone	ļ	Į.	
		ADSE00417	į		ļ
	1	/NB0200417		· .	
216748 at	0.010202	Consensus includes	AK024890	 	
210140_at	0.019292	1 '	ANU24690		
	ľ	gb:AK024890.1 /DEF=Homo			·
	ł	sapiens cDNA: FLJ21237 fis,			1
•		clone COL01114. /FEA=mRNA			1
		/DB_XREF=gi:10437303	4	1	1
	ļ	/UG=Hs.306720 Homo sapiens		ļ	į.
	Į	cDNA: FLJ21237 fis, clone			,
	Į	COL01114	ļ ·		Į.
216751 at	0.046749	Consensus includes	AK024879		t
-		gb:AK024879.1 /DEF=Homo]		
•		sapiens cDNA: FLJ21226 fis,		1]
		clone COL00721. /FEA=mRNA	1]
		· .	1		}
	}	/DB_XREF=gi:10437291	1	•	}
•		/UG=Hs.306715 Homo sapiens		-	
		cDNA: FLJ21226 fis, clone			
	l	COL00721		l	[

		ng to Figure 19 - Coronary Artery		1	ln
Gen	p-value	Description	Gene	Unigene	Protein
ldentifier			Accession	Accession	Accession
			No.	No.	No.
216983_s_at	0.033533	Consensus includes	BC002889		
हिसा च	<u> </u>	gb:BC002889.1 /DEF=Homo	l		
		sapiens, clone IMAGE:3941350,			
	ì	mRNA, partial cds. /FEA=mRNA		1	
		/PROD=Unknown (protein for		1	
· 	ŀ	IMAGE:3941350)	!		
	Į.	/DB_XREF=gi:12804072	· ·		
* !		1 s = ===			
		/UG=Hs 122605 Homo sapiens			
		cDNA: FLJ22124 fis, clone			
	}	HEP19352			
<u> </u>			<u> </u>	<u> </u>	
216996_s_at	0.018222	Consensus includes	AK021557		NP_055744
		gb:AK021557.1 /DEF=Homo			
		sapiens cDNA FLJ11495 fis,			
		clone HEMBA1001950, highly			
	-	similar to Homo sapiens mRNA			
		for KIAA0971 protein.			·
		/FEA=mRNA			I
		/DB_XREF=gi:10432760			
		/UG=Hs.84429 KIAA0971 protein			Ì
4.5		,			
217143 s at	0.018023	Consensus includes gb:X06557.1	X06557		
		/DEF=Human mRNA for TCR-	, 10000.		
		delta chain. /FEA=mRNA			
	ļ · · ·	/DB_XREF=gi:37003			
•	į,	/UG=Hs.2014 T cell receptor		1	
		delta locus		1	1.
247452 -4	0.005000	Canada includes	A1(004420	 	
217152_at	0.025293	Consensus includes	AK024136		,
		gb:AK024136.1 /DEF=Homo			
		sapiens cDNA FLJ14074 fis,		1,	:
		clone HEMBB1001869.		1	
		//FEA=mRNA		,	
		/DB_XREF=gi:10436442			
	1	/UG=Hs.141208 Homo sapiens			<u>.</u>
		cDNA FLJ14074 fis, clone		1	
		HEMBB1001869		1.	
217164_at	0.034721	Consensus includes	AK024108		V
		gb:AK024108.1 /DEF=Homo			
		sapiens cDNA FLJ14046 fis,			
	1	clone HEMBA1006461.	,		
		/FEA=mRNA		1	
		//DB XREF=gi:10436406	1 .	1	1
		//UG=Hs.142677 Homo sapiens		{	
		CDNA FLJ14046 fis, clone		ł .	1
				1	5 6
<u> </u>		HEMBA1006461	1	1	<u> </u>

		<u> </u>	اب						to Figure 19 - Coronary Artery		
217200_x_at 0.025284 Consensus includes gb:U06715.1 U06715 \(\text{DEF=Human cytochrome B561} \) \(\text{HCYTO B561, mRNA, partial cds. } \) \(\text{FEA=mRNA / GEN=B561} \) \(\text{PROD=HCYTO B561} \) \(\text{PROD=HCYTO B561} \) \(\text{PROD=HCYTO B561} \) \(\text{PROD=HCYTO B561} \) \(\text{PROD=HCYTO B561} \) \(\text{PROD=HCYTO B561} \) \(\text{PROD=HCYTO B561} \) \(\text{PROD=HCYTO B561} \) \(\text{PROD=HCYTO B561} \) \(\text{PROD=HCYTO B561} \) \(\text{PROD=HCYTO B561} \) \(\text{PROD=HCYTO B561} \) \(\text{PROD=HCYTO B561} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \) \(\text{PSOME AC06530} \	rotein	Prot	* * ')	ger	Unig	٠.	Gene	escription	p-valu	Gene
217200_x_at	ccession	Acc	n				n	Accession			ldentifier
217200_x_at		I				-	**				, , ,
/ÖEF=Human cytochrome B561, HCYTO B561, MRNA, partial cds. /FEA=mRNA /GEN=B561 //PROD=HCYTO B561 //PROD=HCYTO B561 //PROD=HCYTO B561 //DB_XREF=gi:476590 //UG=Hs.153028 cytochrome b- 561 217202_s_at	.	140.		-		110.	3-1-		onsensus includes ab U06715.1	0.025284	217200 x at
HCYTO B561, mRNA, partial cds. /FEA=mRNA /GEN=B561 /PROD=HCYTO B561 /DB_XREF=gi:476590 /UG=Hs.153028 cytochrome b-561 217202_s_at								000,-10			
cds. /FEA=mRNA /GEN=B561 //PROD=HCYTO B561 //PROD=HCYTO B561 //DB_XREF=gi:476590 //UG=Hs.153028 cytochrome b- 561 217202_s_at											
//ROD=HCYTO B561 //DB_XREF=gi:476590 //UG=Hs.153028 cytochrome b- 561 217202_s_at									The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	. *	•
/DB_XREF=gi:476590 //UG=Hs.153028 cytochrome b- 561 217202_s_at	•							t in the second		,	
/UG=Hs.153028 cytochrome b- 561 217202_s_at			,								
217202_s_at 217202_s_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216_x_at 217216			- 1								
217202_s_at 0.034721 Homo sapiens glutamine synthetase pseudogene, complete sequence. 217216_x_at 0.028893 Consensus includes gb:AC006530 /DEF=untitled /FEA=CDS_5 /DB_XREF=gi:4680764 /UG=Hs.153820 hypothetical protein 217274_x_at 0.040064 Consensus includes gb:X52005.1 X52005 /DEF=H.sapiens skeletal embryonic myosin light chain 1 (MLC1) mRNA. /FEA=mRNA /GEN=MCL1 /PROD=myosin light chain 1 /DB_XREF=gi:34677 /UG=Hs.159218 H.sapiens skeletal embryonic myosin light chain 1 (MLC1) mRNA 217340_at 0.040064 Consensus includes gb:AL024509 /DEF=Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs /FEA=CDS_1 //DB_XREF=gi:3947836 /UG=Hs.247780 Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous hordone) for the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the fi								,	•		· ·
synthetase pseudogene, complete sequence. 217216_x_at 0.028893 Consensus includes gb:AC006530 /DEF=untitled /FEA=CDS_5 /DB_XREF=gi:A680764 /UG=Hs.153820 hypothetical protein 217274_x_at 0.040064 Consensus includes gb:X52005.1 /DEF=H.sapiens skeletal embryonic myosin light chain 1 (MLC1) mRNA. /FEA=mRNA /GEN=MCL1 /PROD=myosin light chain 1 /DB_XREF=gi:34677 /UG=Hs.159218 H.sapiens skeletal embryonic myosin light chain 1 (MLC1) mRNA 217340_at 0.040064 Consensus includes gb:AL024509 /DEF=Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs /FEA=CDS_1 /DB_XREF=gi:3947836 /UG=Hs.247780 Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Portein L21 pseudogene and an HNRNP A3 (Heterogenous Portein L21 pseudogene and an HNRNP A3 (Heterogenous Portein L21 pseudogene and an HNRNP A3 (Heterogenous Protein L21 pseudogene and an HNRNP A3 (Heterogenous								•	51		
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Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs /FEA=CDS_1 //DB_XREF=gi:3947836 //UG=Hs.247780 Human DNA sequence from clone 522P13 on chromosome 6p21:31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous							. ,		quence from clone 522P13 on		
Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs /FEA=CDS_1 //DB_XREF=gi:3947836 //UG=Hs.247780 Human DNA sequence from clone 522P13 on chromosome 6p21:31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous			- 1		•			•	romosome 6p21.31-22.3.]	
Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs /FEA=CDS_1 //DB_XREF=gi:3947836 //UG=Hs.247780 Human DNA sequence from clone 522P13 on chromosome 6p21:31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous				٠.					•		. ,
HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs /FEA=CDS_1 //DB_XREF=gi:3947836 //UG=Hs.247780 Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous			- [;
Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs /FEA=CDS_1 /DB_XREF=gi:3947836 /UG=Hs.247780 Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous	,		- [1	,		
pseudogene. Contains ESTs, STSs and GSSs /FEA=CDS_1 //DB_XREF=gi:3947836 //UG=Hs.247780 Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous		-								,	
STSs and GSSs /FEA=CDS_1 //DB_XREF=gi:3947836 //UG=Hs.247780 Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous											
/DB_XREF=gi:3947836 /UG=Hs.247780 Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous											_
/UG=Hs.247780 Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous											
sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous										1	
chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous			ı							1	
Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous									•		* *
Protein L21 pseudogene and an HNRNP A3 (Heterogenous			1								
HNRNP A3 (Heterogenous		_					<i>*</i> '				
			- 1								
			l			'					
Nuclear Riboprotein A3, FBRNP)			Į				*				
pseudogene Contains ESTs,					•		İ				
STSs and GSSs									rss and Gsss		
			- 1								

G ne	p-value	ng to Figure 19 - Coronary Artery Description	Gene	Unigene	Protein .
Identifier	p value		Accession	Accession	Accession
lucillilei			No.	No.	No.
217477_at	0.018603	Consensus includes gb:U78581.1		INO.	NP_003549
217 4 /7_at	0.010093	/DEF=Human type I	070001		-0000-0
		phosphatidylinositol-4-phosphate			
		5-kinase beta (STM7) mRNA,			
		partial cds. /FEA=mRNA			
	100	/GEN=STM7 /PROD=type I			
•		phosphatidylinositol-4-phosphate			
] .	5-kinasebeta	* :		
		/DB_XREF=gi:1743882			
		/UG=Hs.78406			
	**	phosphatidylinositol-4-phosphate			· .
,	w'	5-kinase, type I, beta			*
`		. 1		•	-
217497_at	0.046749	ESTs, Weakly similar to	AW613387	Hs.388345	NP_001944
		hypothetical protein FLJ20378			
		[Homo sapiens] [H.sapiens]			, ,
217527_s_at	0.046749	ESTs, Weakly similar to neuronal	AI478300	Hs.351454	e e e e e e e e e e e e e e e e e e e
		thread protein [Homo sapiens]			. '
	*,	[H.sapiens]			
217549_at	0.025284	ESTs, Weakly similar to	AW574933	Hs.248844	
_		hypothetical protein FLJ20489			
		[Homo sapiens] [H.sapiens]			
217627 at	0.018023	hypothetical protein FLJ30921	BE515346	Hs.278871	NP 689573
217654_at		ESTs, Weakly similar to	R71245	Hs.174303	
		hypothetical protein FLJ11267	, , , , , ,		
	1	[Homo sapiens] [H.sapiens]			
217722 s at	0.034721		NM_016645		NP_057729
217722 <u>.</u> 0_at	0.001721	sapiens mesenchymal stem cell	1111_010010		-001720
	-	protein DSC92 (LOC51335),			
		mRNA. /FEA=mRNA			-
		/GEN=LOC51335			
		■ • T1			
].	/PROD=mesenchymal stem cell			
1		protein DSC92		\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	
		/DB_XREF=gi:7706195			
		/UG=Hs.323467 mesenchymal			
		stem cell protein DSC92	,		
		/FL=gb:AB029315.1			
	1	gb:AF242770.1 gb:NM_016645.1		1.	1

G ne List Co	rrespondir	ng to Figure 19 - Coronary Artery	Disease		
Gen	p-valu	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
		· ·	No.	No.	No.
217732_s at	0.034721	gb:AF092128.1 /DEF=Homo	AF092128	***	NP_068839
		sapiens putative transmembrane			
		protein E3-16 mRNA, complete			
		cds. /FEA=mRNA		1	† .
		/PROD=putative transmembrane			
	,	protein E3-16		€	[
	,	/DB_XREF=gi:5138905	·		[
		/UG=Hs.239625 integral	·		·
		membrane protein 2B			}
*		/FL=gb:NM_021999.1		∤ .	ł
		gb:AF136973.1 gb:BC000554.1			•
		gb:AF092128.1 gb:AF152462.1	. •		
1		gb:AF246221.1	1	1	[
217738 at	0.046749	pre-B-cell colony-enhancing factor	BF575514	Hs.239138	NP_005737
217741 s at	0.034721	zinc finger protein 216	AW471220	Hs.3776	NP 005998
217752 s at		gb:NM 018235.1 /DEF=Homo	NM 018235		NP_060705
		sapiens hypothetical protein	_		
		FLJ10830 (FLJ10830), mRNA.		ŀ	
		/FEA=mRNA /GEN=FLJ10830		. The second	
,	* .	/PROD=hypothetical protein		1	ļ
		FLJ10830 /DB_XREF=gi:8922698	1		
		/UG=Hs.273230 hypothetical	ł	. ر.	},
		protein FLJ10830	1		
į l		/FL=gb:BC001375.1	1	· ·	1
	·	gb:BC003176.1 gb:NM_018235.1	. .		•
			} .		ļ
				}	
217774_s_at	0.034721	gb:NM_016404.1 /DEF=Homo	NM_016404		NP_057488
(sapiens hypothetical protein			
		(HSPC152), mRNA. /FEA=mRNA]		Į ·
	₹	/GEN=HSPC152	1		·
1		/PROD=hypothetical protein	N	1	·
1		/DB_XREF=gi:7705476	{·	}	
{ ·		/UG=Hs.79259 hypothetical	1	ł	
		protein /FL=gb:AF110774.1	1		1
j		gb:AF161501.1 gb:NM_016404.1]]	[.
	<u> </u>	gb:AF229068.1	<u> </u>	1.	
217775_s_at	0.020576	gb:NM_016026.1 /DEF=Homo	NM_016026		NP_057110
		sapiens CGI-82 protein		1	
		(LOC51109), mRNA.	1		l `
* * * * * * * * * * * * * * * * * * * *		/FEA=mRNA /GEN=LOC51109	1		ĺ
j i	,	/PROD=CGI-82 protein	1		
		/DB_XREF=gi:7705790	1	1	
1		/UG=Hs.179817 CGI-82 protein	1		
1		/FL=gb:BC000112.1	1	1	} .
}		gb:AF151840.1 gb:NM_016026.1	1	1	
L	L	gb:AF167438.1	l	<u> </u>	L

Gene	p-value	ng to Figure 19 - Coronary Artery I Description	Gene	Unigene	Protein
Identifier	p-value	Description	Accession		
identiller	[· · · · · · · · · · · · · · · · · · ·	Acc ssion	Accession
047707 ***	0.046740	Ch.N.M. 046406 4 /DEE-Home	No.	No.	No.
217797_at	0.046749	gb:NM_016406.1 /DEF=Homo	NM_016406		NP_057490
:		sapiens hypothetical protein			
, a		(HSPC155), mRNA. /FEA=mRNA			}
	ŀ	/GEN=HSPC155	·		
		/PROD=hypothetical protein		}	· . :
		/DB_XREF=gi:7705480			
	1	/UG=Hs.177507 hypothetical		}	
		protein /FL=gb:BC005187.1	,]	
	1	gb:AF151884.1 gb:AF161504.1			i
		gb:NM_016406.1			1
217830_s_at	0.018023	Consensus includes	AL109658	 	† · · · · · · · · · · · · · · · · · · ·
- 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1		gb:AL109658 /DEF=Human DNA	1		1
		sequence from clone RP4-			}
		776F14 on chromosome 20p12.2	4		
	Į.	13. Contains the 5 end of the)	
		FKBP1A gene for FK506-binding			}
		protein 1A (12kD), the gene for			∤
	} `			1	1
		P47 protein, part of a novel			ł
•	1	member of the PTPNS (protein		1	1
	1	tyrosine phosphatase, non-	1		
	! .	recepto /FEA=mRNA			1
	}	/DB_XREF=gi:7161806		1.)
	Ì	/UG=Hs.12865 p47			
		/FL=gb:BC002801.1			
		gb:AF078856.1 gb:NM_016143.1			1
			l	<u> </u>	
217832_at	0.034721	Consensus includes	NM_006372		NP_006363
	{	gb:BE672181 /FEA=EST			
•		/DB_XREF=gi:10032712	1	1	1
		/DB_XREF=est:7b51c08.x1	1		
	[/CLONE=IMAGE:3231758			}
1 1 4 4 4		/UG=Hs.155489 NS1-associated			ļ
		protein 1 /FL=gb:AF155568.1		1	1
		gb:NM_006372.1			
217858_s_at	0.018023	gb:NM_016607.1 /DEF=Homo	NM 016607	 	NP_808817
217000_3_dt	0.010020	sapiens ALEX3 protein (ALEX3),	11111_010007	}	
	· .	mRNA. /FEA=mRNA	1	1	1
		/GEN=ALEX3 /PROD=ALEX3	1.		
		· ·		1	1
		protein /DB_XREF=gi:7705273	1	(
		/UG=Hs.172788 ALEX3 protein		1	İ
	1	/FL=gb:AB039669.1		1	
		gb:NM_016607.1		1	,

		ng to Figure 19 - Coronary Artery I		Unicono	Droto:
Gene Identifier	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
initia	}		No.	No.	No
217888_s_at	0.036254	gb:NM 018209.1 /DEF=Homo	NM 018209	140.	NP_783202
2.17000_s_at	0.000204	sapiens hypothetical protein	114141_010200		
		FLJ10767 (FLJ10767), mRNA.	1		
	·	/FEA=mRNA /GEN=FLJ10767			
* * *]	/PROD=hypothetical protein	·		}
	}	FLJ10767 /DB_XREF=gi:8922651	} ·		
	}	/UG=Hs.25584 hypothetical	<u> </u>	ļ	
		protein FLJ10767		ł	
		/FL=gb:NM_018209.1		1	
		/ L gb./tiii_010200.1	<u> </u>		İ
217899_at	0.046749	gb:NM_017727.1 /DEF=Homo	NM_017727	 	NP 060197
_ ,	0.040140	sapiens hypothetical protein			
	'	FLJ20254 (FLJ20254), mRNA.	}		
		/FEA=mRNA /GEN=FLJ20254	}		1.0
	İ	/PROD=hypothetical protein		1	,
		FLJ20254 /DB XREF=gi:8923227	l		1
		/UG=Hs 15356 hypothetical		.	{
		protein FLJ20254	1		
		/FL=gb.BC002467.1	ļ		
		gb:NM_017727.1	, , , , , , , , , , , , , , , , , , ,		} ·
			1		
217906 at	0.034721	gb:NM_014315.1 /DEF=Homo	NM 014315		NP 055130
. –		sapiens host cell factor homolog	\	· ·	· -
1		(LCP), mRNA. /FEA=mRNA)]	1
,	} .	/GEN=LCP /PROD=host cell	}	}	
	1	factor homolog		1	
		/DB_XREF=gi:7657300		1	ł
·		/UG=Hs.20597 host cell factor		į ·	
		homolog /FL=gb:BC002335.1		}	-
	}	gb:AF113131.1 gb:NM_014315.1)	1
		gb:AF244137.1			
217909_s_at	0.026013	transcription factor-like 4	BF056105	Hs.78185	NP_733753
217922_at		mannosidase, alpha, class 1A,	H97940	Hs.367638	
·	1	member 2	<u> </u>		<u> </u>
217928_s_at	0.025284	gb:NM_018312.2 /DEF=Homo	NM_018312		NP_060782
		sapiens chromosome 11 open	_	1	, "
		reading frame 23 (C11ORF23),		1	1
1	1	mRNA. /FEA=mRNA	1.	}	1
1		/GEN=C11ORF23	}		ł
		/PROD=sporulation-induced		1	+
•		transcript 4-associatedprotein	ļ.,	1	ĺ
		/DB_XREF=gi:13489082		,	
		/UG=Hs.180817 chromosome 11		1	
] ;		open reading frame 23	}	<u>}</u> .	1
·		/FL=gb:AF264779.1	}	1	
1	1 .	gb:NM_018312.2	1		1

		ng to Figure 19 - Coronary Artery I		 	
Gene	p-value	Description	Gene	Unigene	Protein
ld ntifi r	4.	` .	Accession	Accession	Accession
			No.	No.	No.
217932_at	0.038017	gb:NM_015971.1 /DEF=Homo	NM 015971	-	NP 057055
- 1,002_dt	0.000017	sapiens 30S ribosomal protein	5,55,		
	•	S7 homolog (LOC51081),			
·		mRNA /FEA=mRNA			
		/GEN=LOC51081 /PROD=30S			
		ribosomal protein S7 homolog		,	٠.
1 A	*	/DB_XREF=gi:7705737			
		/UG=Hs.71787 30S ribosomal			
		protein S7 homolog	*,		
		/FL=gb:BC000241.1	,		
		gb:AF077042.1 gb:NM_015971.1			
217937 s at	0.026842	gb:NM_016596.2 /DEF=Homo	NM_016596		NP_057680
	_ *	sapiens histone deacetylase 7A			· -
	N	(HDAC7), transcript variant 2,			
	-	mRNA. /FEA=mRNA			i i
	* *	/GEN=HDAC7 /PROD=histone		1	•
·		deacetylase 7A, isoform b			
		/DB XREF=gi:13259523			
		. –			
		/UG=Hs.275438 histone			
		deacetylase 7A			
, ,	,	/FL=gb:NM_016596.2	•		
		gb:AF239243.1		<u> </u>	
217940_s_at	0.018693	gb:NM_018210.1 /DEF=Homo	NM_018210		NP_060680
		sapiens hypothetical protein			
		FLJ10769 (FLJ10769), mRNA.			
		/FEA=mRNA /GEN=FLJ10769			
		/PROD=hypothetical protein		1. 5	
		FLJ10769 /DB_XREF=gi:8922653			
`		/UG=Hs.8083 hypothetical protein			
	1	FLJ10769 /FL=gb:AF151071.1		- • '	
		gb:NM 018210.1	1.	·	
		955 152.15.			
		A Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Comp			
217945_at	0.046740	gb:NM_025238.1 /DEF=Homo	NM_025238	<u> </u>	NP 079514
21/940_at	0.040749	sapiens BTB (POZ) domain	14101_020200		NI = _07 93 12
]	1			
		containing 1 (BTBD1), mRNA.			
		/FEA=mRNA /GEN=BTBD1	i i	_	1
		/PROD=BTB (POZ) domain		· · ·	1.
		containing 1			· .
		/DB_XREF=gi:13376847			· ·
	-	/UG=Hs.21332 BTB (POZ)			
		domain containing 1		•	
4		/FL=gb:AL136853.1			
		gb:AF257241.1 gb:NM_025238.1	1	'	1
	1	gb:AF355402.1	1	1	

		ng to Figure 19 - Coronary Artery I	Disease		
Gene	p-value	Description	Gene	Unigene	Protein
Identifier	,		Accession	Accession	Accession
· ' ' [No.	No.	No.
217957_at	0.046749	gb:NM_013242.1 /DEF=Homo	NM_013242	110.	NP 037374
	0.010110	sapiens similar to mouse Glt3	11111_013242	İ	_00/0/4
	•	1			· · · · · · · · · · · · · · · · · · ·
		or D. malanogaster transcription	}	ł	
		factor IIB (AF093680), mRNA.		j	
		/FEA=mRNA /GEN=AF093680	1		· .
i		/PROD=similar to mouse Glt3 or	ľ	l	Í
		D. malanogastertranscription	1		[]
	:	factor IIB /DB_XREF=gi:8392874			ł
	·	/UG=Hs.279818 similar to mouse		``	j
		Glt3 or D. malanogaster			
	•	transcription factor IIB	}		l
		/FL=gb:BC005152.1	1		j .
			1		
		gb:AF093680.1 gb:NM_013242.1	ł		i
	F.				1
	, 				
217964_at	0.046749	gb:NM_017775.1 /DEF=Homo	NM_017775		NP_060245
		sapiens hypothetical protein			
1	* *	FLJ20343 (FLJ20343), mRNA.	ł	}	} ·
		/FEA=mRNA /GEN=FLJ20343	1	1	
		/PROD=hypothetical protein	}		
	* -	FLJ20343 /DB_XREF=gi:8923319			
			1		1
		/UG=Hs.252692 hypothetical			}
		protein FLJ20343	ļ		l
		/FL=gb:NM_017775.1			}
			<u></u>	<u> </u>	
217987_at	0.034721	gb:NM_019048.1 /DEF=Homo	NM_019048		NP_061921
, A B	•	sapiens hypothetical protein	·	ł	ł
		(FLJ20752), mRNA /FEA=mRNA		1	S
3.4 5.4	4	/GEN=FLJ20752			
		/PROD=hypothetical protein		} ·	{
		/DB_XREF=gi:9506696	Į.] ,
		/UG=Hs.101364 hypothetical			}
					{
		protein /FL=gb:BC001243.1		1	1
10.40005		gb:NM_019048.1	<u> </u>	<u> </u>	
218005_at		zinc finger protein 22 (KOX 15)	AA744771	Hs.108642	NP_008894
218025_s_at	0.034721	gb:NM_006117.1 /DEF=Homo	NM_006117		NP_006108
		sapiens peroxisomal D3,D2-enoyl-			{
		CoA isomerase (PECI), mRNA.			j .
		/FEA=mRNA /GEN=PECI	:		<u> </u>
• .		pr ==	1		ł ·
•		PROD=peroxisomal_D3 D2-enovl-	Į.		
• .		/PROD=peroxisomal D3,D2-enoyl-			}
		CoA isomerase			
		CoA isomerase /DB_XREF=gi:5174624			
		CoA isomerase /DB_XREF=gi:5174624 /UG=Hs.15250 peroxisomal			
		CoA isomerase /DB_XREF=gi:5174624 /UG=Hs.15250 peroxisomal D3,D2-enoyl-CoA isomerase			
		CoA isomerase /DB_XREF=gi:5174624 /UG=Hs.15250 peroxisomal D3,D2-enoyl-CoA isomerase /FL=gb:AL136642.1			
		CoA isomerase /DB_XREF=gi:5174624 /UG=Hs.15250 peroxisomal D3,D2-enoyl-CoA isomerase			
		CoA isomerase /DB_XREF=gi:5174624 /UG=Hs.15250 peroxisomal D3,D2-enoyl-CoA isomerase /FL=gb:AL136642.1 gb:BC002668.1 gb:AF069301.1			
		CoA isomerase /DB_XREF=gi:5174624 /UG=Hs.15250 peroxisomal D3,D2-enoyl-CoA isomerase /FL=gb:AL136642.1			

		ng to Figur 19 - Coronary Artery I			
	p-value	Description	Gene	Unigene	Protein
Identifier	1		Accession	Accession	Accession
		*	No.	No	No.
218041 x at	0.034721	gb:NM_018573.1 /DEF=Homo	NM 018573	,	
		sapiens hypothetical protein	·		
1		PRO1068 (PRO1068), mRNA.			
		/FEA=mRNA /GEN=PRO1068			
	· 1				ĺ
		/PROD=hypothetical protein			. '
	, ,	PRO1068 /DB_XREF=gi:8924006			1
	. *	/UG=Hs.321158 hypothetical			1
		protein PRO1068)	1	
		/FL=gb:AF116620.1	ž		ļ. · .
•		gb:NM_018573.1			
·					!
218050_at	0.046749	gb:NM_016617.1 /DEF=Homo	NM 016617	 	NP_057701
	2.5.0.	sapiens hypothetical protein (BM-		1.67	
		002), mRNA /FEA=mRNA	· .		
		•	• • .	} ;	
	- 1	/GEN=BM-002			.
		/PROD=hypothetical protein			
		/DB_XREF=gi:7705299		1	}
j.		/UG=Hs.5862 hypothetical protein)
		/FL=gb:BC005193.1			1.0
		gb:AF208844.1 gb:NM_016617.1			1 T 4
218052_s_at	0.025284	gb:NM_020410.1 /DEF=Homo	NM 020410	 	NP 065143
		sapiens CGI-152 protein			-
		(LOC57130), mRNA.			ļ
				1	
	1	/FEA=mRNA /GEN=LOC57130		1	
	." 	/PROD=CGI-152 protein	J		
		/DB_XREF=gi:9966896			
(8)	*	/UG=Hs.9275 CGI-152 protein	. '		
	٠.	/FL=gb:AF288687.1] .		
	.*	gb:NM_020410.1			}
218076_s_at	0.046749	gb:NM_018054.1 /DEF=Homo	NM 018054	1	NP 060524
		sapiens homolog of rat nadrin		}	
·		(FLJ10308), mRNA. /FEA=mRNA	·	1	}
		/GEN=FLJ10308 /PROD=homolog			
` .		of rat nadrin			
		/DB_XREF=gi:8922343			
		/UG=Hs 14169 homolog of rat		1	
. '		nadrin /FL=gb:AF113218.1		` 	
		gb:NM_018054.1	<u> </u>	<u> </u>	
218100_s_at	0.036254	gb:NM_018010.1 /DEF=Homo	NM_018010		NP_060480
		sapiens hypothetical protein		[
(.		FLJ10147 (FLJ10147), mRNA.		1	[.
		/FEA=mRNA /GEN=FLJ10147		1	
		/PROD=hypothetical protein			
	·	FLJ10147 /DB_XREF=gi:8922255			1
		/UG=Hs.170318 hypothetical	i		
		protein FLJ10147			ł
		/FL=gb:AF139576.1	1		
		gb:AF245220.1 gb:NM_018010.1	l		
· ·					

		ng to Figure 19 - Coronary Artery			
G ne	p-value	Description	Gene	Unigene	Protein
Identifier	. 1		Accession	Accession	Accession
·			No	No.	No
218103_at	0.046749	gb:NM 017647.1 /DEF=Homo	NM_017647		NP_060117
2,10109_at	0.0401.43	sapiens hypothetical protein	14141_017047		141 -000117
v I					
		FLJ20062 (FLJ20062), mRNA.		1	
	., •	/FEA=mRNA /GEN=FLJ20062		}	ł
		/PROD=hypothetical protein			
1		FLJ20062 /DB_XREF=gi:8923066			
		/UG=Hs.257486 hypothetical			
		protein FLJ20062			1
• •		/FL=gb:BC000131.1		1	
		gb:NM_017647.1		1	
		gb.14141_017047.1]		
646444	0.010711				
218114_at	0.048741	gb:NM_013365.1 /DEF=Homo	NM_013365		NP_037497
		sapiens ADP-ribosylation factor]		
		binding protein GGA1 (GGA1),		i e	
		mRNA. /FEA=mRNA			
		/GEN=GGA1 /PROD=ADP-	į	15	
		ribosylation factor binding protein			{
		GGA1 /DB_XREF=gi:9558728	1		
		1	1		{
		/UG=Hs.238296 ADP-ribosylation			
		factor binding protein GGA1		l	1
		/FL=gb:AF190862.1			
		gb:AF233521.1 gb:AF218584.1		;	
•		gb:NM_013365.1		1	
				İ	
				4	
218122 s at	0.036254	gb:NM 021627.1 /DEF=Homo	NM_021627	 	NP 067640
2 10 122_0_at	0.000204	sapiens sentrin-specific protease	111111_021027	1	141 _007040
*			}	1	·
		(SENP2), mRNA /FEA=mRNA			
		/GEN=SENP2 /PROD=sentrin-	}		
* .		specific protease	'		
	1, 1	/DB_XREF=gi:11055993		}	[·
		/UG=Hs.3355 sentrin-specific			
	, ,	protease /FL=gb:AF151697.2			*-
-		gb:NM_021627.1)		
218123_at	0.018023	gb:NM_017835.1 /DEF=Homo	NM_017835		NP_067077
2,10120_qt	0.010020	sapiens chromosome 21 open	14141_017000	ļ	_007077
	•				
		reading frame 59 (C21ORF59),	1) ~
		mRNA. /FEA=mRNA		}	le de la company
		/GEN=C21ORF59		}	
		/PROD=hypothetical protein)	1	
<u>.</u>		FLJ20467 /DB_XREF=gi:8923436]	1
٠		/UG=Hs.5811 chromosome 21]		
		open reading frame 59	ì		
	•	/FL=gb:NM_021254.1			[
,			[[[
		gb:BC000709.1 gb:NM_017835.1	[
. ve		gb:AF282851.1	(:	ŀ	1
	l	,	1	1	1

Gene	p-value	ng to Figure 19 - Coronary Artery I Description	Gene	Unigen	Protein
Identifier	p-value	Description	Accession	Accession	1
laenuner	1				Accession
040405 -6	0.040740	L NIM 040570 4 /DEE 11	No.	No.	No.
218135_at	0.046749	gb:NM_016570.1 /DEF=Homo	NM_016570		NP_057654
		sapiens CDA14 (LOC51290),		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
* -	1	mRNA. /FEA=mRNA			İ.,
·		/GEN=LOC51290 /PROD=CDA14			
		/DB_XREF=gi:7706104			
		/UG=Hs.26813 CDA14			
	· ·	/FL=gb:BC000887.1			
		gb:AF216751.1 gb:NM_016570.1		} . • • •	ł
	}	gb:AF183410.1			ļ
		:			
218143 s at	0.034721	gb:NM_005697.2 /DEF=Homo	NM 005697		NP_005688
2 10 140_9_at	0.00-1121	sapiens secretory carrier	11111_000007		141 _000000
	**	membrane protein 2 (SCAMP2),			
-*		mRNA. /FEA=mRNA		1	[-1
		/GEN=SCAMP2 /PROD=secretory			`,
,		carrier membrane protein 2	· ·		
	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	/DB_XREF=gi:5730030			l
,		/UG=Hs.238030 secretory carrier			*-
		membrane protein 2		l .	
		/FL=gb:BC001376.1		}	}
	ļ .	gb:BC004385.1 gb:AF005038.2	194		
	Į.	gb:NM_005697.2			
	[•	
218152_at	0.034721	gb:NM 018200.1 /DEF=Homo	NM 018200		NP 060670
	ļ · .	sapiens high-mobility group 20A	-	<u>l</u>	- '
_		(HMG20A), mRNA /FEA=mRNA		* .	
		/GEN=HMG20A /PROD=high-		· ·	
	ì	mobility group 20A		*	
	1.	/DB XREF=gi:8922632		<u> </u>	į
(· · · · · · · · · · · · · · · · · · ·		/UG=Hs.69594 high-mobility			
;	.[group 20A /FL=gb:AF146222.1	,	A.	
	1	gb:NM_018200.1			
218164 at	0.004070	ab NM 022827 1 /DEE=Homo	NM 022827	 	NP 073738
218164_at	0.021876	13502202 /22	NIVI_022827	j	NP_0/3/38
		sapiens hypothetical protein			
	1	FLJ21347 (FLJ21347), mRNA.	1		ļ
	}.	/FEA=mRNA /GEN=FLJ21347		*	
	}	/PROD=hypothetical protein	J	1]
		FLJ21347			
		/DB_XREF=gi:12383067	(* .
	1	/UG=Hs.103147 hypothetical		1	}
)	protein FLJ21347	J		ļ
	1	/FL=gb:NM_022827.1			1

Gene List Co	rrespondir	ng to Figure 19 - Coronary Artery I	Disease	<u> </u>	
Gene Identifier	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
			No.	No.	No.
218167_at	0.034721	gb:NM_016627 1 /DEF=Homo	NM_016627	1	NP_057711
	· '	sapiens hypothetical protein			-
		(LOC51321), mRNA.		İ	
		/FEA=mRNA /GEN=LOC51321	,	· ·	
•		/PROD=hypothetical protein		1	
	}	/DB_XREF=gi:7706167		1	l '
	}	/UG=Hs.268122 hypothetical protein /FL=gb:AF208856.1			
		gb:NM 016627.1			
218175_at	0.018603	gb:NM 025140.1 /DEF=Homo	NM_025140	 	NP_079416
210175_at	0.010093	sapiens hypothetical protein	14141_023140		1019410
*		FLJ22471 (FLJ22471), mRNA.			
	:	/FEA=mRNA /GEN=FLJ22471			
		/PROD=hypothetical protein			1
		FLJ22471			[.
		/DB_XREF=gi:13376724			
1		/UG=Hs.288909 hypothetical			
		protein FLJ22471	İ		
	}	/FL=gb:NM_025140.1	}		1
218192 at	0.018023	gb:NM 016291.1 /DEF=Homo	NM 016291	·	NP 057375
	1	sapiens mammalian inositol		•	
,		hexakisphosphate kinase 2			
		(IP6K2), mRNA /FEA=mRNA	٠.		,
		/GEN=IP6K2 /PROD=mammalian	1		ļ
		inositol hexakisphosphate kinase			
		2 /DB_XREF=gi:7705552		1	
	•	/UG=Hs.323432 mammalian		} ,	
·		inositol hexakisphosphate kinase			1
		2 /FL=gb:AF177145.1	[·,
		gb:NM_016291.1			1
218201_at	0.046749	gb:NM_004546.1 /DEF=Homo	NM_004546		NP_004537
ļ		sapiens NADH dehydrogenase	}	,	
		(ubiquinone) 1 beta subcomplex,			
		2 (8kD, AGGG) (NDUFB2),	ſ.	1.	,
		mRNA. /FEA=mRNA			
		/GEN=NDUFB2 /PROD=NADH			
		dehydrogenase (ubiquinone) 1	· ·	1	
	ļ·	betasubcomplex, 2 (8kD, AGGG))		
·		/DB_XREF=gi:4758777	1	1	
1		/UG=Hs.198272 NADH	1	1	}
<u> </u>	}	dehydrogenase (ubiquinone) 1	<u> </u>]	}
		beta subcomplex, 2 (8kD,			
		AGGG) /FL=gb:BC001168.1		l	1
		gb:AF050639.1 gb:NM_004546.1	<u> </u>	1 .	
		gb:AF067166.1			
L	<u> </u>	1	<u> </u>	<u></u>	

		ng to Figure 19 - Coronary Artery		Unigona	Drotoin
Gene Id ntifier	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
218209 s at	0.018023	gb:NM_018170.1 /DEF=Homo	NM 018170	INO.	NP 060640
216209 <u>_</u> S_at	0.016023	sapiens hypothetical protein FLJ10656 (FLJ10656), mRNA. /FEA=mRNA /GEN=FLJ10656 /PROD=hypothetical protein	NIM_016170		INF_000040
# 1.		FLJ10656 /DB_XREF=gi:8922574 /UG=Hs:300906 hypothetical protein FLJ10656 /FL=gb:NM_018170.1			
218216_x_at	0.036254	gb:NM_016638.1 /DEF=Homo sapiens SRp25 nuclear protein (LOC51329), mRNA. /FEA=mRNA /GEN=LOC51329 /PROD=SRp25 nuclear protein /DB_XREF=gi:7706183	NM_016638)		NP_061164
		/UG=Hs.103561 SRp25 nuclear protein /FL=gb:BC001958.1 gb:AB035384.1 gb:NM_016638.1			
218223_s_at	0.025284	gb:NM_016274.1 /DEF=Homo sapiens CK2 interacting protein 1; HQ0024c protein (LOC51177), mRNA. /FEA=mRNA /GEN=LOC51177 /PROD=CK2 interacting protein 1; HQ0024c protein /DB_XREF=gi:7705918 /UG=Hs.173380 CK2 interacting protein 1; HQ0024c protein 1; HQ0024c protein	NM_016274		NP_057358
		/FL=gb:AF291105.1 gb:AF073836.1 gb:NM_016274.1 gb:AF168676.1			
218224_at	0.034721	gb:NM_006029.2 /DEF=Homo sapiens paraneoplastic antigen MA1 (PNMA1), mRNA. /FEA=mRNA /GEN=PNMA1 /PROD=paraneoplastic antigen MA1 /DB_XREF=gi:11141858 /UG=Hs.194709 paraneoplastic antigen MA1 /FL=gb:AF037364.2	NM_006029		NP_006020

		ng to Figure 19 - Coronary Artery	2.1.1	115:55	D4-:-
Gene	p-value	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
			No.	No.	No.
218237_s_at	0.018023	gb:NM_030674.1 /DEF=Homo	NM_030674		NP_109599
		sapiens amino acid transporter		- 1	.
- '		system A1 (ATA1), mRNA.			i i
		/FEA=mRNA /GEN=ATA1			
		/PROD=amino acid transporter			
		system A1	· ·	·	ĺ
		/DB_XREF=gi:13492978			
·		/UG=Hs.18272 amino acid			(
		I			
		transporter system A1	·		
		/FL=gb:AF271070.1		•	
, to		gb:NM_030674.1			
218238_at	0.025284	gb:NM_012341.1 /DEF=Homo	NM_012341	1	NP_036473
		sapiens GTP-binding protein	. ,		
		(NGB), mRNA. /FEA=mRNA	· .		
	•	/GEN=NGB /PROD=GTP-binding			
		protein /DB_XREF=gi:6912531	,		
	1	/UG=Hs.215766 GTP-binding			
		protein /FL=gb:AF325353.1		1	1
	٠,	gb:AF120334.1 gb:NM_012341.1			1
		gb.Ai 120334.1 gb.NiVI_012341.1			1.
040000 0 04	0.024704		NIM 004044		ND 007004
218263_s_at	0.034721	gb:NM_021211.1 /DEF=Homo	NM_021211		NP_067034
		sapiens transposon-derived			
		Buster1 transposase-like protein	: .		
		(LOC58486), mRNA.			
•		/FEA=mRNA /GEN=LOC58486	,		
	1	/PROD=transposon-derived			ŀ
•		Buster1 transposase-likeprotein	1		
		/DB_XREF=gi:10864022			ì
7.		/UG=Hs.25726 transposon-			
		derived Buster1 transposase-like			ì
		protein /FL=gb:NM 021211.1		111	
	i ·	(,			
·		gb:AF205600.1	4.1		
040005	0.000040				,
218285_s_at	0.026842	gb:NM_020139.1 /DEF=Homo	NM_020139		NP_064524
		sapiens oxidoreductase UCPA	}	ľ	ł
	i	(LOC56898), mRNA.	ĺ		1
-		/FEA=mRNA /GEN=LOC56898		}	ŀ
# · · ·		/PROD=oxidoreductase UCPA			
		/DB_XREF=gi:10047131	1		1 to 16
		/UG=Hs.124696 oxidoreductase		1	
		UCPA /FL=gb:NM_020139.1	1	ļ	1
	17	gb:AF164790.1	I	1	I

		ng to Figure 19 - Cor nary Artery [Unia	Duntain
G ne	p-value	D scription	Gene	Unig ne	Protein
Identifier	,		Accession	Accession	Accession
			No.	No.	No.
218309_at	0.019292	gb:NM_018584.1 /DEF=Homo	NM_018584		NP_061054
		sapiens hypothetical protein			
		PRO1489 (PRO1489), mRNA.	v.]	1
		/FEA=mRNA /GEN=PRO1489			
4.7	!	/PROD=hypothetical protein			1
	1	PRO1489 /DB_XREF=gi:8924051			
		/UG=Hs 107767 hypothetical		1 .	
)	protein PRO1489			1
		/FL=gb:AF116637.1			
4.5	ł	gb:NM 018584.1		1	1
		gb. v v _016564.1		ļ ^r .	-
24222	0.04000=		104 045455	ļ	LID COSE
218329_at	0.019292	gb:NM_012406.2 /DEF=Homo	NM_012406	* * *	NP_036538
		sapiens PR domain containing 4			
		(PRDM4), mRNA. /FEA=mRNA		1	
		/GEN=PRDM4 /PROD=PR			
	٠.	domain containing 4	Y	1	
]	/DB_XREF=gi:9055315			
	1.	/UG=Hs.21807 PR domain	* **		
)	containing 4 /FL=gb:AF144757.2			
		gb:NM_012406.2			
	•		*		1
218331 s at	0.034721	gb:NM 017782.1 /DEF=Homo	NM 017782		NP 060252
210001_0_at	0.00 772	sapiens hypothetical protein	11111_017 702	ļ	
		FLJ20360 (FLJ20360), mRNA.	* .	<u>'</u>	
		//FEA=mRNA /GEN=FLJ20360			
				}	ľ.
•		/PROD=hypothetical protein			
	1	FLJ20360 /DB_XREF=gi:8923334		,	`
	}	/UG=Hs.26434 hypothetical		. :	
		protein FLJ20360			*
	· ·	/FL=gb:BC001759.1			
		gb:NM_017782.1	_	Į	
					Ĺ
218366 x at	0.018023	gb:NM_022734.1 /DEF=Homo	NM_022734		NP_07357
		sapiens hypothetical protein.			
	1	FLJ20859 (FLJ20859), mRNA.	1		
		/FEA=mRNA /GEN=FLJ20859		.	
		/PROD=hypothetical protein	<u> </u>	İ	1
	;	FLJ20859].]	
,	:	· ·	,		Į.
4		/DB_XREF=gi:12232388	·		1
		/UG=Hs.6311 hypothetical protein			1.
	1.	FLJ20859 /FL=gb:NM_022734.1	Į.	1	1 .

		ng to Figure 19 - Coronary Artery			<u> </u>
G ne	p-value	Description	Gene	Unigene	Protein
ld ntifier	4.		Accession	Accession	Accession
			No.	No	No.
218422_s_at	0.034721	gb:NM_022118.1 /DEF=Homo	NM_022118		NP_071401
		sapiens cutaneous T-cell	*** *** *** * * * * * * * * * * * * * *		
,		lymphoma tumor antigen se70-2		1.5	<u> </u>
	,	(SE70-2), mRNA. /FEA=mRNA			
		/GEN=SE70-2 /PROD=cutaneous		,	ч .
		T-cell lymphoma tumor antigen			1
land the second		se70-2 /DB_XREF=gi:11545836			
		/UG=Hs.39140 cutaneous T-cell		` ·	
	,	lymphoma tumor antigen se70-2			
		/FL=gb:AF273052.1	l en e		
	,	gb:NM_022118.1 gb:BC000791.1			
		gb.14141_022110.1	1		
	,				* * .
218428 s at	0.046749	gb:NM 016316.1 /DEF=Homo	NM_016316	-	NP 057400
2 10420_5_al	0.040749	sapiens REV1 (yeast homolog)-	NN _0 103 10 .		JINF_05/400
		like (REV1L), mRNA.	}		V.
		/FEA=mRNA /GEN=REV1L			· .
		/PROD=REV1 (yeast homolog)-	1.	ł	1
		like /DB_XREF=gi:7706680		5	
		/UG=Hs.110347 REV1 (yeast			
		homolog)- like			
		/FL=gb:AB047646.1	1.		
		gb:AF151538.1 gb:AF206019.1			
	1	gb:NM_016316.1			<u> </u>
218456_at	0.018023	gb:NM_023925.1 /DEF=Homo	NM_023925		NP_115532
,	ĺ	sapiens hypothetical protein			·
		FLJ22569 (FLJ22569), mRNA.			
	1	/FEA=mRNA /GEN=FLJ22569			İ
		/PROD=hypothetical protein			
	[FLJ22569		,	
		/DB_XREF=gi:12965192	,	1.	,
,		/UG=Hs.234355 hypothetical	[:	1	
		protein FLJ22569	<i>r</i> .		
		/FL=gb:NM_023925.1			
218517 at	0.034721	gb:NM_024900.1 /DEF=Homo	NM 024900	 	NP_079176
12,10011_ai	0.004721	sapiens hypothetical protein	1411_024300		-0/01/0
]		FLJ22479 (FLJ22479), mRNA.			
		/FEA=mRNA /GEN=FLJ22479	·		
} .	1 .		}	· .	
		/PROD=hypothetical protein			
	1	FLJ22479		1.7	, , ,
		/DB_XREF=gi:13376356			
		/UG=Hs.238246 hypothetical			1
· ·		protein FLJ22479			
1	1	/FL=gb:NM_024900.1		<u>L</u>	<u></u>

Gene List C	rrespondir	ng to Figure 19 - Coronary Artery I	Diseas	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
Gene	p-value	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
			No.	No.	No.
218518_at	0.034721	gb:NM_016603.1 /DEF=Homo	NM_016603		NP_057687
		sapiens GAP-like protein	[- -	- · · · · · · · · · · · · · · · · · · ·	
,		(LOC51306), mRNA.	•. "	-	
		/FEA=mRNA /GEN=LOC51306		1	**
•		/PROD=GAP-like protein			i
		/DB_XREF=gi:7706136	:		
		/UG=Hs.82035 potential nuclear			
		protein C5ORF5; GAP-like	.	1	
		protein /FL=gb:AF251038.1		4.	· ·
	[gb:AF157316.1 gb:NM_016603.1			
218521 s at	0.046749	gb:NM 018299.1 /DEF=Homo	NM_018299		NP_060769
		sapiens hypothetical protein			
		FLJ11011 (FLJ11011), mRNA.			
)	/FEA=mRNA /GEN=FLJ11011	1		j ·
	100	/PROD=hypothetical protein	,		٠
		FLJ11011 /DB_XREF=gi:8922821	· · ·		
1 20		/UG=Hs.21275 hypothetical			
	1.	protein FLJ11011			[
1	,	/FL=gb:NM 018299.1			
				1	
218526 s at	0.026013	gb:NM 014185.1 /DEF=Homo	NM 014185	- 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 To 10 T	NP_057576
-		sapiens HSPC165 protein	_].	-
		(HSPC165), mRNA. /FEA=mRNA			
		/GEN=HSPC165	t ·	1	1
		/PROD=HSPC165 protein			(
		/DB_XREF=gi:7661825			
		/UG=Hs.13605 HSPC165 protein			!
		/FL=gb:AF161514.1	` \ \	1	
		gb:AF151070.1 gb:NM_014185.1			
) ·		gb:NM_016492.1 gb:AF168714.1	.		ł
		gb:AF265206.1			·
218530_at	0.019657	gb:NM_013241.1 /DEF=Homo	NM_013241		NP_037373
_		sapiens FH1FH2 domain-	-		-
		containing protein (FHOS),			
		mRNA. /FEA=mRNA			1.
		/GEN=FHOS /PROD=FH1FH2			}
ľ		domain-containing protein		1	1
		/DB_XREF=gi:7019374		1	1
		/UG=Hs.95231 FH1FH2 domain-			
		containing protein	1		1
,		/FL=gb:AF113615.1		1	1
		gb:NM_013241.1		<u> </u>	L ·

		ng to Figure 19 - Coronary Artery			
Gene	p-value	Description	Gene	Unigene	Protein
ldentifier			Accession	Accession	Accession
			No.	No.	No.
218533 s at	0.045316	gb:NM 017859.1 /DEF=Homo	NM_017859		NP 060329
		sapiens hypothetical protein	- 		-
		FLJ20517 (FLJ20517), mRNA.		•	
· '		/FEA=mRNA /GEN=FLJ20517	Ì		. •
		/PROD=hypothetical protein			
			ĺ	ľ	
		FLJ20517 /DB_XREF=gi:8923486			. :
	l	/UG=Hs.39850 hypothetical		1	
	ļ	protein FLJ20517			
		/FL=gb:NM_017859.1			l
	The second	<u> </u>	,		
218536_at	0.034721	Consensus includes	AF052167		NP_065713
		gb:AF052167.1 /DEF=Homo		•	-
		sapiens clone 24749 and 24750	ł		
	, .	mRNA sequences. /FEA=mRNA			
	1	/DB_XREF=gi:3360478		1	ł
		/UG=Hs.30057 transporter similar			
			1		.
		to yeast MRS2	li I		:
		/FL=gb:NM_020662.1	1		}
		gb:AF288288.1		r .	
218543_s_at	0.046749	gb:NM_022750.1 /DEF=Homo	NM_022750		NP_073587
	ł	sapiens hypothetical protein	ì	1	ł
	+	FLJ22693 (FLJ22693), mRNA.			
		/FEA=mRNA /GEN=FLJ22693	}		
		/PROD=hypothetical protein		* 4	
	ł	FLJ22693	ŀ		
,		/DB_XREF=gi:12232412	,	,	
	ł	/UG=Hs.12646 hypothetical	ł ·	ŀ	
	1	protein FLJ22693	· \		
		/FL=gb:AL136766.1			
	ļ	gb:NM_022750.1		<u> </u>	
218553_s_at	0.027239	gb:NM_024076.1 /DEF=Homo	NM_024076		NP_076981
	•	sapiens hypothetical protein		} ;:	}
		MGC2628 (MGC2628), mRNA.			
	-	/FEA=mRNA /GEN=MGC2628	1	}	ļ
		/PROD=hypothetical protein	İ		
		MGC2628	1.		
		/DB_XREF=gi:13129063			
٠.			1	,	
		/UG=Hs.171637 hypothetical			
		protein MGC2628	· ·		1
•	,	/FL=gb:BC001185.1			
	1	gb:NM_024076.1			

		ng to Figure 19 - Coronary Artery I	Dis ase		
Gene	p-value	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
		į	No.	No	No.
218555 at	0.027792	gb:NM_013366.2 /DEF=Homo	NM 013366	110.	NP 037498
at	0.021702	sapiens anaphase-promoting	11111_0 10000		
_				·	¥
•		complex subunit 2 (APC2),			
4		mRNA. /FEA=mRNA			
•		/GEN=APC2 /PROD=anaphase-			
		promoting complex 2			
		/DB_XREF=gi:7549800			•
		/UG=Hs.23076 anaphase-			
*	1	promoting complex subunit 2]
		/FL=gb:AF191337.1			
		gb:NM_013366.2		,	
249607	0.024724		NINA 040445	<u> </u>	NID 000505
218607_s_at	0.034721	gb:NM_018115.1 /DEF=Homo ,	NM_018115	,	NP_060585
•		sapiens hypothetical protein		1	,
		FLJ10498 (FLJ10498), mRNA.			
		/FEA=mRNA /GEN=FLJ10498		,	
		/PROD=hypothetical protein			
		FLJ10498 /DB XREF=gi:8922466			
4.		/UG=Hs.109045 hypothetical			
	1	protein FLJ10498		İ	
1.00		1			
	1	/FL=gb:NM_018115.1	<u>.</u>		
040050	0.004704				
218652_s_at	0.034721	gb:NM_017733.1 /DEF=Homo	NM_017733	1.	NP_060203
		sapiens hypothetical protein			
		FLJ20265 (FLJ20265), mRNA		1 -	·
		/FEA=mRNA /GEN=FLJ20265			٠.٠
	1.	/PROD=hypothetical protein		1	
		FLJ20265 /DB_XREF=gi:8923239			
	i ·	/UG=Hs.7099 hypothetical protein	,	1	
		FLJ20265 /FL=gb:BC001249.1			
				} · ·	ł
		gb:BC000937.2 gb:NM_017733.1			
			` .	1	
· · · · · · · · · · · · · · · · · · ·					
218666_s_at	0.022752	gb:NM_017919.1 /DEF=Homo	NM_017919		NP_060389
·	} .	sapiens hypothetical protein		}	
		FLJ20651 (FLJ20651), mRNA.		1	
		/FEA=mRNA /GEN=FLJ20651	1		
in the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of th		/PROD=hypothetical protein			
* .	}				
•	l	FLJ20651 /DB_XREF=gi:8923603			<u> </u>
	1.	/UG=Hs.200332 hypothetical	1	}	
	. .	protein FLJ20651			
į		/FL=gb:NM_017919.1	<u>.</u>] .
	<u> </u>			1.	
218699_at	0.034721	RAB7, member RAS oncogene	BG338251	Hs.115325	NP_003920
_		family-like 1			-
				<u> </u>	<u> </u>

Gene		ng to Figure 19 - Coronary Artery I Description	Gene	Unigene	Protein
	p-value	Description			
ldentifier			Accession	Accession	Accession
			No.	No.	No.
218715_at	0.046749	gb:NM_018428.1 /DEF=Homo	NM_018428		NP_060898
		sapiens hepatocellular carcinoma-		[[
		associated antigen 66 (HCA66),		'	
		mRNA. /FEA=mRNA	-		
		/GEN=HCA66			J
		/PROD=hepatocellular carcinoma-			
•	i i	associated antigen 66			•,
		/DB XREF=gi:8923721			·
		/UG=Hs.30670 hepatocellular		``	
		carcinoma-associated antigen 66			
		/FL=gb:AF244135.1		·	
		gb:AF116631.1 gb:NM_018428.1]
218729_at	0.026013	gb:NM_020169.1 /DEF=Homo	NM 020169		NP 06455
_ · · · · · · · · · · · · · · · · · · ·		sapiens latexin protein (LXN),			-
	'	mRNA. /FEA=mRNA /GEN=LXN			
. *		/PROD=latexin_protein			
		/DB_XREF=gi:9910395			{
• •		/UG=Hs.109276 latexin protein			
		/FL=gb:BC005346.1			
		1		-	
210725 a at	0.024724	gb:AF282626.1 gb:NM_020169.1	AA349848	Hs.388482	ND 05520
		zinc finger protein		IDS.30040Z	NP_05529
218750_at	U.U25284 ¹ 	gb:NM_024116.1 /DEF=Homo	NM_024116		NP_07702
		sapiens hypothetical protein			
		MGC5306 (MGC5306), mRNA.			[-
1.5		/FEA=mRNA /GEN=MGC5306			
• • • • • • • • • • • • • • • • • • •		/PROD=hypothetical protein	4.	1 '	-
	F	MGC5306	ļ	1	
		/DB_XREF=gi:13129135			
		/UG=Hs.301732 hypothetical			;
	·	protein MGC5306			
		/FL=gb:AF275800.1	-		ļ
		gb:NM_024116.1			
218805_at	0.046749	gb:NM_018384.1 /DEF=Homo	NM_018384	, TE - TT	NP_06085
		sapiens hypothetical protein			
		FLJ11296 (FLJ11296), mRNA.			
		/FEA=mRNA /GEN=FLJ11296	٠.		
		/PROD=hypothetical protein			
		FLJ11296 /DB XREF=gi:8922984			
		/UG=Hs.26194 hypothetical	1	}	[·
		protein FLJ11296	1		:
		/FL=gb:NM_018384.1			
	l '	1/1 r-an:14161-0 10304.1			1

		ng to Figure 19 - Coronary Artery I			
Gene	p-value	Description	Gene	Unigene	Protein
dentifier		, , , , , , , , , , , , , , , , , , ,	Accession	Accession	Accession
Ä,		e de	No.	No.	No.
218817_at	0.025284	gb:NM_021928.1 /DEF=Homo	NM 021928		NP 06874
· · · · · · · · · · · · · · · · · · ·	1	sapiens hypothetical protein			· · · · · · · · · · · · · · · · · · ·
		FLJ22649 similar to signal			
•		peptidase SPC2223 (FLJ22649),			
		mRNA. /FEA=mRNA			
		1	<u> </u>		
		/GEN=FLJ22649			· ·
	r	/PROD=hypothetical protein	1		
	·	FLJ22649 similar to	· ·		
		signalpeptidase SPC2223		·	٠.
	ŀ	/DB_XREF=gi:11345461			
	ļ	/UG=Hs.42194 hypothetical	•		
		protein FLJ22649 similar to			,
		signal peptidase SPC2223		. 5. (
	i .	/FL=gb:NM_021928.1	-		
		gb:AL136660.1			115 0000
218819_at	0.018023	gb:NM_012141.1 /DEF=Homo	NM_012141	- %	NP_03627
		sapiens deleted in cancer 1;			
· · ·	1	RNA helicase HDBDICE1		4 °	
• • • • • • • • • • • • • • • • • • • •	7	(DDX26), mRNA. /FEA=mRNA			
		/GEN=DDX26 /PROD=DEADH		,	1.
		(Asp-Glu-Ala-AspHis) box	·		
	1	polypeptide 26			
et en en en en en en		/DB_XREF=gi:11024693			
		/UG=Hs.58570 deleted in cancer]	j
	1	1; RNA helicase HDBDICE1		* . *	
	**	/FL=gb:NM_012141.1		4.4	
		gb:AF097645.1			
	·				
218877_s_at	0.018222	gb:NM_021820.1 /DEF=Homo	NM_021820		NP_06859
	1	sapiens MDS024 protein			
		(MDS024), mRNA. /FEA=mRNA		, '	<u>:</u>
		/GEN=MDS024 /PROD=MDS024	• .		
*		protein /DB_XREF=gi:11141892			
-	, of	/UG=Hs.286122 MDS024 protein			
4		I · · · · · · · · · · · · · · · · · · ·		-	
	Ĭ	/FL=gb:AF182423.1		5	ľ
		gb:NM_021820.1			
218924_s_at	0.034721	gb:NM_004388.1 /DEF=Homo	NM_004388		NP_00437
		sapiens chitobiase, di-N-acetyl-			
		(CTBS), mRNA. /FEA=mRNA			,
	İ	/GEN=CTBS /PROD=chitobiase,		1	
F		Idi-N-acetyl-			
		/DB_XREF=gi:4758091			
	*				
		/UG=Hs 135578 chitobiase, di-N-			
		acetyl- /FL=gb:M95767.1		1	
	1	gb:NM 004388.1	1		

Gene	p-value	ng to Figure 19 - Coronary Artery I Description	Gen	Unigene	Protein
Identifier	p value	Doodilphon	Acc ssion	Accession	Accession
identiner				1 1 1 1 1	
			No.	No.	No.
218927_s_at	0.018222	gb:NM_018641.1 /DEF=Homo	NM_018641		NP_061111
,	[sapiens chondroitin 4-O-		1	· · · · · · · · · · · · · · · · · · ·
	1	sulfotransferase 2 (C4S-2),			
		mRNA. /FEA=mRNA /GEN=C4S-		•	·
		2 /PROD=chondroitin 4-O-		•	
		sulfotransferase 2			
1				,	
	*	/DB_XREF=gi:8922111			
•		/UG=Hs.25204 chondroitin 4-O-			
		sulfotransferase 2			1
		/FL=gb:BC002918.1			
		gb:NM_018641.1 gb:AF239822.1			
218963_s_at	0.049425	gb:NM 015515.1 /DEF=Homo	NM_015515		NP 775320
		sapiens DKFZP434G032 protein	, -		l –
		(DKFZP434G032), mRNA.		• .	
		/FEA=mRNA			
		1	ł		ŀ
	11.5	/GEN=DKFZP434G032			
• .	-	/PROD=DKFZP434G032 protein			
		/DB_XREF=gi:7661573			
	,	/UG=Hs.9029 DKFZP434G032	1	1. ·	
	1.0	protein /FL=gb:AF102848.1		, - ,	
		gb:NM_015515.1			
218982 s at	0.046749	gb:NM 015969.1 /DEF=Homo	NM 015969		NP_057053
		sapiens hypothetical protein	} _	1	_
		(HSPC011), mRNA. /FEA=mRNA			4
		/GEN=HSPC011			
er e		1		:	- 1
	ļ	/PROD=hypothetical protein	1		;
		/DB_XREF=gi:7705424		1	
		/UG=Hs 44298 hypothetical	,	· 1	
·	1	protein /FL=gb:AF077035.1			1 · 1
٠	<u> </u>	gb:NM_015969.1			<u> </u>
218986_s_at	0.046749	gb:NM_017631.1 /DEF=Homo	NM_017631		NP_060101
	·	sapiens hypothetical protein	•		
	· .	FLJ20035 (FLJ20035), mRNA.			İ .
		/FEA=mRNA /GEN=FLJ20035			1
		/PROD=hypothetical protein			
	,				1
, v	1.	FLJ20035 /DB_XREF=gi:8923037		· -	
		/UG=Hs.109309 hypothetical		1	
•		protein FLJ20035			
, .	1	/FL=gb:NM_017631.1			
				*** .	

Gene	p-value	Description	Gene	Unigene	Protein
ldentifi r			Accession	Accession	Accession
identiii i			No.	No.	No.
219002 at	0.038017	gb:NM_024622.1 /DEF=Homo	NM_024622	INO.	NP 078898
2 10002_at	0.000017	sapiens hypothetical protein	14101_02-1022		_070030
		FLJ21901 (FLJ21901), mRNA.			1 :
		/FEA=mRNA /GEN=FLJ21901			
		/PROD=hypothetical protein			
		FLJ21901	1.		1
		/DB_XREF=gi:13375843			*,
		/UG=Hs.32646 hypothetical			
•		protein FLJ21901			
		1.			ĺ
210045 of	0.018222	/FL=gb:NM_024622.1	NIM 040024	 	ND OCAGO
219045_at	0.010222	gb:NM_019034.1 /DEF=Homo	NM_019034		NP_061907
		sapiens hypothetical protein	J] .
		(RIF), mRNA. /FEA=mRNA			
		/GEN=RIF /PROD=hypothetical			
		protein /DB_XREF=gi:9506666			re to the
•		/UG=Hs 96593 hypothetical			Į.
		protein /FL=gb:AF239923.1			
010001	20010548	gb:NM_019034.1			
219081_at	0.046749	gb:NM_024668.1 /DEF=Homo	NM_024668		NP_078944
		sapiens hypothetical protein			
•		FLJ20288 (FLJ20288), mRNA.			
		/FEA=mRNA /GEN=FLJ20288	[:		
		/PROD=hypothetical protein			
		FLJ11979			·
	į.	/DB_XREF=gi:13386461].	j	
		/UG=Hs.84045 hypothetical		. •	
		protein FLJ20288	1		
		/FL=gb:BC004457.1			-
		gb:NM_024668.1			
219117_s_at	0.034721		NM_016594		NP_057678
	1,	sapiens FK506 binding protein			}
		precursor (LOC51303), mRNA.	,		İ
		/FEA=mRNA /GEN=LOC51303		. *	1.
		/PROD=FK506 binding protein			-
		precursor /DB_XREF=gi:7706130	1	1	1
		/UG=Hs 24048 FK506 binding	,		
•		protein precursor			
		/FL=gb:AF238079.1			
		gb:NM_016594.1		1	[·
	1		1	1	l

		ng to Figure 19 - Coronary Artery	Diseas		<u></u>
Gene	p-valu	Description	Gene	Unigene	Protein
Identifier	<u> </u>		Accession	Accession	Accession
			No.	No.	No.
219118_at	0.018023	gb:NM 016594.1 /DEF=Homo	NM 016594	1110.	NP 057678
210.10_ut	0.010020	sapiens FK506 binding protein	111111111111111111111111111111111111111		
	1	precursor (LOC51303), mRNA.		ļ	
		/FEA=mRNA /GEN=LOC51303	l ·		(
				,	
	<u> </u>	/PROD=FK506 binding protein			4
		precursor /DB_XREF=gi:7706130			
	1	/UG=Hs.24048 FK506 binding			
e La companya da sa sa sa sa sa sa sa sa sa sa sa sa sa		protein precursor	`		-
	1	/FL=gb:AF238079.1	ľ.		i .
		gb:NM_016594.1			
219186_at	0.034721	gb:NM_020224.1 /DEF=Homo	NM_020224		NP_064609
ू र		sapiens hypothetical protein	[`	ſ.	
		DKFZp547O146			
0		(DKFZp547O146), mRNA.			İ
		/FEA=mRNA			
		/GEN=DKFZp547O146			
		/PROD=hypothetical protein		-	
		DKFZp547O146			
٠.	j	/DB_XREF=gi:9910203		J , .	
		/UG=Hs.91246 hypothetical			
	j	protein DKFZp547O146			}
		/FL=gb:NM_020224.1			
219198 at	0.019603	gb:NM_012204.1 /DEF=Homo	NINA 040004	 	ND 02022
219190_at	0.016093	. –	NM_012204		NP_036336
	ļ	sapiens general transcription			
	-	factor IIIC, polypeptide 4 (90kD)			
		(GTF3C4), mRNA. /FEA=mRNA			
		/GEN=GTF3C4 /PROD=general		•	
		transcription factor IIIC,			}
		polypeptide 4(90kD)		•	
		/DB_XREF=gi:6912399			1
		/UG=Hs.22302 general			· ·
•	}	transcription factor IIIC,		•	
		polypeptide 4 (90kD)	,		
		/FL=gb:AF142328.1			İ
	l :	gb:NM_012204.1	·		
219235_s_at	0.046651	gb:NM_023923.1 /DEF=Homo	NM 023923		NP_076412
		sapiens hypothetical protein	-		_
		FLJ13171 (FLJ13171), mRNA.	,		
*	ļ	/FEA=mRNA /GEN=FLJ13171		3	
		/PROD=hypothetical protein			1
		FLJ13171			
		/DB_XREF=gi:12965188	1		1
		/UG=Hs.225641 hypothetical			
		· · · · · · · · · · · · · · · · · · ·	1	ľ	[
_		protein FLJ13171	.[1
	ľ	/FL=gb:AF130081.1		ľ	
	L	gb:NM_023923.1	<u> </u>	L	

		ng to Figure 19 - Coronary Artery I	6 7 7 7 1		
	p-value	Description	Gene	Unigene	Protein
Identifi r			Acc ssion	Accession	Accession
			No.	No.	No.
219282_s_at	0.025284	gb:NM_015930.1 /DEF=Homo	NM_015930	А	1
- 19 1 1		sapiens vanilloid receptor-like	-		
		protein 1 (VRL-1), mRNA.			
		/FEA=mRNA /GEN=VRL-1		Í	1
		/PROD=vanilloid receptor-like			l
		protein 1 /DB_XREF=gi:7706764	٠.	· ·	
		/UG=Hs.279746 vanilloid receptor] .	J •
	-	like protein 1 /FL=gb:AF129112.1			,
	ir ir	gb:NM_015930.1			
		gb.14141_015950.1			
			* .	}	:
040000	0.040740	1. NIM 044005 4 (DEE 11	NIM 044005		NID OFFOR
219290_x_at	0.046749	gb:NM_014395.1 /DEF=Homo	NM_014395		NP_055210
v.**		sapiens dual adaptor of			
• •	,	phosphotyrosine and 3-	**		
		phosphoinositides (DAPP1),	.`		
		mRNA. /FEA=mRNA	}		
		/GEN=DAPP1 /PROD=dual			
44 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	•	adaptor of phosphotyrosine and3			1
		phosphoinositides			
		/DB_XREF=gi:7657006			
		/UG=Hs.62643 dual adaptor of			
		phosphotyrosine and 3-		}	}
		phosphoinositides			
] -	/FL=gb:AF186022.1		1	
		gb:NM_014395.1		.*	
219303_at	0.034721	gb:NM_024546.1 /DEF=Homo	NM_024546		NP 078822
	0.001121	sapiens hypothetical protein	102 10 10		
		FLJ13449 (FLJ13449), mRNA.	1.	l sa j	1
		/FEA=mRNA /GEN=FLJ13449			
1		/PROD=hypothetical protein			
					,
		FLJ13449			
		/DB_XREF=gi:13375708			
		/UG=Hs.10711 hypothetical			,
		protein FLJ13449			
_		/FL=gb:AL136651.1	[()	
	<u> </u>	gb:NM_024546.1			
219304_s_at	0.018023	gb:NM_025208.1 /DEF=Homo	NM_025208		NP_149126
		sapiens spinal cord-derived		,	,
		growth factor-B (SCDGF-B),			
	j	mRNA. /FEA=mRNA			j
		/GEN=SCDGF-B /PROD=spinal			
		cord-derived growth factor-B			
•		/DB_XREF=gi:13376807			
		/UG=Hs.112885 spinal cord-		. ^	J
		derived growth factor-B		ĺ	
]	/FL=gb:AB033832.1		1	
	l	gb:AF113216.1 gb:NM_025208.1			
		100 AE 1137 IN 1 00 NW 175798 1	1	4	

G ne	p-value	ng to Figure 19 - Coronary Artery Description	Gene	Unigene	Protein
Identifier	Parale	Description	Accession	Accession	
laentifier		·		1	Accession
210224 0 0	0.024724	gb:NM 022837.1 /DEF=Homo	No. NM 022837	No.	No. NP_073748
219334_s_at	0.034721	1 ·	INIVI_UZZ637	 }	INP_0/3/40
		sapiens hypothetical protein			
	1	FLJ22833 (FLJ22833), mRNA.		·	
		/FEA=mRNA /GEN=FLJ22833			
		/PROD=hypothetical protein		₹	
	1	FLJ22833		,	
	ł	/DB_XREF=gi:12383083			·
_		/UG=Hs.118183 hypothetical			
	1	protein FLJ22833			1
, ,		/FL=gb:NM_022837.1			
219351_at	0.018023	gb:NM_014563.1 /DEF=Homo	NM_014563		NP_055378
		sapiens spondyloepiphyseal			
		dysplasia, late (SEDL), mRNA.			
* •		/FEA=mRNA /GEN=SEDL		1	
		/PROD=spondyloepiphyseal			
*		dysplasia, late		<u> </u>	4
		/DB_XREF=gi:7657547			
	İ	/UG=Hs.174038		·	
. "	14	spondyloepiphyseal dysplasia,			
	Ĺ	late /FL=gb:NM_014563.1			Į
219386_s_at	0.041795	gb:NM_020125.1 /DEF=Homo	NM_020125		NP_064510
		sapiens BCM-like membrane			}
		protein precursor (SBBI42),	, ~	·	
	1	mRNA. /FEA=mRNA	}	ļ.	
·		/GEN=SBBI42 /PROD=BCM-like			
•		membrane protein precursor			ľ
	'	/DB_XREF=gi:9910341			
	1	/UG=Hs.20450 BCM-like			
		membrane protein precursor	*		
, ,		/FL=gb:AF144235.1	ĺ	~	[
		gb:NM 014036.1 gb:AF146761.1			
		gb:NM_020125.1			
219399_at	0.018222	gb:NM_018362.1 /DEF=Homo	NM 018362		NP_060832
		sapiens likely ortholog of mouse		1	
	ļ	LIN-7C; mammalian LIN-7	1) ·
,		protein 3 (LIN-7-C), mRNA.			
		//FEA=mRNA /GEN=LIN-7-C	v	1	
¥*		/PROD=LIN-7 protein 3		1 .	
		//DB_XREF=gi:8922943	i.		}
		/UG=Hs.306206 LIN-7 protein 3			
				1	
		/FL=gb:NM_018362.1		<u> </u>	<u></u>

Gene	p-value	ng to Figure 19 - Coronary Artery Description	Gene	Unigene	Protein
Identifier	Pivalac		Accession	Accession	Accession
identinei			1		No.
040544 -4	0.020525	Th.NM 047906 4 /DEE-Home	No. NM 017806	No.	NP 060276
219541_at	0.038535	gb:NM_017806.1 /DEF=Homo	114141_017606		NF_000276
		sapiens hypothetical protein			
*		FLJ20406 (FLJ20406), mRNA.			
•		/FEA=mRNA /GEN=FLJ20406		1	
]	/PROD=hypothetical protein			
•] .	FLJ20406 /DB_XREF=gi:8923377			
•		/UG=Hs.149227 hypothetical			
		protein FLJ20406			
· .		/FL=gb:NM_017806.1	ļ]	
:		7. 2 gb.(tim_0 1.000.1			
219574_at	0.034721	gb:NM 017923.1 /DEF=Homo	NM 017923		NP 060393
218014_al	0.034721	10			141000393
		sapiens hypothetical protein		j '	
		FLJ20668 (FLJ20668), mRNA.			
		/FEA=mRNA /GEN=FLJ20668			-
		/PROD=hypothetical protein			
		FLJ20668 /DB_XREF=gi:8923612			
,		/UG=Hs 12920 hypothetical	ř		
4		protein FLJ20668			
		/FL=gb:NM 017923.1		* * * * * * * * * * * * * * * * * * * *	
. 1	ļ ·				
219582 at	0.018023	gb:NM 024576.1 /DEF=Homo	NM_024576		NP 078852
		sapiens hypothetical protein	-		- ·
		FLJ21079 (FLJ21079), mRNA.			
	1.7	/FEA=mRNA /GEN=FLJ21079			ļ
	i .	/PROD=hypothetical protein		K 9	
		FLJ21079			
		•			,
, *		/DB_XREF=gi:13375751		1	
	1	/UG=Hs.16512 hypothetical		•	
	6.0 Tu	protein FLJ21079		Į.	
		/FL=gb:NM_024576.1		<u> </u>	<u> </u>
219599_at	0.034721		NM_018507		NP_06097
		sapiens hypothetical protein			1 :
		PRO1843 (PRO1843), mRNA.			
		/FEA=mRNA /GEN=PRO1843			
		/PROD=hypothetical protein		i	l
		PRO1843 /DB_XREF=gi:8924082		1 .	
		/UG=Hs.283330 hypothetical			
i i		protein PRO1843			
		/FL=gb:AF119854.1			
	1		·		
,		gb:NM_018507:1			
l	<u>i</u>		1	L	

		ng to Figure 19 - Coronary Artery I		11	Ducto!-
Gene	p-value	D scription	Gene	Unigene	Protein
ldentifier	,		Accession	Acc ssion -	Accession
		· · · · · · · · · · · · · · · · · · ·	No	No.	No.
219600 s at	0.046749	gb:NM_006134.2 /DEF=Homo	NM 006134		NP 006125
		sapiens chromosome 21 open	-	ļ _.	∦ - -
		reading frame 4 (C21ORF4),	• •		
		mRNA. /FEA=mRNA		, 7	
		/GEN=C21ORF4		`	
		/PROD=chromosome 21 open			
		reading frame 4			1
		/DB_XREF=gi:8659558			
		/UG=Hs.284142 chromosome 21			1
all english	1 1	open reading frame 4			
		/FL=gb:BC000569.1			
		gb:AF045606.2 gb:NM_006134.2			,
0400074	0.020254		NM 017935	 	NP 060405
219667_s_at	0.036254	gb:NM_017935.1 /DEF=Homo	1001/935		111-000403
		sapiens hypothetical protein		l'	
	* -	FLJ20706 (FLJ20706), mRNA.	•		
		/FEA=mRNA /GEN=FLJ20706			
		/PROD=hypothetical protein			
		FLJ20706 /DB_XREF=gi:8923635			
		/UG=Hs.193736 hypothetical		[
. '		protein FLJ20706			
		/FL=gb:NM_017935.1			·
		/FL=gb.NW_01/933.1			
	0.007000	1 NIM 0004004 /DEE 11	NIM 000400		ND 005420
219669_at	0.027239	gb:NM_020406.1 /DEF=Homo	NM_020406		NP_065139
		sapiens polycythemia rubra vera			1
# . # .		1; cell surface receptor (PRV1),			· .
•		mRNA. /FEA=mRNA		·	
		/GEN=PRV1			,
		/PROD=polycythemia rubra vera		, ,	
		1; cell surfacereceptor			
		/DB_XREF=gi:9966888			,
	•				
		/UG≂Hs.232165 polycythemia			
1.		rubra vera 1; cell surface	•		. 1
,		receptor /FL=gb:AF146747.1			
		gb:NM_020406.1		<u> </u>	
219679 s at	0.026013	gb:NM_018604.1 /DEF=Homo	NM_018604		
		sapiens hypothetical protein		1	
'		PRO1741 (PRO1741), mRNA.	. ,	1	
		/FEA=mRNA /GEN=PRO1741	,		
		/PROD=hypothetical protein			
		PRO1741 /DB XREF=gi:8924074			
,				Į.	:
		/UG=Hs.306067 hypothetical			
	1	protein PRO1741			
	1	/FL=gb:AF116666.1	1	1	1 ' .'
		// L gb./ (1 10000.)			
		gb:NM_018604.1			

Gene	p-value	Description	Gene	Unigene	Protein
ldentifier			Accession	Accession	Accession
identifier			No.	No.	No.
219717_at	0.049425	gb:NM 017741.1 /DEF=Homo	NM 017741	110.	NP 06021
z (9) 11 _at	0.043423	sapiens hypothetical protein			_00021
	ı	FLJ20280 (FLJ20280), mRNA.			
•		/FEA=mRNA /GEN=FLJ20280			
					•
		/PROD=hypothetical protein			1.
		FLJ20280 /DB_XREF=gi:8923256		1.	
	ı	/UG=Hs.270134 hypothetical	•	\	
		protein FLJ20280			
	ļ ·	/FL=gb:NM_017741.1			
219757_s_at	0.036254	gb:NM_017799.1 /DEF=Homo	NM_017799	1	NP 060269
210101_8_at	3.000204	sapiens hypothetical protein			
J	1 × ×	FLJ20392 (FLJ20392), mRNA.	! :	1 2 2	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		/FEA=mRNA /GEN=FLJ20392			
		/PROD=hypothetical protein			
		FLJ20392 /DB_XREF=gi:8923365			
4		/UG=Hs.27047 hypothetical)	
•		protein FLJ20392			
		/FL=gb:NM_017799.1			
040000	0.004704	-b-NIM 0040544 (DEE-Horse	NNA 024054	 	ND 07042
219802_at	0.034721	gb:NM_024854.1 /DEF=Homo	NM_024854		NP_07913
**		sapiens hypothetical protein			
		FLJ22028 (FLJ22028), mRNA.		.	
		/FEA=mRNA /GEN=FLJ22028			
		/PROD=hypothetical protein		•	
,		FLJ22028			
		/DB_XREF=gi:13376278	·		ļ
**		/UG=Hs.192570 hypothetical			
		protein FLJ22028	. :		
		/FL=gb:NM_024854.1			
219812_at	0.018222		NM_024070	1 .	
•	5	sapiens hypothetical protein			
		MGC2463 (MGC2463), mRNA.			
		/FEA=mRNA /GEN=MGC2463			
	!	/PROD=hypothetical protein		1	1
		MGC2463			
		/DB_XREF=gi:13129051			
	~	/UG=Hs.323634 hypothetical		1	
		protein MGC2463	·	-[1
		/FL=gb:BC001129.1			
		gb:NM_024070.1		1	

Gene	p-value	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
identinier		**	No.	No.	No.
219878 s_at	0.03018	gb:NM 015995.1 /DEF=Homo	NM 015995	110.	NP 057079
<u></u>	}	sapiens Kruppel-like factor 13			
		(KLF13), mRNA. /FEA=mRNA			$\overline{}$
	i	/GEN=KLF13 /PROD=Kruppel-like	•		
		factor 13 /DB_XREF=gi:7706289			
		/UG=Hs.7104 Kruppel-like factor			1
		13 /FL=gb:AF132599.1			
		gb:AF150628.1 gb:NM_015995.1		l .	
		gb.AF 150028.1 gb.NM_0 15995.1			
219941 at	0.042466	gb:NM 018279.1 /DEF=Homo	NM_018279	· · · · · · · · · · · · · · · · · · ·	NP 060749
2 15541_at	0.042400	sapiens hypothetical protein	14141_010275		Jul _000743
	÷	FLJ10936 (FLJ10936), mRNA.			
		/FEA=mRNA /GEN=FLJ10936		-	,
-	V	/PROD=hypothetical protein			
		FLJ10936 /DB_XREF=gi:8922782			200
1		/UG=Hs.7337 hypothetical protein			
	1	FLJ10936 /FL=gb:NM_018279.1			
		FE3 10930		• .	
				,	
219957_at	0.018023	gb:NM 017987.1 /DEF=Homo	NM 017987	 	NP_06045
	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	sapiens hypothetical protein			
		FLJ10063 (FLJ10063), mRNA.			
		/FEA=mRNA /GEN=FLJ10063	4.5	1	
•		/PROD=hypothetical protein \		ł	∦.
	'.	FLJ10063 /DB_XREF=gi:8922215			
	4.5	/UG=Hs.154091 hypothetical			
		protein FLJ10063	1		
•		/FL=gb:NM_017987.1		1	ì
219983_at	0.021165	gb:NM_020386.1 /DEF=Homo	NM 020386		NP 065119
, -	ļ	sapiens H-REV107 protein-] -
		related protein (LOC57110),			
		mRNA. /FEA=mRNA			
	~	/GEN=LOC57110 /PROD=H-			
	}	REV107 protein-related protein	1		1
		/DB XREF=gi:9966858		'	
		/UG=Hs.36761 H-REV107 protein		1	
		related protein	1		
	1	/FL=gb:AB030816.1		1	
•,		gb:NM 020386.1		1 /	

Gene Accession Accession No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No.
No. No. No. No. No. F=Homo NM_018150 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP_06062 NP
F=Homo NM_018150 NP_06062 protein), mRNA. LJ10597 protein =gi:8922541 netical F=Homo NM_018113 NP_06058 protein), mRNA.
protein), mRNA. LJ10597 protein =gi:8922541 netical F=Homo protein), mRNA. NP_06058
), mRNA. LJ10597
LJ10597 protein =gi:8922541 netical F=Homo
F=Homo NM_018113 NP_06058 protein), mRNA.
=gi:8922541
F=Homo NM_018113 NP_06058 protein), mRNA.
F=Homo NM_018113 NP_06058 protein), mRNA.
F=Homo NM_018113 NP_06058 protein), mRNA.
F=Homo
F=Homo
protein), mRNA.
protein), mRNA.
), mRNA
1.110494
protein
=gi:8922462
thetical
linelical
F-11 NIM 000000 NID 07470
F=Homo NM_022336 NP_07173
11,
EDAR),
1,
30
ysplasin 1,
F=Homo NM_016371 NP_05745
d (17-beta)
SD17B7),
d (17-beta)
0
pxysteroid
ase 7
asc /

Gene	p-value	ng to Figure 19 - Coronary Artery I Description	Gene	Unigene	Protein
	b-yaine	Description		Accession	Accession
ldentifier		,	Accession	1 :	
	<u> </u>	<u> </u>	No.	No.	No.
220187_at	0.034721	gb:NM_024636.1 /DEF=Homo	NM_024636	· .	NP_078912
		sapiens hypothetical protein			:
	1	FLJ23153 (FLJ23153), mRNA.			<i>.</i>
	ľ	/FEA=mRNA /GEN=FLJ23153	t		
	1 .	/PROD=hypothetical protein			
	1	FLJ23153]
		/DB XREF=gi:13375867			
	ŀ	/UG=Hs.44208 hypothetical		1.00	
		protein FLJ23153			
		/FL=gb:NM_024636.1	i		i .
220207 -4	0.00000		NM_016382	 	NP 057466
220307_at	0.028893	gb:NM_016382.1 /DEF=Homo	NIVI_0 10302	'	[NP_05/460
	1.	sapiens natural killer cell		· ·	
		receptor 2B4 (CD244), mRNA			a constraint
		/FEA=mRNA /GEN=CD244			1
		/PROD=natural killer cell			
		receptor 2B4	·	!	Ì
	1	/DB_XREF=gi:7706528			1
•		/UG=Hs.157872 natural killer cell		•	
•	-	receptor 2B4 /FL=gb:AF242540.1		ł	
		gb:AF105261.1 gb:AF145782.1			
		gb:AF107761.2 gb:AF117711.1	1	1.	· • •
		lgb.NM_016382.1			
	-{	19p.14W_010502.1			
220336 s at	0.022856	gb:AB043821.1 /DEF=Homo	AB043821	 	NP 05744
ai	0.023030	1 -			_05/44/
	•	sapiens GPVI mRNA for platelet		1	,
	Λ	glycoprotein VI-3, complete cds.	-		
	[/FEA=mRNA /GEN=GPVI		J	
ļ.		/PROD=platelet glycoprotein VI-3	1	1	ļ
	1	/DB_XREF=gi:9955913			
		/UG=Hs.272216 glycoprotein VI		ì	1
; .		(platelet) /FL=gb:AB035073.1	* .		<u> </u>
		gb:NM_016363.1 gb:AB043819.1	[·	1	
	1	gb:AB043821.1		}	,
			A		
220342 x at	0.018222	gb:NM_017992.1 /DEF=Homo	NM 017992	1	1
2200 12_X_0	0.01022	sapiens hypothetical protein	1111_511.002		
	1	FLJ10083 (FLJ10083), mRNA.	· ·		
		/FEA=mRNA /GEN=FLJ10083	J		1
• .		I '		1	
	1	/PROD=hypothetical protein	}		1
		FLJ10083 /DB_XREF=gi:8922223	ŀ		
		/UG=Hs.279951 hypothetical	1	1	1
		protein FLJ10083			1
	,	/FL=gb:NM_017992.1	1		
1	1	1	1	1	1

		ng to Figure 19 - Coronary Artery I			
Gene	p-value	Description	Gene	Unig ne	Protein
ldentifi r			Accession	Acc ssion	Accession
	,	•	No.	No.	No.
220547_s at	0.025284	gb:NM_019054.1 /DEF=Homo	NM_019054		NP_061927
	**********	sapiens hypothetical protein	-	. +	_
		MGC5560 (MGC5560), mRNA.			
,	* .	/FEA=mRNA /GEN=MGC5560	•		
		/PROD=hypothetical protein			
		MGC5560			
			· ·	ļ .·	
	. '	/DB_XREF=gi:12963480	* -		
		/UG=Hs.233150 hypothetical			. ;
		protein MGC5560			
		/FL=gb:NM_019054.1			
220580_at	0.034721	gb:NM_025044.1 /DEF=Homo	NM_025044	4	NP_079320
		sapiens hypothetical protein	1		
·		FLJ22476 (FLJ22476), mRNA.		,	*.
	,	/FEA=mRNA /GEN=FLJ22476	l		·
		/PROD=hypothetical protein			
*		FLJ22476			
		/DB_XREF=gi:13376569			
•		/UG=Hs.287696 hypothetical			
100		protein FLJ22476]		
		/FL=gb:NM_025044.1			
220607 x at	0.034721	gb:NM_016397.1 /DEF=Homo	NM 016397		NP_05748
220001_x_at	0.004121	Isapiens TH1 drosophila homolog			_03740
				}.	
	<u> </u>	(HSPC130), mRNA. /FEA=mRNA		!	
A .	Į.	/GEN=HSPC130 /PROD=TH1			
		drosophila homolog			
•,*	17	/DB_XREF=gi:7705462			
. ·	ł	/UG=Hs.5184 TH1 drosophila			
	,	homolog /FL=gb:AF161479.1	ŀ		
		gb:NM_016397.1_			<u> </u>
220646 s at	0.026013	gb:NM_016523.1 /DEF=Homo	NM_016523	1	NP_057607
· · · · · · · · · · · · · · · · · · ·		sapiens killer cell lectin-like	-		
	}	receptor F1 (KLRF1), mRNA.			
		/FEA=mRNA /GEN=KLRF1		•	
•	[/PROD=killer cell lectin-like			
		receptor F1	1	1	
		1		1	
	{	//DB_XREF=gi:7705573	1	J	
		/UG=Hs.183125 killer cell lectin-			
	* .	like receptor F1		1	
]	/FL=gb:AF175206.1			,
 		gb:NM_016523.1			
220684_at	0.025284	gb:NM_013351.1 /DEF=Homo	NM_013351		NP_03748
		sapiens T-box 21 (TBX21),			
		mRNA. /FEA=mRNA			}
		/GEN=TBX21 /PROD=T-box 21			
	1	/DB_XREF=gi:7019548			
·		/UG=Hs.272409 T-box 21] .		
		/FL=gb:AF093098.1		1	
1					

		ng to Figure 19 - Coronary Artery I	Jisease		
Gene	p-value	Description	Gene	Unigene	Protein
Identifier			Accession	Accession	Accession
			No.	No.	No.
220704 at	0.046749	gb:NM 018563.1 /DEF=Homo	NM_018563		NP_006051
,- <u></u>	. 0. 9. 19.1. 19.	sapiens hypothetical protein			
P. Carlotte		PRO0758 (PRO0758), mRNA.			·
		1]	
-		/FEA=mRNA /GEN=PRO0758		·	ļ
	Ì	/PROD=hypothetical protein	. ±		
		PRO0758 /DB_XREF=gi:8923974			} · .
		/UG=Hs.283708 hypothetical			
	, '	protein PRO0758			·
,		/FL=gb:AF116605.1		-/	t v r
,		gb:NM_018563.1			
• .			,		
220740 s at	0.034721	gb:NM 005135.1 /DEF=Homo	NM_005135		NP 005126
2207-10_5_at	0.004721	sapiens solute carrier family 12	11111_000100		_000120
* :		(potassiumchloride transporters),			1 * .
	1			* · ·	
	, .	member 6 (SLC12A6), mRNA.		1	
	· · · · · · · · · · · · · · · · · · ·	/FEA=mRNA /GEN=SLC12A6	{	<u> </u>	1
		/PROD=solute carrier family 12			1
		(potassiumchloridetransporters),	·		
		member 6			
	}	/DB_XREF=gi:4826779	· ·		
		/UG=Hs.4876 solute carrier			
,		family 12 (potassiumchloride			
	i ·	transporters), member 6	1.		
i	·			40.0	
	l .	/FL=gb:AF108831.1		11. The second	
;	•	gb:NM_005135.1	[
			 	<u> </u>	
220753_s_at	0.048741	gb:NM_015974.1 /DEF=Homo	NM_015974		NP_057058
:	·	sapiens lambda-crystallin			
		(LOC51084), mRNA.			
	l ' '	/FEA=mRNA /GEN=LOC51084			l
1		/PROD=lambda-crystallin			
.'		/DB_XREF=gi:7705743			* .
	1	/UG=Hs.108896 lambda-crystallin			<u>'</u>
•		/FL=gb:AF077049.1	·		
		, -)	,	
000704	0.040000	gb:NM_015974.1	1111 04 4400		NE 05 1050
220791_x_at	0.018023	gb:NM_014139.1 /DEF=Homo	NM_014139		NP_054858
		sapiens sodium channel, voltage-		}	
		gated, type XII, alpha			ľ
·		polypeptide (SCN12A), mRNA.			l .
		/FEA=mRNA /GEN=SCN12A			i i
•	,	/PROD=sodium channel, voltage-	}	1	\ ' '
		gated, type XII, alphapolypeptide	ļ.		j
	2.0	/DB_XREF=gi:7657541			
		/UG=Hs.186877 sodium channel,		1	
		I " ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' '	1.	1	J .
		voltage-gated, type XII, alpha			1
	[polypeptide /FL=gb:AF109737.1			
		gb:NM_014139.1		1	
	· ·	190.jun_014100.1	1	1	ſ
		JB. 14105. 1	· .		

		ng to Figure 19 - Coronary Artery I		Unic no	Drotois
Gene Identifier	p-value	Description	Gene Accession	Unig ne Accession	Protein Accession
			No.	No.	No.
220905_at	0.038535	gb:NM_025007.1 /DEF=Homo	NM_025007		}
		sapiens hypothetical protein		1 1 T 1 W 1 T 1	
		FLJ13501 (FLJ13501), mRNA.			(
	•	/FEA=mRNA /GEN=FLJ13501			
•		/PROD=hypothetical protein			
		FLJ13501			•
		/DB_XREF=gi:13376524		1	1
•		/UG=Hs.287576 hypothetical			
	[protein FLJ13501			
	ł	/FL=gb:NM_025007.1			
220918 at	0.026842	gb:NM 025143.1 /DEF=Homo	NM_025143		NP 079419
		sapiens hypothetical protein	-		
		FLJ20856 (FLJ20856), mRNA.			1
	1	/FEA=mRNA /GEN=FLJ20856			l
		/PROD=hypothetical protein			
		FLJ20856			,
, s = 1		/DB_XREF=gi:13376728			
		/UG=Hs.288916 hypothetical		k 15	
		protein FLJ20856	<u> </u>	,	
		/FL=gb:NM_025143.1			
220925 at	0.018022	gb:NM 021929.1 /DEF=Homo	NM 021929		NP 068748
220925_at	0.010023	sapiens hypothetical protein	14141_02 1929	· ·	141 _0007 40
	1:	FLJ21613 similar to rat corneal	1	·	1
		wound healing related protein			1
		•			
-		(FLJ21613), mRNA. /FEA=mRNA	1.		į
	· .	/GEN=FLJ21613			1
		/PROD=hypothetical protein			
·		FLJ21613 similar to ratcorneal			
1		wound healing related protein	1		ł
]		/DB_XREF=gi:11345463]		
		/UG=Hs.300952 hypothetical	-		1
•		protein FLJ21613 similar to rat			1
		corneal wound healing related			
 	ļ	protein /FL=gb:NM_021929.1			1
220940_at	0.025284		NM_025190	İ	NP_079466
	}	sapiens KIAA1641 protein	ŀ	}	
		(KIAA1641), mRNA. /FEA≃mRNA			
1		/GEN=KIAA1641			
		/PROD=hypothetical protein	1	1	1
		FLJ21281			
		/DB_XREF=gi:13449272		·	1
1		/UG=Hs.44566 KIAA1641 protein		1	
1	1	/FL=gb:NM_025190.1	1	l	

		ng to Figure 19 - Coronary Artery I			
Gene	p-value	Description	Gene	Unigene	Prot in
ld ntifier			Accession	Accession	Accession
•] .		No.	No.	No.
220941_s at	0.034721	gb:NM 017447.1 /DEF=Homo	NM 017447	1	NP_059143
		sapiens hypothetical protein	-	4.40	
	i .	LOC54149 (YG81), mRNA.			
	[•	ĺ
		/FEA=mRNA /GEN=YG81			
	1	/PROD=hypothetical protein			
	1.	LOC54149			}
. *		/DB_XREF=gi:8394546			
-		/UG=Hs.49391 hypothetical	•		
]	protein LOC54149	,	}- *	
	1	/FL=gb:NM_017447.1			
220942 x at	0.034721	gb:NM_014367.1 /DEF=Homo	NM 014367		NP_055182
		sapiens hypothetical protein,	_		
		estradiol-induced (E2IG5),		ì	1
		mRNA /FEA=mRNA	* . * ·		
		/GEN=E2IG5 /PROD=hypothetical			3 %
	1	protein, estradiol-induced		1	
		/DB_XREF=gi:7657049			1
٠.		/UG=Hs.5243 hypothetical			
		protein, estradiol-induced			
		/FL=gb:AF191020.1			·
		gb:NM 014367.1			
	1			į	
220966 x at	0.026842	gb:NM_030978.1 /DEF=Homo	NM 030978	11.11.11	NP_112240
	}	sapiens hypothetical protein	1		_
	l	similar to actin related protein			
		23 complex, subunit 5			ĺ
,	J			ļ	
	·	(MGC3038), mRNA. /FEA=mRNA	\ · · · · · · · · · · · · · · · · · · ·		
		/GEN=MGC3038			
	1	/PROD=hypothetical protein			· ·
1	,	similar to actin relatedprotein 23			1
		complex, subunit 5		1	
	1	/DB_XREF=gi:13569955	1		
		/FL=gb:NM_030978.1		·	1_
220969 s at	0.042057		NM_030892		
		sapiens hypothetical protein	-	· .	1
	1.	FLJ11786 (FLJ11786), mRNA.		1 '	
		/FEA=mRNA /GEN=FLJ11786	,		1
		/PROD=hypothetical protein		1	
		FLJ11786		· .	
;		1	1.	1	1
'		/DB_XREF=gi:13569855			
004607	0.010=	/FL=gb:NM_030892.1	NINA BOOGGE	 	NB 43544
221027_s_at	0.046749	gb:NM_030821.1 /DEF=Homo	NM_030821		NP_110448
		sapiens group XII secreted		1	
1	1	phospholipase A2 (PLA2G12),	ļ		1
		mRNA. /FEA=mRNA			
1	- [/GEN=PLA2G12 /PROD=group	1 .		
		XII secreted phospholipase A2	!		1
		/DB_XREF=gi:13540619			1
	-	/FL=gb:NM_030821.1	-		
L	<u> </u>	IN E-GD.14141_03002 1.1	<u> </u>	1	

		ig to Figure 19 - Coronary Artery [
Gene	p-value	Description	Gene	Unigene	Protein
dentifier			Accession	Accession	Accession
40			No	No.	No.
221080 s at	0.034721	gb:NM 024898.1 /DEF=Homo	NM_024898	INO.	NP 079174
221060_s_at	0.034721	-	NIVI_U24090	ŀ	NP_0/91/4
		sapiens hypothetical protein			
		FLJ22757 (FLJ22757), mRNA.			
		/FEA=mRNA /GEN=FLJ22757			
		/PROD=hypothetical protein		The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	
		FLJ22757	* .		
	!	/DB_XREF=gi:13376352			
		/UG=Hs.236449 hypothetical			+1
		protein FLJ22757		* *	
		/FL=gb:NM_024898.1			
221090_s_at	0.018023	gb:NM_018233.1 /DEF=Homo	NM 018233		NP 060703
	0.010020	sapiens hypothetical protein	0,0200		
				<u> </u>	
		FLJ10826 (FLJ10826), mRNA.	. 1		
		/FEA=mRNA /GEN=FLJ10826			
and the state of	(/PROD=hypothetical protein	[
		FLJ10826 /DB XREF=gi:8922693		** * *	
•	ł .	/UG=Hs.24809 hypothetical			† .
	ł	protein FLJ10826			
	l ·	/FL=gb:NM_018233.1			100
221203 s at	0.025284	gb:NM_018023.2 /DEF=Homo	NM 018023		NP 060493
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	sapiens hypothetical protein	_		
•		FLJ10201 (FLJ10201), mRNA.			
e de la companya de la companya de la companya de la companya de la companya de la companya de la companya de					
		/FEA=mRNA /GEN=FLJ10201			
		/PROD=hypothetical protein			
		FLJ10201		н	
		/DB_XREF=gi:13492976			
	1	/UG=Hs.318127 hypothetical	1.		
			and the second		
		protein FLJ10201		l de la companya de la companya de la companya de la companya de la companya de la companya de la companya de	1
·		/FL=gb:NM_018023.2			
221211_s_at	0.034721	gb:NM_020152.1 /DEF=Homo	NM_020152		NP_064537
		sapiens c21orf7 form A-D			
		(C21orf7), mRNA. /FEA=mRNA		·	
	1 "	/GEN=C21orf7 /PROD=c21orf7	1		
		1 :			
	i ·	form A-D /DB_XREF=gi:9910145		1	1
	\ \ \	/UG=Hs.41267 c21orf7 form A-D			
the second second	1.	//FL=gb:AF269161.1	ì	}	}
	· ·	gb:NM_020152.1	. '		
• , .		95020		.}	
0040004	0.000054	SHAM 047000 4 /DEC-Home	NIM 017960	<del>                                     </del>	ND 060220
221222_s_at	0.036254	gb:NM_017860.1 /DEF=Homo	NM_017860		NP_060330
		sapiens hypothetical protein		· [ ·	
	J·	FLJ20519 (FLJ20519), mRNA.			1
		/FEA=mRNA /GEN=FLJ20519		1	
		/PRQD=hypothetical protein		1	
				1	1
	1	FLJ20519 /DB_XREF=gi:8923488	,		
	1	/UG=Hs.79457 hypothetical	1	1	} .
**	1	protein FLJ20519			1
		/FL≃gb:NM 017860.1	.1	} .	}
	· · · · · · · · · · · · · · · · · · ·				l
	<u></u>	<u> </u>		li	<u> </u>

		ng to Figure 19 - Coronary Artery		10-1	D-4
Gene Identifier	p-value	Description	Gene Accession No.	Unigene Accession	Protein Accession
221260 s at	0.045316	gb:NM_030809.1 /DEF=Homo	NM 030809	No.	<b>No.</b> NP 110436
221200_5_at	0.040310	sapiens chromosome 12 open	14141_020009		INP_110430
·		reading frame 2 (C12orf2),			ļ
	,:	mRNA. /FEA=mRNA			J
		/GEN=C12orf2		•	
			1		
		/PROD=chromosome 12 open reading frame 2	1	ł	1
		/DB_XREF=gi:13540601		ļ	C 1.
		/FL=gb:NM_030809.1			
221306 at	0.025294	gb:NM 018971.1 /DEF=Homo	NM 018971		NP_061844
221300_at	0.025264	17 = -	ININI_0 1097 1		NP_001044
		sapiens G protein-coupled			<b> </b>
		receptor 27 (GPR27), mRNA. /FEA=CDS /GEN=GPR27		1	
				٠.	
		/PROD=super conserved			
		receptor expressed in brain 1	[	<u> </u>	Ì .
		/DB_XREF=gi:9506746	1		
		/UG=Hs.278283 G protein-	1 :		}
		coupled receptor 27	10		<b>]</b> . '
		/FL=gb:AB040799.1	i.		
004440	0.040740	gb:NM_018971.1	1114 040007		<del>                                     </del>
221419_s_at	0.046749	gb:NM_013307.1 /DEF=Homo	NM_013307		} .
		sapiens non-functional folate			
	<b> </b>	binding protein (HSAF000381),	1	jes 💰	·
		mRNA: /FEA=CDS			
		/GEN=HSAF000381 /PROD=non-			
		functional folate binding protein			
		//DB_XREF=gi:7019412			
• • • • • • • • • • • • • • • • • • •	<u>.</u>	/FL=gb:NM_013307.1			1 C
221499 s at	0.018222	Consensus includes	AF008936	<del> </del>	NP 003754
22 1433_3_at	0.010222	gb:AK026970.1 /DEF=Homo	AI 000930		111-003/34
	1	sapiens cDNA: FLJ23317 fis,		· -	
e .		clone HEP12062, highly similar	1		10 to 10 to 10
* - 2		to AF008936 Homo sapiens		1	1.00
		syntaxin-16B mRNA.			
	1	I/FEA=mRNA			
		//DB_XREF=gi:10439960			
		/UG=Hs.102178 syntaxin 16			1 .
		/FL=gb:AF008936.1		· .	1
221518_s_at	0.025284	Consensus includes	BC000226	<del>                                     </del>	NP 060414
22 10 10_5_dt	0.020204	gb:BE966019 /FEA=EST	DC000220		1117 _000412
, ** 		/DB_XREF=gi:11770993			
	1 .	/DB_XREF=gi.11770993 /DB_XREF=est:601659921R1	,		1.
	1	//CLONE=IMAGE:3905741	1		1
		· ·		<b>∤</b>	1.
	1	/UG=Hs.300700 hypothetical	1	1	1
į.		protein FLJ20727		<b>i</b> .	1.0

		ng to Figure 19 - Coronary Artery I	A A	<u> </u>	
Gene Identifier	p-value	Description	Gene Accession	Unigene Accession	Prot in Accession
204540	0.00000		No.	N	No.
221519_at	0.02008	gb:AF281859.1 /DEF=Homo	AF281859		NP_071322
		sapiens dactylin mRNA,			
		complete cds. /FEA=mRNA		1	
		/PROD=dactylin			1
İ	1	/DB_XREF=gi:10764487			
 	· .	/UG=Hs.24307 split handfoot			
		malformation (ectrodactyly) type			
•		3 /FL=gb:AF281859.1			
		gb:NM_022039.1			
221555_x at	0.018222	CDC14 cell division cycle 14	AU145941	Hs.22116	NP_201589
		homolog B (S. cerevisiae)			_
221559_s_at	0.034721	gb:BC000229.1 /DEF=Homo	BC000229		NP 076944
	0.002.	sapiens, clone MGC:2488,			
•		mRNA, complete cds.			
		/FEA=mRNA /PROD=Unknown	]		
		(protein for MGC:2488)			
	1	/DB_XREF=gi:12652942			
	1				
:	1	/UG=Hs 267194 hypothetical	1		
	.}	protein MGC2488			1
	1	/FL=gb:BC000229.1	-		
221565_s_at	0.034721	gb:BC000039.1 /DEF=Homo	BC000039		NP_057000
		sapiens, Similar to hypothetical			
		protein, clone MGC:1824,	1		
	1	mRNA, complete cds.	<b>!</b>	1	
	1	/FEA=mRNA /PROD=Similar to	1	}	ľ
,	1	hypothetical protein			1.
	1	/DB_XREF=gi:12652592		]	
		/UG=Hs.241545 hypothetical			
		protein /FL=gb:BC000039.1			
. : *		gb:NM_015916.1			1 . 2
221601_s_at	0.049425	regulator of Fas-induced apoptosis	AI084226	Hs.58831	NP_005440
221675 s at	0.034721	gb:AF195624.1 /DEF=Homo	AF195624	<del>    -  </del>	NP 06462
	1 3.33	sapiens	, 10002		
		cholinephosphotransferase 1 beta			
		mRNA, complete cds.			
		//FEA=mRNA	4 % L		
	1	/PROD=cholinephosphotransferas	· .		
	1		·	1	
		e 1 beta /DB_XREF=gi:9502012	). · · · · · · · · · · · · · · · · · · ·		
j	]	/UG=Hs.171889			1
		cholinephosphotransferase 1		1	1.
	1	/FL≈gb:AF195624.1	,		
l '.	1	• · · · · ·	1	1	1

Gene		ng to Figure 19 - Coronary Artery I		Unigene	Protein
A CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR	p-value	Description	Gene	7	
ldentifier		•	Accession	Accession	Accession
			No	No.	No.
221688 s_at	0.025284	gb:AL136913.1 /DEF=Homo	AL136913		NP_060755
		sapiens mRNA; cDNA	e e e e e e e e e e e e		[ <del>-</del>
4		DKFZp586L0118 (from clone		* ,	
		DKFZp586L0118); complete cds.			, · · · · · · · · · · · · · · · · · · ·
		/FEA=mRNA		<b>*</b> .	{
		/GEN=DKFZp586L0118			
		/PROD=hypothetical protein			
		/DB_XREF=gi:12053320		- '	
		/UG=Hs.6118 hypothetical protein		·	
N 4		FLJ10968 /FL=gb:AL136913.1			
221708 s at	0.036254	gb:BC006214.1 /DEF=Homo	BC006214		NP 061141
52 11 00_2_ar	0.000201	sapiens, clone MGC:999, mRNA,		1	_001141
					ł
		complete cds. /FEA=mRNA			, .
- A		/PROD=Unknown (protein for			
		MGC:999)			
# T 1		/DB_XREF=gi:13623232			
		/FL=gb:BC006214.1	<b>!</b>		
221742 at	0.026013	DnaJ (Hsp40) homolog, subfamily	BF037823	Hs.9683	
<del>-</del>		C, member 3			
221750 at	0.034721	3-hydroxy-3-methylglutaryl-	BG035985	Hs.396266	NP 002121
	0.00	Coenzyme A synthase 1 (soluble)			
	[	(Soluble)		**	}
224769 of	0.025294	splicing factor proline/glutamine	AV705803	Hs.180610	
221768_at	0.023264		AV/05605	IDS. 100010	
· . •	1	rich (polypyrimidine tract binding	}	1	
	<u> </u>	protein associated)			
221821_s_at	0.046749	Consensus includes	AK022732		NP_060292
		gb:AK022732.1 /DEF=Homo	``		1
	1	sapiens cDNA FLJ12670 fis,	{ · ·		
		clone NT2RM4002301.			1
		/FEA=mRNA			} .
	1	/DB_XREF=gi:10434303		1	l,
	ł · · ·	/UG=Hs.268189 hypothetical		1	]
	1				
004040+	0.040000	protein FLJ20436	DE070204	110 70740	:
221842_s_at	0.018023	zinc finger protein 131 (clone pHZ-	BE972394	Hs.78743	İ
<del> </del>	<del></del>	[10]			
221860_at	0.018023	heterogeneous nuclear	AL044078	Hs.2730	NP_001524
		ribonucleoprotein L			
221873_at	0.046749	zinc finger protein 143 (clone pHZ-	AW162015	Hs.374355	NP_003433
	ĺ	(1)			}
221874_at	0.049425	Consensus includes	AB037745		
· . ·		gb:AB037745.1 /DEF=Homo			
	Ì	sapiens mRNA for KIAA1324	,		
		protein, partial cds. /FEA=mRNA			[ ]
	]	1. ·			
•		/GEN=KIAA1324		ļ.	
	[	/PROD=KIAA1324 protein	1	1	1
	1	/DB_XREF=gi:7243028		1.	1
		/UG=Hs 104696 KIAA1324		*.	1
	)	protein		l	1 .

		ng to Figure 19 - Coronary Artery I	Disease		
Gene	p-value	Description	Gene	Unigene	Protein
Identifier	1		Accession	Accession	Accession
	1		No.	No.	No.
221957 at	0.034721	pyruvate dehydrogenase kinase,	BF939522	Hs.193124	NP 005382
,	1 9.00 1721	isoenzyme 3	DI 000022	113.135124	-000002
221978_at	0.046740	major histocompatibility complex,	BE138825	Hs.377850	ND 061022
221910_at	0.040749		DE 130023	IU8.311920	NP_061823
004005	0.005004	class I, F	10000750		
221985_at		hypothetical protein FLJ20059	AW006750	Hs.246875	NP_060114
221986_s_at		hypothetical protein FLJ20059	AW006750	Hs.246875	NP_060114
221989_at		ribosomal protein L10	AW057781	Hs.77091	NP_006004
221992_at	0.036254	ESTs, Moderately similar to	Al925734	Hs.409134	,
		nuclear pore complex interacting			
	ł	protein [Homo sapiens] [H.sapiens]			
	ì	 			
222024 s_at	0.025284	Consensus includes	AK022014		NP_658913
22202-1_3_at	0.020204	gb:AK022014.1 /DEF=Homo	711022014	ł	1111 _0000
		179			
*	l .	sapiens cDNA FLJ11952 fis,		l. · · ·	<b>.</b>
4.0		clone HEMBB1000831, weakly	•		
1.		similar to Homo sapiens breast			
		cancer nuclear receptor-binding	,	Ì	(
	ľ	auxiliary protein (BRX) mRNA.	}	}	1
		/FEA=mRNA			
	1	/DB_XREF=gi:10433327			1
,	ļ	/UG=Hs.306619 Homo sapiens		1	
		cDNA FLJ11952 fis, clone			
		HEMBB1000831, weakly similar	ì		1
	<b>}</b>	to Homo sapiens breast cancer		}	}
		• ·			
,	į .	nuclear receptor-binding auxiliary			
000000		protein (BRX) mRNA			115 0000
222058_at		goliath protein	AW194818	Hs.102737	NP_060904
222064_s_at		hypothetical protein MGC2744	AI093187	Hs.317403	NP_079543
222108_at	0.034721	Homo sapiens BAC clone GS1-	AC004010	1	
		99H8 from 7, complete sequence.			
* .					
222115_x_at	0.040064	Consensus includes	BC003693		NP_115958
		gb:BC003693.1 /DEF=Homo		ŀ	
·	ď	sapiens, Similar to RIKEN cDNA			<b>∤</b> ·
	1	3930401K13 gene, clone		)	ļ
,		IMAGE:3454556, mRNA, partial			Į.
		cds. /FEA=mRNA /PROD=Similar	•		İ
		to RIKEN cDNA 3930401K13			
		gene /DB_XREF=gi:13277567			}
		/UG=Hs.90998 KIAA0128 protein;		ŀ	j
		septin 2			,
	}		}		1
222122_s_at	0.018023	Tho2	BG403671	Hs.16411	

		ng to Figure 19 - Coronary Artery I			12-
Gene	p-value	Description	Gene	Unigene	Protein
ldentifier			Accession	Accession	Accession
			No.	N .	No.
222125 s at	0.046749	Consensus includes	BC000580	13.3	NP 808808
### (# <b>##</b> ####	1.0.0 10.110	gb:BC000580.1 /DEF=Homo			-
		sapiens, clone IMAGE:3162218,			
				· ·	
•	ĺ	mRNA, partial cds. /FEA=mRNA			
	ł,	/PROD=Unknown (protein for			
t	<b>†</b>	IMAGE:3162218)		Ì	
		/DB_XREF=gi:12653606			ľ
		/UG=Hs.5014 hypothetical protein	: "		
1		FLJ20262		<b>∤</b> 4. ∓	
			}	<b>,</b>	
222132 s at	0.049425	Consensus includes	AJ278150	<del>                                     </del>	NP 060708
	0.010120	gb:AJ278150.1 /DEF=Homo	, 102, 0.00		
	J	sapiens mRNA for putative lipid			f .
		kinase. /FEA=mRNA		1	1
* -	1	1			<b>)</b>
		/PROD=putative lipid kinase	· .		
	1	/DB_XREF=gi.8250242			
	<b>J</b>	/UG=Hs.260238 hypothetical		[	1
		protein FLJ10842		<u> </u>	<u> </u>
222140_s_at	0.018973	Consensus includes	AK021758	- W 1-40	NP_057418
_	1	gb:AK021758.1 /DEF=Homo			
+ \$ · · ·	}	sapiens cDNA FLJ11696 fis,			,
		clone HEMBA1005029, highly		A .	* · ·
	1	similar to Homo sapiens CGI-13			ľ
		protein mRNA. /FEA=mRNA	1		
	1.	1.		1	
* •	1	//DB_XREF=gi:10433004	1		1
		/UG=Hs 16085 putative G-protein	} .	: 1	
* *		coupled receptor			ſ
<u> </u>				<u> </u>	1
222158_s_at	0.018222	Consensus includes	AF229834		NP_057160
		gb:AF229834.1 /DEF=Homo	1		
		sapiens apoptosis-related protein		) .	)
* . *	1	PNAS-4 (PNAS-4) mRNA, partial			
		cds. /FEA=mRNA /GEN=PNAS-4			1
· ·		/PROD=apoptosis-related protein			(
,		PNAS-4 /DB XREF=gi:7229639		1 -	1
		/UG=Hs.42409 CGI-146 protein		ļ	
\.\.\.\.\.\.\.\.\.\.\.\.\.\.\.\.\.\.\.		700-113.42409 CGI-140 PIOLEIII		1	
	1.				1
000400	0.040740	CORA NOT	D0405004	11. 000700	ND 055055
222182_s_at	0.046749	CCR4-NOT transcription complex,	BG105204	Hs.239720	NP_055330
.*	1	subunit 2			1

E - 1 22		ng to Figure 19 - Coronary Artery I	Disease		
Gene	p-value	Description	Gene	Unigene	Protein
ldentifier	9		Accession	Accession	Accession
	L _		No	No.	No.
222239_s_at	0.034721	Consensus includes	AL117626	(	NP 036273
		gb;AL117626.1 /DEF=Homo	·		
	1	sapiens mRNA; cDNA			
		DKFZp434B105 (from clone			
		DKFZp434B105); partial cds.			
	]	/FEA=mRNA			1
*		/GEN=DKFZp434B105			
*-		/PROD=hypothetical protein			
		/DB_XREF=gi:5912207		1	
* * * * * * * * * * * * * * * * * * * *	t in the second	/UG=Hs.58570 deleted in cancer			
		1; RNA helicase HDBDICE1		ł	
		T, KINA Helicase FIDEDICET	,	1	
222252 v ot	0.040064	Conseque	AK023354		NID 004540
222252_x_at	0.040004	Consensus includes	AKU23354		NP_064516
		gb:AK023354.1 /DEF=Homo			
	1	sapiens cDNA FLJ13292 fis,	[		ŀ
		clone OVARC1001180, weakly			
		similar to UBIQUITIN-LIKE			
		PROTEIN DSK2 /FEA=mRNA			
	ļ	/DB_XREF=gi:10435253		<b>)</b>	1
	<b>.</b>	/UG=Hs.283739 ataxin-1 ubiquitin			-
		like interacting protein	[		
222282_at	0.046749	AV761453 MDS Homo sapiens	AV761453	,	
	1	cDNA clone MDSBZA03 5', mRNA			ľ
<u> </u>		sequence.		L	<u> </u>
222316_at	0.025284	ESTs	AW973253	Hs.292689	
222366_at	0.046749	ESTs	W86781	Hs.293736	
222369_at	0.035763	ESTs, Moderately similar to	AW971254	Hs.178433	
	:  -	hypothetical protein FLJ20489	1.5		
	1	[Homo sapiens] [H.sapiens]			(
222380 s at	0.034721		AI907083	Hs 124620	:
32541_at		protein phosphatase 3 (formerly	NM 005605	Hs.75206	NP 005596
<del>-</del>		2B), catalytic subunit, gamma		1	} <b>5</b> 0000
		isoform (calcineurin A gamma)	1		]
35201_at	0.046749	heterogeneous nuclear	NM 001533	Hs.2730	NP_001524
30201 <u>-</u> 41	0.0 107 10	ribonucleoprotein L	11111_001000	113.2700	100 1324
35671 at	0.036254	general transcription factor IIIC,	NM_001520	Hs 331	NP 001511
ooor,i_at	0.000204	polypeptide 1, alpha 220kDa	111111_001320	1115.551	NF_001311
35685_at	0.018022	ring finger protein 1	NIM 002021	Un 25204	ND 002022
			NM_002931	Hs.35384	NP_002922
36545_s_at		KIAA0542 gene product	AB011114	Hs.62209	ND 50000
38398_at	0.046749	MAP-kinase activating death	AB002356	Hs.82548	NP_569832
206 f at	0.010444	domain	NIM COCACA	Up 407000	ND 000445
396 f at		erythropoietin receptor	NM_000121	Hs.127826	NP_000112
39650_s_at		KIAA0435 gene product	NM_014801	Hs.31438	NP_055616
41113_at		hypothetical protein AF447587	Al871396	Hs.101414	
44673_at		sialoadhesin	N53555	Hs.31869	NP_075556
45572_s_at	0.034721	golgi associated, gamma adaptin	AW009695	Hs.238296	NP_037497
		ear containing, ARF binding	J		] ':
		protein 1		1.	

Gene List Co		ng to Figure 19 - Coronary Artery			<u></u>
Gene	p-value	Description	Gene	Unigene	Protein
ld ntifi r	,		Accession	Accession	Accession
	i.		No.	No.	No.
46665_at	0.034721	sema domain, immunoglobulin	AI949392	Hs.7188	NP_060259
		domain (lg), transmembrane			· · · ·
•		domain (TM) and short			· ·
		cytoplasmic domain, (semaphorin)			İ
		4C			
47069 at	0.034721	Rho GTPase activating protein 8	AA533284	Hs.102336	NP 851852
47560 at	0.02008	hypothetical protein FLJ11939	AI525402	Hs.94229	NP 078955
50277 at		golgi associated, gamma adaptin	AW001443	Hs.238296	NP 037497
·		ear containing, ARF binding			-
*.		protein 1			
51200_at	0.034721	hypothetical protein FLJ20850	A1744084	Hs.30783	NP_060437
51228 at		ESTs, Weakly similar to RNA	N36928	Hs.33540	
		binding motif protein 12; putative			
		brain nuclearly-targeted protein			
		[Homo sapiens] [H.sapiens]			
51774 s at	0.046749	ESTs, Moderately similar to	AW014299	Hs.237946	
. 14. <del>1-1-1</del>		hypothetical protein FLJ20489			
		[Homo sapiens] [H.sapiens]	ļ ·		
52940 at	0.038017	single lg IL-1R-related molecule	AA085764	Hs.11809	NP 068577
57539 at		hypothetical protein FLJ14972	AA535065	Hs.11900	NP 115916
57715 at		hypothetical protein LOC51063	W72694	Hs.241545	NP 057000
63825_at		chromosome 11 open reading	AI557319	Hs.5258	NP_008917
<b>-</b>		frame2		: '	
64064_at	0.046749	immune associated nucleotide 4	Al435089	Hs.26194	NP_060854
. <del>-</del>		like 1 (mouse)			<u> </u>
64474_g_at	0.019292	hypothetical protein FLJ22127	AA203219	Hs.59457	NP 073612
74694 s at	0.034721	hypothetical protein FLJ23282	AA907940	Hs.170253	NP_079092
91816 f at		Homo sapiens mRNA for OK/SW-	C18318	Hs.123469	
		CL.4, complete cds			
91952 at	0.026013	hypothetical protein BC002926	Al363375	Hs.298553	NP 612362
AFFX-BioC-5		J04423 E coli bioC protein (-5	J04423		
	T v	and -3 represent transcript			
		regions 5 prime and 3 prime			1
		respectively)			, i
AFFX-HUMG.	0.046749	glyceraldehyde-3-phosphate	NM_002046	Hs.169476	NP_002037
		dehydrogenase			_
AFFX-M2783	0.018023	Human 28S ribosomal RNA gene,	M27830		
		complete cds.			
AFFX-r2-Hs2	0.03018	Human 28S ribosomal RNA gene.	M11167		
AFFX-r2-Hs2	0.035763	Human 28S ribosomal RNA gene.	M11167	<u> </u>	<u> </u>
	1	1	1	1	I .

Gene	p-value	Description	Gene	Unigene	Protein
ldentifier		4	Acc ssion	Accession	Accession
	e* -		No.	No.	No.
AFFX-r2-P1-c	0.025284	Bacteriophage /REF=X03453	X03453		
. Para di Larra di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Carte di Ca		/DEF=Bacteriophage P1 cre		- 5,	
		recombinase protein			
*		corresponding to nucleotides 581			
	\$4. S.	1001 of X03453 /LEN=1058 (-5			
* * * * * * * * * * * * * * * * * * *		and -3 represent transcript			•
		regions 5 prime and 3 prime			
		respectively)			

<u> </u>		TABLE 3M		<u> </u>	
3en s	Correspoi	nding To Diff rentially Expr ssed Gen	es in Figure 20 -	RA	
	p-value	Description	Gene Accession No.	Unigene Accession	Prot in Acc ssion
*				No.	No.
1	0.022106	vacuolar protein sorting 28 (yeast)	NM_016208	Hs.339697	NP_057292
		(VPS28), mRNA /cds=(62,727)			-
		/gb=NM_016208 /gi=7705884			
		/ug=Hs.339697 /len=928			ļ
-4	0.040751	tetraspan 3 (TSPAN-3), mRNA	NM 005724	Hs.100090	NP 005715
		/cds=(218,979) /gb=NM_005724	<del></del> '		
		/gi=21264581 /ug=Hs.100090	*		
		/len=1842			F. H
14	0.011238	mRNA for KIAA0638 protein, partial	AB014538	Hs.432813	
		cds. /cds=(87,4241) /gb=AB014538		1	9.0
		/gi=20521112 /ug=Hs.432813		1	
4.12		/len=5449			
15	0.010277	603041572T1 NIH_MGC_116 cDNA	BI517954	Hs.398211	
*		clone IMAGE:5163112 3', mRNA			
	5.5	sequence /clone=IMAGE:5163112			
		/clone_end=3' /gb=BI517954		1	
	1	/gi=15342746 /ug=Hs.398211 /len=964			
25	0.002565	sialyltransferase SThM (sthm)	Ú14550		NP_006447
28	0.031362	602184410T1 NIH_MGC_42 cDNA	BF569051	Hs.352114	
		clone IMAGE:4300347 3', mRNA			
		sequence /clone=IMAGE:4300347			
٠.		/clone_end=3' /gb=BF569051			
		/gi=11642431 /ug=Hs.352114	· · · · · · · · · · · · · · · · · · ·		
		/len=1899	·		<u> </u>
37	0.002602	thyroid hormone receptor-associated	NM_005119	Hs.108319	NP_005110
		protein, 150 kDa subunit (TRAP150),	1	, ,	* * * *
		mRNA /cds=(203,3070)			
		/gb=NM_005119 /gi=4827039		1	
		/ug=Hs.108319 /len=3618			
49	0.032636	B cell RAG associated protein	NM_014863	Hs.6079	NP_056976
	] .	(GALNAC4S-6ST), mRNA			J
		/cds=(582,2267) /gb=NM_014863			
. <u>.</u>	<u>-</u>	/gi=7662195 /ug=Hs.6079 /len=4712		<u> </u>	
95	8.37E-04	Kreisler (mouse) maf-related leucine	NM_005461		NP_005452
		zipper homolog (KRML)	1	· ·	
		(=MAFB/Kreisler basic region/leucine			
		zipper transcription factor (MAFB))			ł
		Length = 3071			
98	0.012276	mitochondrion, complete genome	NC_001807		
104		proteasome (prosome, macropain)	NM_002818	Hs.433810	NP_002809
		activator subunit 2 (PA28 beta)			
	6.5	(PSME2), mRNA /cds=(66,785)			
		/gb=NM_002818 /gi=4506236	1	1	
		/ug=Hs.433810 /len=828		1	1

Genes	Correspon	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
141	1.76E-04	mel transforming oncogene (derived from cell line NK14)- RAB8 (MEL), mRNA /cds=(77,700) /gb=NM_005370 /gi=16933566 /ug=Hs.5947 /len=2048	NM_005370	Hs.5947	NP_005361
158	0.015895	CD36 antigen (collagen type I receptor, thrombospondin receptor) (CD36), mRNA /cds=(133,1551) /gb=NM_000072 /gi=4557418 /ug=Hs.75613 /len=1820	NM_000072	Hs.75613	NP_000063
178		zinc finger protein 161 (ZNF161), mRNA /cds=(42,1592) /gb=NM_007146 /gi=6005967 /ug=Hs.223754 /len=2306	NM_007146	Hs.223754	NP_009077
179	0.009388	ubiquitin specific protease 9, X chromosome (fat facets-like Drosophila) (USP9X), transcript variant 1, mRNA /cds=(60,7751) /gb=NM_004652 /gi=11641424	NM_004652	Hs.77578	NP_068706
194	0.009388	/ug=Hs.77578 /len=8171 hypothetical protein FLJ33215 (FLJ33215), mRNA /cds=(118,1626) /gb=NM_148894 /gi=22507398	NM_148894	Hs.205442	NP_683692
196	0.004825	/ug=Hs.205442 /len=2610 integrin-binding sialoprotein (bone sialoprotein, bone sialoprotein II) (IBSP), mRNA /cds=(143,1096) /gb=NM_004967 /gi=13259536 /ug=Hs.49215 /len=1108	NM_004967	Hs.49215	NP_004958
206		calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA /cds=(69,518) /gb=NM_001743 /gi=20428653 /ug=Hs.425808 /len=1128	NM_001743	Hs.425808	NP_001734
210		protein tyrosine phosphatase type IVA, member 1 (PTP4A1), mRNA /cds=(650,1171) /gb=NM_003463 /gi=17986281 /ug=Hs.227777 /len=4394	NM_003463	Hs.227777	NP_003454
221		zinc finger protein 271 (ZNF271), mRNA /cds=(710,1981) /gb=NM_006629 /gi=24586660 /ug=Hs.367734 /len=2195	NM_006629	Hs.367734	NP_006620
228	0.002337	KIAA0182 mRNA, complete cds. /cds=(1,3475) /gb=D80004 /gi=1136423 /ug=Hs.75909 /len=7133	D80004	Hs.75909	

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
	i.			No.	No.
259	0.015895	ornithine decarboxylase antizyme	NM 015878	Hs.223014	NP 680479
	0.0,000	inhibitor (OAZIN), transcript variant 1,		1,0.220011	
		mRNA /cds=(721,2067)			
	1	/gb=NM_015878 /gi=22538416			
		/ug=Hs.223014 /len=2882		<del>                                     </del>	
261	0.017288	serine (or cysteine) proteinase inhibitor,	NM_004155	Hs.104879	NP_004146
		clade B (ovalbumin), member 9			
		(SERPINB9), mRNA /cds=(93,1223)			
		/gb=NM_004155 /gi=19923258		. *	
		/ug=Hs.104879 /len=4130			1
-					
277	0.002096	reticulon 3 (RTN3), mRNA	NM 006054	Hs.252831	NP 006045
	1	/cds=(125,835) /gb=NM_006054			
		/gi=5174654 /ug=Hs.252831 /len=2524			1
		/gi-51740347dg-113.2520317leti-2524			
270	0.005324	adaium/admadulia danandant parina	NIM 002600	Un 151460	ND 002670
279	0.000324	calcium/calmodulin-dependent serine	NM_003688	Hs.151469	NP_003679
		protein kinase (MAGUK family) (CASK),			
		mRNA /cds=(28,2793) /gb=NM_003688			
		/gi=4502566 /ug=Hs.151469 /len=3122			
281	0.043799	16.7Kd protein (LOC51142), mRNA	NM_016139	Hs.180859	NP_057223
4.		/cds=(82,537) /gb=NM_016139		ļ.	
		/gi=7705850 /ug=Hs.180859 /len=841			
282	0.001501	protein phosphatase 1, regulatory	NM 005398	Hs.303090	NP 005389
		(inhibitor) subunit 3C (PPP1R3C),			
	1	mRNA /cds=(58,1011) /gb=NM_005398		1	,
		/gi=21314622 /ug=Hs.303090			
•	<b>)</b>				
000	0.000400	/len=2524	NA 000500	112 0000	ND 000500
283	0.006463	syntaxin 7 (STX7), mRNA	NM_003569	Hs.8906	NP_003560
	<b>∤</b> ·	/cds=(80,865) /gb=NM_003569			
		/gi=4507294 /ug=Hs.8906 /len=1614			
284	0.014599	translin-associated factor X (TSNAX),	NM_005999	Hs.96247	NP_005990
	1	mRNA /cds=(159,1031)			
		/gb=NM_005999 /gi=20302159	- I	1	
	<b>.</b>	/ug=Hs.96247 /len=2667			
290	0.030249	Niemann-Pick disease, type C2	NM 006432	Hs.433222	NP 006423
	,	(NPC2), mRNA /cds=(116,571)	7		<del>-</del>
		/gb=NM 006432 /gi=20149580	<b>]</b>		
		/ug=Hs.433222 /len=929			
	0.000566	origin recognition complex, subunit 2-	NM_006190	Hs.41694	NP 006181
.311.1			1141M 000 1A0	113.41094	ואַר_חֹחָסוַסוֹ
302	0.000500	Hite (venet) (OPCOL)			1
302	0.000300	like (yeast) (ORC2L), mRNA		· [	1
302	0.000000	/cds=(215,1948) /gb=NM_006190			
302	0.000300				
	0.000000	/cds=(215,1948) /gb=NM_006190			
302		/cds=(215,1948) /gb=NM_006190	AB011370		NP_033801
	0.012276	/cds=(215,1948) /gb=NM_006190 /gi=21359879 /ug=Hs.41694 /len=2815	AB011370 NM_004673	Hs.241519	NP_033801 NP_004664
311	0.012276	/cds=(215,1948) /gb=NM_006190 /gi=21359879 /ug=Hs.41694 /len=2815 Ankhzn mRNA, angiopoietin-like 1 (ANGPTL1), mRNA		Hs.241519	
311	0.012276	/cds=(215,1948) /gb=NM_006190 /gi=21359879 /ug=Hs.41694 /len=2815 Ankhzn mRNA,		Hs.241519	

		nding To Differentially Expr ssed Gen			D-4-:-	
Spot	p-valu	D scription	Gene	Unigene	Protein	
			Accession No.	Accession	Accession	
				No.	No.	
320	0.035177	hypothetical protein DKFZp564K142	NM_032121	Hs.323562	NP_115497	
		similar to implantation-associated	مين ۽ حمل جي ديو ٿيا			
		protein (DKFZp564K142), mRNA		-		
		/cds=(30,1037) /gb=NM_032121	,		l.	
		/gi=14149774 /ug=Hs.323562				
		/len=2241	and the			
321	0.007107	serologically defined breast cancer	NM 015966	Hs.169992	NP_057050	
		antigen 84 (SDBCAG84), mRNA	·		-	
		/cds=(28,1179) /gb=NM_015966			ŀ	
٠, .		/gi=7706277 /ug=Hs.169992 /len=1337				
		· g. , , , , , , , , , , , , , , , , , ,				
336	0.03788	mRNA for KIAA0570 protein, partial	AB011142	Hs.180948		
550	5.55.56	cds. /cds=(480,10718) /gb=AB011142		1.0.1000.10		
		/gi=20521084 /ug=Hs.180948				
- 1		/len=11269		*		
337	0.00168	yippee protein (CGI-127), mRNA	NM_016061	Hs.184542	NP 057145	
337	0.00100	/cds=(126,491) /gb=NM_016061	14141_010001	1115, 104342	145	
		/gi=7706340 /ug=Hs.184542 /len=2183				
		/gi=//00340/ug=ns.104342/len=2103				
25.4	0.044000	etromal call derived factor 2 (CDE2)	NIM OOCOOO	11- 440004	ND 000054	
354	0.011238	stromal cell-derived factor 2 (SDF2),	NM_006923	Hs.118684	NP_008854	
		mRNA /cds=(40,675) /gb=NM_006923				
2.00		/gi=14141194 /ug=Hs.118684				
		/len=1075				
356	0.015895	RAB21, member RAS oncogene family	NM_014999	Hs.184627	NP_055814	
		(RAB21), mRNA /cds=(256,933)			, · · ·	
,		/gb=NM_014999 /gi=7661921				
. 4.		/ug=Hs.184627 /len=2630				
				<u></u>		
358	0.003947	hypothetical protein FLJ35613	NM_173653	Hs.30022	NP_775924	
		(FLJ35613), mRNA /cds=(126,2063)				
		/gb=NM_173653 /gi=27734934		· ·		
		/ug=Hs.30022 /len=3568		1 - 2		
359	0.001062	plakophilin 2=X97675 plakophilin 2b	NP_004563			
* .		(ORF 38%)				
364	0.030249	microphthalmia-associated transcription	NM_000248	Hs.166017	NP_000239	
		factor (MITF), mRNA /cds=(121,1380)	_		-	
		/gb=NM 000248 /gi=4557754				
	] ,	/ug=Hs.166017 /len=1788				
٠.						
369	0.002602	mRNA for KIAA1147 protein, partial	AB032973	Hs.233044	<del>                                     </del>	
	1	cds. /cds=(1,570) /gb=AB032973				
		/gi=6330032 /ug=Hs.233044 /len=6496				
370	0.005335	carboxypeptidase E (CPE), mRNA	NM 001873	Hs.75360	NP_001864	
310	0.000020	1	114101-00 1073	113.73300	141 _00 1004	
	1.	/cds=(291,1721) /gb=NM_001873				
	1	/gi=4503008 /ug=Hs.75360 /len=2443	<u></u>	<u> </u>	1	

		nding To Diff rentially Expr ssed Gen			<del> </del>	
Spot	p-value		Gene	Unigene	Protein	
			Accession No.	Accession	Accession	
			·	No.	No.	
371	0.02801	ecotropic viral integration site 2A	NM_014210	Hs.70499	NP_055025	
	Ta	(EVI2A), mRNA /cds=(220,918)				
		/gb=NM_014210 /gi=7657074				
		/ug=Hs.70499 /len=1563				
390	0.023945	UDP-galactose transporter related	NM_005827	Hs.154073	NP_005818	
		(UGTREL1), mRNA /cds=(88,1056)				
S		/gb=NM_005827 /gi=5032212				
		/ug=Hs.154073 /len=1186				
393	0.040751	microsomal epoxide hydrolase	AF253417	***		
		(EPHX1) gene, complete cds				
395	0.025911	cysteine and histidine-rich domain	NM 012124	Hs.22857	NP 036256	
		(CHORD)-containing, zinc binding	, * 1 <del>4  </del> 1			
		protein 1 (CHORDC1), mRNA				
		/cds=(85,1083) /gb=NM_012124	A Section 1			
		/gi=6912303 /ug=Hs.22857 /len=2058				
396	0.010277	hypothetical protein FLJ20445	NM 017824	Hs.343748	NP 060294	
555	3.0.02.7	(FLJ20445), mRNA /cds=(293,1129)			-333254	
		/gb=NM 017824 /gi=19923500				
		/ug=Hs.343748 /len=3896				
400	0.007107	leukemia inhibitory factor receptor	NM 002310	Hs.2798	NP 002301	
400	0.007 107	(LIFR), mRNA /cds=(154,3447)	14141_002310	115.2780	147_002301	
		/gb=NM_002310 /gi=6042197				
400	0.004000	/ug=Hs.2798 /len=5252	NINA 004070	Hs.181301	ND 004070	
403	0.001339	cathepsin S (CTSS), mRNA	NM_004079	IHS. 181301	NP_004070	
	1	/cds=(134,1129) /gb=NM_004079				
		/gi=23110961 /ug=Hs.181301	e de la company	1.00		
		/len=4100				
409	0.020388	S-phase kinase-associated protein 1A	NM_006930	Hs.171626	NP_733779	
	* :	(p19A) (SKP1A), transcript variant 1,		4 "		
		mRNA /cds=(140,622) /gb=NM_006930				
		/gi=25777710 /ug=Hs.171626				
		/len=2172				
417	0.02801	LATS, large tumor suppressor, 2	NM_014572	Hs.432314	NP_055387	
		(Drosophila) (LATS2), mRNA				
		/cds=(375,3641) /gb=NM_014572		1		
		/gi=18959199 /ug=Hs.432314				
		/len=4098		<u> </u>		
425	0.030249	myeloid cell nuclear differentiation	NM_002432	Hs.153837	NP_002423	
		antigen (MNDA), mRNA				
		/cds=(201,1424) /gb=NM_002432			1	
		/gi=4505226 /ug=Hs.153837 /len=1670			*	
					; 	
427	0.002893	hypothetical protein FLJ20508	NM_017850	Hs.272673	NP_060320	
		(FLJ20508), mRNA /cds=(191,802)				
		/gb=NM 017850 /gi=8923468				
	1	/ug=Hs.272673 /len=2376		1.		

		nding To Differentially Expr ssed G n			A 100
Spot	p-value	Description	G ne	Unigene	Prot in
•			Accession No.	Accession	Acc ssion
				No. 6	No.
428	0.040751	golgi complex associated protein 1,	NM 022735	Hs.6831	NP 073572
420	0.040751	60kDa (GOCAP1), mRNA	14141_022130	113.0001	-073372
				· · · · · · · · · · · · · · · · · · ·	
		/cds=(56,1642) /gb=NM_022735			
		/gi=15826851 /ug=Hs.6831 /len=3598			
432	0.011238	DKFZp586L081 (from clone	AL080234	Hs.8078	
- 1		DKFZp586L081) /cds=UNKNOWN			
. •		/gb=AL080234 /gi=5262727			
		/ug=Hs.8078 /len=2159			
40.4	0.044000		NIM. 000201	Ua 70774	ND .000292
434	0.011238	phosphoglycerate kinase 1 (PGK1),	NM_000291	Hs.78771	NP_000282
-		mRNA /cds=(70,1323) /gb=NM_000291		1	
		/gi=22095338 /ug=Hs.78771 /len=2338			
437	0.015895	TCAAP1D11790 Pediatric acute	BM144590	Hs.425539	
70.		myelogenous leukemia cell (FAB M1)	5,		
		Baylor-HGSC project=TCAA cDNA			
		clone TCAAP1179, mRNA sequence			
		/clone=TCAAP1179 /gb=BM144590			
		/gi=17161827 /ug=Hs.425539 /len=178			
``		<b>3</b>			h ta
452	0.047031	aldehyde dehydrogenase 2 family	NM 000690	Hs.195432	NP 000681
404	0.047031			1113.130402	1145 _000001
•		(mitochondrial) (ALDH2), nuclear gene			
	•	encoding mitochondrial protein, mRNA			
		/cds=(442,1995) /gb=NM_000690	2.5		
		/gi=25777731 /ug=Hs.195432	·		
		/len=2445			4 1 N 1
466	0.001878	activity-dependent neuroprotector	NM 015339	Hs.3657	NP 056154
400	0.001070		14141_010000	113.0007	141 _000 104
		(ADNP), mRNA /cds=(346,3654)		].	
		/gb=NM_015339 /gi=12229216			
		/ug=Hs.3657 /len=4713			
478	0.047031	glyceraldehyde-3-phosphate	NM_002046	Hs.169476	NP_002037
,	I	dehydrogenase (GAPD), mRNA	_		
		/cds=(76,1083) /gb=NM_002046			
	1	/gi=7669491 /ug=Hs.169476 /len=1283			
		/g =/669491/ug=ns.169476/left=1265			
·	200				
479	0.023117		NM_017719	Hs.79025	NP_060189
		/cds=(642,2939) /gb=NM_017719			
		/gi=21361642 /ug=Hs.79025 /len=5519			
	1,	, <u> </u>			
484	0.005001	troponin T1, skeletal, slow (TNNT1),	NM 003283	Hs.73980	NP 003274
404 *	0.000881		_	113.7 9300	111 _0032/4
	1	mRNA /cds=(149,904) /gb=NM_003283			
	•	/gi=21359857 /ug=Hs.73980 /len=1018			
			<u>l -                                    </u>	<u> </u>	<u> </u>
485	6.56E-04	GNAS complex locus (GNAS),	NM 080425	Hs.374523	NP 536351
	1	transcript variant 3, mRNA			·
		li i i i i i i i i i i i i i i i i i i			
	1	/cds=(1,2730) /gb=NM_080425			
		/gi=18426897 /ug=Hs.374523		1	1
	ł	/len=3091		1.	1

		nding To Differentially Expressed Gen			D4-:-
Spot	p-value	Description	Gen Acc ssion No.	Unigene Accession No.	Protein Accession No.
487	3.19E-04	proteasome (prosome, macropain) 26S	NM 153822	Hs.148495	NP_722544
		subunit, non-ATPase, 4 (PSMD4),			
		transcript variant 2, mRNA			
1.	:	/cds=(63,869) /gb=NM_153822			***
	-	/gi=25121957 /ug=Hs.148495	•		• '
400	0.040070	/len=1508	NIA 000704	11 70474	ND 000750
489	0.013076	tyrosine 3-monooxygenase/tryptophan	NM_006761	Hs.79474	NP_006752
• • • •	*	5-monooxygenase activation protein,			
		epsilon polypeptide (YWHAE), mRNA		٠.	
	*	/cds=(80,847) /gb=NM_006761			
	* .	/gi=21328449 /ug=Hs.79474 /len=1776			1
• .					
499	0.030075	troponin C2, fast (TNNC2), mRNA	NM_003279	Hs.182421	NP_003270
* <i>i</i>		/cds=(65,547) /gb=NM_003279			
1.		/gi=4507616 /ug=Hs.182421 /len=677			
510	0.006665	uroporphyrinogen decarboxylase	NM 000374	Hs.78601	NP 000365
,		(UROD), mRNA /cds=(19,1122)	_		
	l .	/gb=NM_000374 /gi=9845521			
:	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	/ug=Hs.78601 /len=1296		1	
513	0.004220		NM_014172	Hs.297214	NP 054891
513	0.004339	phosphohistidine phosphatase	NIVI_U 14172	IDS.29/214	148_034691
		(PHP14), mRNA /cds=(334,711)			
		/gb=NM_014172 /gi=24475860			
		/ug=Hs.297214 /len=903			
517	6.36E-04	galactokinase 1 (GALK1), mRNA	NM_000154	Hs.92357	NP_000145
		/cds=(64,1242) /gb=NM_000154			
·		/gi=4503894 /ug=Hs.92357 /len=1361			
519	0.012792	splicing factor (45kD) (SPF45), mRNA	NM_032905	Hs.107001	NP_116294
		/cds=(148,1353) /gb=NM_032905		14 - 4	
		/gi=14249677 /ug=Hs.107001	1	t	
		/len=1566		1	
526	0.026485	GDP dissociation inhibitor 1 (GDI1),	NM 001493	Hs.74576	NP_001484
h		mRNA /cds=(81,1424) /gb=NM_001493		,	
		/gi=4503970 /ug=Hs.74576 /len=2225	. , , , ,		
532	2 32F-04	ferritin, light polypeptide (FTL), mRNA	NM 000146	Hs.430150	NP 000137
552	2.5212-04	/cds=(189,716) /gb=NM_000146	14141_000140	113.400100	
	1			1	
		/gi=20149497 /ug=Hs.430150 /len=878		1	i
600	0.000500		NINA 000404	Un 200055	ND 000475
533	0.003563	hemoglobin, gamma G (HBG2), mRNA	NN_000184	Hs.386655	NP_000175
	,	/cds=(54,497) /gb=NM_000184	·		
		/gi=28302132 /ug=Hs.386655 /len=583			
					<u>                                     </u>
534	0.038043	eukaryotic translation initiation factor 3,	NM_003751	Hs.57783	NP_003742
		subunit 9 eta, 116kDa (EIF3S9), mRNA			
		/cds=(54,2675) /gb=NM_003751	<b>]</b> .	1	
		/gi=4503526 /ug=Hs.57783 /len=2995			
	1		I		j

		nding To Differentially Expr ssed Gen			
Spot p	p-value		Gen	Unigene	Protein
			Acc ssion No.	Accession	Accession
.554	0.033876	ribosomal protein L29 (RPL29), mRNA	NM 000992	<b>No.</b> Hs.430207	No. NP 000983
.00 1	0.000070	/cds=(95,574) /gb=NM 000992		113.400207	
		/gi=17105395 /ug=Hs.430207 /len=737			
		/gi=17 103393 /ug=118.430207 /ieii=737			
563	0.004349	activating transcription factor 4 (tax-	NM_001675	Hs.181243	NP_001666
١.		responsive enhancer element B67)	1, 3, 1,		
		(ATF4), mRNA /cds=(882,1937)			•
		/gb=NM_001675 /gi=4502264			
		/ug=Hs.181243 /len=2015	* * .		
565	0.040751	topoisomerase (DNA) III alpha	NM 004618	Hs.91175	NP 004609
		(TOP3A), mRNA /cds=(230,3235)			-
		/gb=NM_004618 /gi=20143947			
		/ug=Hs.91175 /len=3807			
566	0.016299	jun D proto-oncogene (JUND)	NM 005354	The second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon	
567		coactosin-like 1 (Dictyostelium)	NM 021149	Hs.289092	NP 066972
, :		(COTL1), mRNA /cds=(150,578)			· · · - · · · · · · ·
		/gb=NM_021149 /gi=23510452			
		/ug=Hs.289092 /len=1850			
570	0.00168	cycA gene for cyclin A	X68303	<del>, , , , , , , , , , , , , , , , , , , </del>	
573		ancient ubiquitous protein 1 (AUP1),	NM_012103	Hs.173736	NP_036235
0,0	0.00100	mRNA /cds=(69,1499) /gb=NM_012103		113.170700	141 _030233
	1	/gi=6912259 /ug=Hs.173736 /len=1664			h.,
		/gi=0.9 (2209 /dg=115.17 37 30 /ieii= 1004			
574	0.002297	mRNA for KIAA1274 protein, partial	AB033100	Hs.300646	**************************************
,		cds. /cds=(265,2850) /gb=AB033100			
	-	/gi=20521819 /ug=Hs.300646			
		/len=4569			•
595	0.02236	NS1-associated protein 1 (NSAP1),	NM_006372	Hs.373499	NP_006363
		mRNA /cds=(526,2397)	- 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1		
		/gb=NM 006372 /gi=23397426			·
		/ug=Hs.373499 /len=2932			
596	0.001549	tubulin, alpha 3 (TUBA3), mRNA	NM_006009	Hs.433394	NP_006000
		/cds=(100,1455)/gb=NM 006009			
,		/gi=17986282 /ug=Hs.433394			
		/len=1677	· ·		
600	0.007171	fascin 1, actin-bundling protein	NM 003088	Hs.118400	NP_003079
, -	.,	(Strongylocentrotus purpuratus)			
		(FSCN1), mRNA /cds=(112,1593)			
		/gb=NM 003088 /gi=4507114			
ζ.		/ug=Hs.118400 /len=2767		*.	
602	0.029005	helicase with zinc finger domain	NM 014877	Hs.3085	NP 055692
552	5.525555	(HELZ), mRNA /cds=(146,5974)	3,,,,,,,	.5.5555	
•		/gb=NM 014877 /gi=7661883		1	
		/ug=Hs:3085 /len=6274			
613	0.019794	PEF protein with a long N-terminal	NM 012392	Hs.241531	NP_036524
013	0.010704	hydrophobic domain (peflin) (PEF),	14101_012382	1113.27 1001	141 _000024
		myarophobic aomain (pellin) (FEF),	1	1 .	1
				1	
• •		mRNA /cds=(13,867) /gb=NM_012392 /gi=6912581 /ug=Hs.241531 /len=1641		,	

Genes	Correspo	nding To Differentially Expr ssed Gen	es in Figure 20 -	RA	
Spot	p-value	Description	Gene Accession No.	Unigene Acc ssion No.	Protein Accession No.
625	0.020388	fragile X mental retardation 1 (FMR1),	NM 002024	Hs.89764	NP 002015
4-4	0.02000	mRNA /cds=(220,2118)			1111 _002010
		/gb=NM 002024 /gi=4503764			
		/ug=Hs.89764 /len=4362			
629	0.014599	nuclear cap binding protein subunit 1,	NM 002486	Hs.89563	NP 002477
		80kDa (NCBP1), mRNA /cds=(31,2403)	l <del>-</del>		_
		/gb=NM 002486 /gi=4505342	1. 134		
		/ug=Hs.89563 /len=2828			
633	0.040751	A kinase (PRKA) anchor protein 13	NM 007200	Hs.301946	NP 658913
		(AKAP13), transcript variant 2, mRNA			
		/cds=(214,8655) /gb=NM 007200			
1,		/gi=21493028 /ug=Hs.301946			
		/len=10156			
635	0.023945	cDNA FLJ37956 fis, clone	AK095275	Hs.170141	
		CTONG2009527. /gb=AK095275			
•		/gi=21754500 /ug=Hs.170141	_		
e		/len=2753			
636	0.006463	hypothetical protein FLJ14775	NM 032837	Hs.334878	NP 116226
		(FLJ14775), mRNA /cds=(172,534)			
		/gb=NM_032837 /gi=14249549	r.		
		/ug=Hs.334878 /len=2697			
640	0.007171	adrenomedullin (ADM), mRNA	NM 001124	Hs.394	NP 001115
		/cds=(157,714) /gb=NM_001124	· ▽ ·		_
		/gi=4501944 /ug=Hs 394 /len=1449			
641	0.005927	mRNA for KIAA1119 protein, partial	AB032945	Hs.172506	
		cds. /cds=(1,3783) /gb=AB032945	•		
_	1	/gi=6329707 /ug=Hs.172506 /len=7438		÷	
642	0.002096	centrin, EF-hand protein, 2 (CETN2),	NM_004344	Hs.82794	NP_004335
		mRNA /cds=(48,566) /gb=NM_004344			
		/gi=4757901 /ug=Hs.82794 /len=1087			
645	0.013394	hematopoietic-derived zinc	NP_004867		
		fingerprotein (RefSeq aa 1e-48)			
667	0.007107	complement component 3a receptor 1	NM_004054	Hs.155935	NP_004045
		(C3AR1), mRNA /cds=(93,1541)			
		/gb=NM_004054 /gi=21314629			
		/ug=Hs.155935 /len=1985			
669	0.036556	putative zinc finger protein NY-REN-34	NM_016119	Hs.279799	NP_057203
· .	· ·	antigen (NY-REN-34), mRNA			
		/cds=(129,704) /gb=NM_016119			
		/gi=7705832 /ug=Hs.279799 /len=1323			
672	0.003183	C-terminal binding protein 2 (CTBP2),	NM_022802	Hs.171391	NP_073713
		transcript variant 2, mRNA			
		/cds=(137,3094) /gb=NM_022802			
		/gi=12746589 /ug=Hs.171391			
	1	/len=3780		<u> </u>	

	p-value	nding To Differentially Expressed Gen Description	Gene	Unigene	Protein
Opor	P-value		Accession No.	Accession	Accession
			Accession No.	No.	No.
673	0.040070	fatty-acid-Coenzyme A ligase, long-	NM 022977	Hs.81452	NP 075266
0/3	0.049079		NIVI_022911	1715.01452	NP_0/5200
•		chain 4 (FACL4), transcript variant 2,			***, * * *
		mRNA /cds=(507,2642)			
:		/gb=NM_022977 /gi=12669908			
		/ug=Hs.81452 /len=5356	. =		
678	0.030075	clone alpha_est218/52C1 mRNA	AF001542	Hs.356442	
		sequence /gb=AF001542 /gi=2529714			
		/ug=Hs.356442 /len=2992			
686	0.001878	HTGN29 protein (HTGN29), mRNA	NM_020199	Hs.283437	NP_064584
	1.	/cds=(205,1002) /gb=NM_020199			
	1.00	/gi=9910277 /ug=Hs.283437 /len=2371			
691	0.003213	U5 snRNP-specific protein, 200-KD (U5	NM_014014	Hs.246112	NP_054733
4		200KD), mRNA /cds=(189,5624)			
		/gb=NM_014014 /gi=24307974			
		/ug=Hs.246112 /len=5898			
696	0.015895	discoidin domain receptor family,	NM 006182	Hs.71891	NP_006173
		member 2 (DDR2), mRNA			_
		/cds=(354,2921) /gb=NM 006182			
		/gi=5453813 /ug=Hs.71891 /len=3096			
709	0.007171	ATP synthase, H_transporting,	NM 001697	Hs.433960	NP 001688
		mitochondrial F1 complex, O subunit			
		(oligomycin sensitivity conferring			
		protein) (ATP5O), mRNA /cds=(37,678)		·	
	•	/gb=NM_001697 /gi=4502302			,
		/ug=Hs.433960 /len=772			
715	0.013304	galactosamine (N-acetyl)-6-sulfate	NM_000512	Hs.159479	NP 000503
7 13	0.013394	sulfatase (Morquio syndrome,	NIVI_000312	115.135475	INF_000303
,		mucopolysaccharidosis type IVA)			•
					'
	. *	(GALNS), mRNA /cds=(56,1624)			
* * * .	1	/gb=NM_000512 /gi=9945384		No.	
740	0.000400	/ug=Hs.159479 /len=2328	NIN 047004		NID 000074
716	0.022106	chromosome 6 open reading frame 49	NM_017601	Hs.347297	NP_060071
		(C6orf49), mRNA /cds=(777,1715)			
	. :	/gb=NM_017601 /gi=8922168	•		
		/ug=Hs.347297 /len=3316			
718	0.025911	angiomotin (AMOT), mRNA	NM_133265	Hs.9271	NP_573572
		/cds=(797,2824) /gb=NM_133265			
*		/gi=19111149 /ug=Hs.9271 /len=6888			
722	0.035177	glutamic-oxaloacetic transaminase 1,	NM_002079	Hs.597	NP_002070
		soluble (aspartate aminotransferase 1)			
		(GOT1), mRNA /cds=(25,1266)			1
		/gb=NM_002079 /gi=4504066			
		/ug=Hs.597 /len=1941		1	

Genes	Correspon	nding To Differentially Expressed G n	s in Figur 20 -	RA	g a same a gradus
Spot	p-value	Description	Gen	Unigene	Protein
			Acc ssion No.	Accession	Accession
				No.	No.
726	0.007107	tyrosine 3-monooxygenase/tryptophan	NM 012479	Hs.25001	NP 036611
		5-monooxygenase activation protein,	<del>-</del>		
		gamma polypeptide (YWHAG), mRNA			, · · · · · · · · · · · · · · · · · · ·
		/cds=(192,935) /gb=NM_012479			
	, J.	/gi=21464100 /ug=Hs.25001 /len=3747			
100		1			
728	0.013394	netrin 4 (NTN4), mRNA	NM 021229	Hs.102541	NP_067052
'	0.010001	/cds=(452,2338) /gb=NM_021229	1402 1220	110.102011	741 _907 002
		/gi=24475651 /ug=Hs.102541			
	1	/len=3607			1
729	0.02801	sprouty 2 (Drosophila) (SPRY2), mRNA	NIM 005942	Hs.18676	NP 005833
123	0.02001	/cds=(382,1329) /gb=NM_005842	14141_003042	1 13. 10070	TVF _000000
			100		
,		/gi=22209007 /ug=Hs.18676 /len=2126	1		
700-	0.000000	DTD046 (LC054400) 5114	NINA DAGGOS	115 20454	ND 057000
730	0.020388	PTD016 protein (LOC51136), mRNA	NM_016125	Hs.30154	NP_057209
, ,		/cds=(183,809) /gb=NM_016125			
		/gi=21361528 /ug=Hs.30154 /len=1917	9		
731	0.014946	mitochondrial ribosomal protein S21	NM_018997	Hs.81281	NP_114107
		(MRPS21), transcript variant 2, nuclear			
		gene encoding mitochondrial protein,			
		mRNA /cds=(519,782) /gb=NM_018997			
		/gi=16950592 /ug=Hs.81281 /len=939			
,		THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE S			
733	0.004367	squamous cell carcinoma antigen	NM_014706	Hs.116875	NP_055521
1.5		recognised by T cells 3 (SART3),		· · · · · · · · · · · · · · · · · · ·	1
		mRNA /cds=(8,2899) /gb=NM_014706			;
		/gi=21327689 /ug=Hs.116875			
	A	/len=3776			
751	0.007807	cDNA FLJ38678 fis, clone	AK095997	Hs.378546	
		KIDNE2000227. /gb=AK095997			
	· .	/gi=21755370 /ug=Hs.378546		l	
	* * * * * * * * * * * * * * * * * * * *	/len=2292			
759	0.011238	chemokine (C-X-C motif) receptor 4	NM 003467	Hs.89414	NP_003458
1	5.5.1250	(CXCR4), mRNA /cds=(89,1147)	1 555 151		-550,00
		/gb=NM 003467 /gi=4503174			
		/ug=Hs.89414 /len=1679			
761	0.013304	caldesmon 1 (CALD1), transcript	NM 033138	Hs.325474	NP 149347
'01	0.013394		14141-022120	1113.323474	148941
'		variant 1, mRNA /cds=(230,2611)		1	
	·	/gb=NM_033138 /gi=15149460			
700	0.035.64	/ug=Hs.325474 /len=3610	NINA 000440	11. 70440	ND 000 too
769	3.04E-04	1	NM_000442	Hs.78146	NP_000433
ŀ		molecule (CD31 antigen) (PECAM1),	1		
		mRNA /cds=(194,2410)			
		/gb=NM_000442 /gi=21314616	1		
		/ug=Hs.78146 /len=3189		L	

Genes	Correspon	nding To Differ ntially Expressed Gen	s in Figure 20 -		
	p-value	Description	Gene	Unigene	Prot in
			Accession No.	Accession No.	Acc ssion No.
770	0.008566	of Tom7 (S. cerevisiae) (TOM7), mRNA /cds=(94,261) /gb=NM 019059	NM_019059	Hs.112318	NP_061932
		/gi=9506858 /ug=Hs.112318 /len=487			
775	0.030249	cofilin isoform 1	AF134802		NP 068733
796		poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA	NM_005016	Hs.63525	NP_114366
		/cds=(89,1189) /gb=NM_005016 /gi=14141167 /ug=Hs.63525 /len=1362			
797	0.043799	C-type (calcium dependent, carbohydrate-recognition domain)	NM_005752	Hs.287364	NP_005743
•		lectin, superfamily member 1 (cartilage-derived) (CLECSF1), mRNA			
	18	/cds=(80,673) /gb=NM_005752 /gi=5031636 /ug=Hs.287364 /len=673			
806	0.040751	ring finger protein 19 (RNF19), mRNA /cds=(318,2834) /gb=NM_015435	NM_015435	Hs.48320	NP_056250
		/gi=19923421 /ug=Hs.48320 /len=4357			
807	0.020388	KIAA0102 gene product (KIAA0102), mRNA /cds=(308,679) /gb=NM_014752	NM_014752	Hs.77665	NP_055567
		/gi=7661907 /ug=Hs.77665 /len=1370			
824	0.047031	lipoprotein lipase (LPL), mRNA /cds=(175,1602) /gb=NM_000237	NM_000237	Hs.180878	NP_000228
		/gi=4557726 /ug=Hs.180878 /len=3549			
829	5.11E-04	zinc finger protein 103 (mouse) (ZFP103), mRNA /cds=(923,2980)	NM_005667	Hs.155968	NP_005658
		/gb=NM_005667 /gi=5031824 /ug=Hs.155968 /len=3423			
830	0.02801	signal transducer and activator of transcription 1, 91kDa (STAT1),	NM_007315	Hs.21486	NP_644671
		transcript variant alpha, mRNA /cds=(352,2604) /gb=NM_007315			
	2	/gi=21536299 /ug=Hs.21486 /len=4157			
832	0.014599	heat shock 105kD (HSP105B), mRNA /cds=(314,2758) /gb=NM 006644	NM_006644	Hs.36927 ⇒	NP_006635
		/gi=5729878 /ug=Hs.36927 /len=3448			
834	0.004367	tetraspan 3 (TSPAN-3), mRNA /cds=(218,979) /gb=NM_005724	NM_005724	Hs.100090	NP_005715
		/gi=21264581 /ug=Hs.100090 /len=1842			

		nding To Differentially Expressed Gen			
Spot	p-value	Description	G ne	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
835	0.010277	likely ortholog of mouse tumor	NM_020755	Hs.146668	NP_065806
		differentially expressed 1, like (TDE1L),			
		mRNA /cds=(76,1437) /gb=NM_020755			ľ
11		/gi=24308212 /ug=Hs.146668			
		/len=3149			
839	0.03788	KIAA0781	AB018324		
841		v-Ki-ras2 Kirsten rat sarcoma 2 viral	NM 033360	Hs.433714	NP 203524
Ų-T,I	0.000177	oncogene (KRAS2), transcript variant a,	1441_000000	10.100711	111 _20002 1
		mRNA /cds=(182,751) /gb=NM_033360			
		/gi=15718762 /ug=Hs.433714			
		/len=1486	* * * * * * * * * * * * * * * * * * *		
042	0.025011	CDC42 effector protein (Rho GTPase	NM 006449	Hs.260024	NP 006440
843	0.025911		14101_000449	1 15.200024	UVF_000440
		binding) 3 (CDC42EP3), mRNA			
		/cds=(969,1733) /gb=NM_006449			
		/gi=19923355 /ug=Hs.260024			
		/len=2768			
845	0.007107	tetratricopeptide repeat domain 3	NM_003316	Hs.118174	NP_003307
	1	(TTC3), mRNA /cds=(1470,7547)			
		/gb=NM_003316 /gi=21359840		L pa	
		/ug=Hs.118174 /len=9078			
857	0.018784	mitochondrial carrier 1 (MTCH1),	NM_014341	Hs.279939	NP_055156
		nuclear gene encoding mitochondrial	* .		•
		protein, mRNA /cds=(1,1119)			
		/gb=NM_014341 /gi=7657344			i .
		/ug=Hs.279939 /len=1890			
858	0.025911	calpastatin (CAST), transcript variant 2,	NM 173060	Hs 359682	NP 775085
		mRNA /cds=(155,2215)	<del>-</del>		
		/gb=NM_173060 /gi=27765084			
		/ug=Hs.359682 /len=4296			-
863	0.015805	heterogeneous nuclear	NM 005968	Hs.79024	NP_112480
OOO	0.013033	ribonucleoprotein M (HNRPM),	11111_00000	113.75024	111 _1.12400
		transcript variant 1, mRNA			
		/cds=(231,2423) /gb=NM_005968			
			1		
	:	/gi=14141151 /ug=Hs.79024 /len=2703			
005	0.005477		NO 004007	,	<del> </del>
865		mitochondrion, complete genome	NC_001807	11- 7000	ND 057074
869	0.023945	receptor associated protein 80	NM_016290	Hs.7889	NP_057374
		(RAP80), mRNA /cds=(110,2269)			
,		/gb=NM_016290 /gi=21361592		: .	
		/ug=Hs.7889 /len=2516			1
871	0.030249	phosphodiesterase 4D interacting	NM_014644	Hs.265848	NP_055459
		protein (myomegalin) (PDE4DIP),	· ·		
		mRNA /cds=(658,4056)			
		/gb=NM_014644 /gi=11036643			
		/ug=Hs.265848 /len=5676		1	
873	0.015895	dynactin 4 (p62) (DCTN4), mRNA	NM 016221	Hs.328865	NP 057305
		/cds=(22,1404) /gb=NM_016221	1 -	1.	1 -
			I '	1	1
		/gi=19923450 /ug=Hs.328865			

Correspor	nding To Differentially Expressed Gen		KA	
p-value	Description	Gene	Unigene	Protein
		Accession No.	Accession	Accession
i			No.	No.
0.032636	proline rich 2 (PROL2), mRNA	NM_006813	Hs.75969	NP 006804
	/cds=(114,1097) /gb=NM 006813	- 1		
		•		
		NM 002291	Hs.82124	NP_002282
		· -		- T
			•	,
		AL833217	Hs.348420	
· /				
	, , ,			
	, ,	<b>(</b>		
0.025911		BI490626	Hs 347727	
			· · · · · · · · ·	
·				
0.025911		NM 006451	Hs 109643	NP_006442
0.0200				
		*		
				.,
0.025911		NM 000969	Hs 180946	NP 000960
0.02.0011		11111_000000	11.0.100010	
			*	1
0.03788		NM 000366	Hs 77899	NP_000357
	, g,,,,,,,,,			
8.58E-05	ubiquitin-conjugating enzyme E2F 3	NM 006357	Hs.4890	NP_006348
	T T			
		NM 003270	Hs.121068	NP 003261
			1	
				]
0.001878	splicing factor, arginine/serine-rich 11	NM 004768	Hs.433581	NP_004759
, , , , , , ,				_
	• -			
0.006463		NM 173812	Hs.125472	NP_776173
1 2.23330	(FLJ32949), mRNA /cds=(1,2277)	[		1
,	1(EL332343), HINNA /COS-LL////L	l.	· .	
,	/gb=NM_173812 /gi=27883873			
ı	0.032636 0.017288 0.012276 0.025911 0.025911 0.03788 8.58E-05 0.002096	p-value         Description           0.032636         proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813 /gi=5802981 /ug=Hs.75969 /len=2061           0.017288         laminin, beta 1 (LAMB1), mRNA /cds=(336,5696) /gb=NM_002291 /gi=4504950 /ug=Hs.82124 /len=5831           0.012276         mRNA; cDNA DKFZp667D087 (from clone DKFZp667D087) /gb=AL833217 /gi=21733848 /ug=Hs.348420 /len=3440           0.025911         603031929T1 NIH_MGC_115 cDNA clone IMAGE:5173326 3', mRNA sequence /clone=IMAGE:5173326 /clone_end=3' /gb=Bl490626 /gi=15329854 /ug=Hs.347727 /len=1255           0.025911         polyadenylate binding protein- interacting protein 1 (PAIP1), mRNA /cds=(188,1627) /gb=NM_006451 /gi=17511254 /ug=Hs.109643 /len=2764           0.025911         ribosomal protein L5 (RPL5), mRNA /cds=(63,956) /gb=NM_000969 /gi=14591908 /ug=Hs.180946 /len=1033           0.03788         tropomyosin 1 (alpha) (TPM1), mRNA /cds=(151,1005) /gb=NM_000366 /gi=27597084 /ug=Hs.77899 /len=1265           8.58E-05         ubiquitin-conjugating enzyme E2E 3 (UBC4/5 yeast) (UBE2E3), mRNA /cds=(120,743) /gb=NM_006357 /gi=5454145 /ug=Hs.4890 /len=1294	Description	Description

		nding To Differentially Express d Gen			
Spot	p-value	Description	Gene Accession No.	Unigene Accession	Protein Accession
899	0.017288	chromosome 21 open reading frame 59	NM 017835	No. Hs.5811	No. NP 067077
099	0.017200	(C21orf59), mRNA-/cds=(361,777)		115.5011	NP_007077
		/gb=NM_017835 /gi=8923436			
		/ug=Hs:5811 /len=1245			
900	0.032636	RAB11A, member RAS oncogene	NM 004663	Hs.75618	NP 004654
- ; -		family (RAB11A), mRNA			
-	'	/cds=(104,754) /gb=NM_004663			
		/gi=20149549 /ug=Hs.75618 /len=2474			
901	1.53E-04	signal transducing adaptor molecule	NM_005843	Hs.17200	NP_005834
		(SH3 domain and ITAM motif) 2			
		(STAM2), mRNA /cds=(351,1928)			
		/gb=NM_005843 /gi=21265030			Company of the
	,	/ug=Hs.17200 /len=3928			
902	0.002602	H2A histone family, member Z	NM_002106	Hs.119192	NP_002097
	-	(H2AFZ), mRNA /cds=(107,493)	enalis de la servicio		:
1.1		/gb=NM_002106 /gi=20336749			
	<u> </u>	/ug=Hs.119192 /len=873			
903	0.007107	S100 calcium binding protein A10	NM_002966	Hs.400250	NP_002957
		(annexin II ligand, calpactin I, light			
		polypeptide (p11)) (S100A10), mRNA			
		/cds=(112,405) /gb=NM_002966			
004	0.045005	/gi=4506760 /ug=Hs.400250 /len=649			N.D. 000000
904	0.015895	tumor susceptibility gene 101	NM_006292	Hs.118910	NP_006283
		(TSG101), mRNA /cds=(127,1299)	grade views		
		/gb=NM_006292 /gi=18765712			
905	0.002562	/ug=Hs.118910 /len=1550	NM 014814	110 22400	ND 055000
905	0.003563	KIAA0107 gene product (P44S10), mRNA /cds=(26,1195) /gb=NM_014814		Hs.23488	NP_055629
		/gi=7661913 /ug=Hs.23488 /len=1308			
		/gi=70019137ug=115.234007ie1i=1300 			
906	0.02801	transaldolase 1 (TALDO1), mRNA	NM 006755	Hs.77290	NP_006746
.500		/cds=(51,1064) /gb=NM_006755	14141_000755	113.77230	_000740
		/gi=5803186 /ug=Hs.77290 /len=1319			
919	0.011238	putative protein tyrosine phosphatase	U93051	Hs.356062	NP_000305
	0.077200	(PTEN) mRNA, complete cds		110.00002	
		/cds=(1,1212) /gb=U93051 /gi=1916351			
		/ug=Hs.356062 /len=1212			
				•	<u>.</u>
936	0.018784	membrane-bound transcription factor	NM_015884	Hs.350970	NP_056968
		protease, site 2 (MBTPS2), mRNA	_	,	_
		/cds=(100,1659) /gb=NM_015884			V v
		/gi=7706692 /ug=Hs 350970 /len=1759		- 4	-
951	0.015895	CDC-like kinase1 (CLK1), mRNA	NM_004071	Hs.2083	NP_004062
		/cds=(156,1610) /gb=NM_004071			
	L	/gi=4758007 /ug=Hs.2083 /len=1834			l* .

		nding To Diff r ntially Express d Gen			
Spot	p-value	Description	Gene	Unigene	Protein
*			Accession No.	Accession	Accession
	1			No.	No.
953	0.001501	mRNA for KIAA0592 protein, partial	AB011164	Hs.439367	
		cds. /cds=(1,4062) /gb=AB011164			
		/gi=3043707 /ug=Hs.439367 /len=4623			
		/gi=3043/07/ug=115.439307/lef1=4023			
050	0.044500	D (0±05)	NINA 447700	11-007000	ND 600000
958	0.014599	cathepsin B (CTSB), transcript variant	NM_147780	Hs.297939	NP_680093
		2, mRNA /cds=(314,1333)		<b>1</b> ',	
		/gb=NM_147780 /gi=22538430		}	
		/ug=Hs.297939 /len=2140			
961	0.035177	SON DNA binding protein (SON),	NM_058183	Hs.92909	NP_620305
tal er		transcript variant e, mRNA			
		/cds=(50,6376) /gb=NM_058183			
		/gi=21040317 /ug=Hs.92909 /len=8482			
		1 3 1 2 1 3 1 3 1 7 4 3 1 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1			
965	0.015805	testis enhanced gene transcript	NM 003217	Hs.74637	NP 003208
900	0.015695		111111_003217	1115.74037	114-003200
٠.	ļ. : : : : : : : : : : : : : : : : : : :	(TEGT), mRNA /cds=(41,754)			ļ
		/gb=NM_003217 /gi=4507432	r,		
		/ug=Hs.74637 /len=2600			Na in
966	0.02801	CGI-81 protein (DREV1), mRNA	NM_016025	Hs.279583	NP_057109
		/cds=(249,1100) /gb=NM_016025			
·	. *	/gi=19923448 /ug=Hs.279583			
		/len=3163			
967	0.015895	hepatoma-derived growth factor (high-	NM 004494	Hs.89525	NP 004485
		mobility group protein 1-like) (HDGF),			
1 1		mRNA /cds=(316,1038)			
		/gb=NM_004494 /gi=4758515			
	1				
	0.000400	/ug=Hs 89525 /len=2376			ND 057500
969	0.022106	cisplatin resistance-associated	NM_016424	Hs.3688	NP_057508
ā, ji		overexpressed protein (LUC7A), mRNA			
		/cds=(154,1452) /gb=NM_016424	**		
		/gi=19923484 /ug=Hs.3688 /len=3451			
971	0.047031	mitochondrion, complete genome	NC 001807		
975		aldo-keto reductase family 1, member	NM_006066	Hs.432896	NP 697021
	3.555.00	A1 (aldehyde reductase) (AKR1A1),		1.5.15255	
	٠.	transcript variant 1, mRNA		ļ	i '
		1 The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the	l		
		/cds=(465,1442) /gb=NM_006066		1::	
		/gi=24497575 /ug=Hs.432896			
	<u> </u>	/len=1556			
977	0.012276	pyruvate dehydrogenase (lipoamide)	NM_000925	Hs.979	NP_000916
		beta (PDHB), mRNA /cds=(19,1098)			l •
* * *	1	/gb=NM_000925 /gi=4505686		1	}
		/ug=Hs.979 /len=1501			
978	0.025911	cyclin D binding myb-like transcription	NM_021145	Hs.5671	NP_066968
910	0.020011	factor 1 (DMTF1), mRNA	1.4.W_OZ 1.140	1.10.007	-000000
			41		
		/cds=(276,2558) /gb=NM_021145			1 .
	1	/gi=10863946 /ug=Hs.5671 /len=3767	1	i	I

		nding To Differentially Expr ssed Gen			
Spot	p-value	Description	Gene	Unig n	Prot in
		"	Accession No.	Acc ssion	Acc ssion
				No.	No.
981	0.030249	wingless-type MMTV integration site	NM_003392	Hs.152213	NP_003383
		family, member 5A (WNT5A), mRNA			
		/cds=(758,1855) /gb=NM_003392			
		/gi=17402917 /ug=Hs.152213			
: -		/len=4428			
983	0.020388	DEAD/H (Asp-Glu-Ala-Asp/His) box	NM 014314	Hs.145612	NP 055129
500	0.020000	polypeptide (RIG-I), mRNA		110.110012	0000
		/cds=(159,2936) /gb=NM_014314			
*		/gi=27881481 /ug=Hs.145612			
			•		
000	0.000000	/len=4372	NINE COCCOO	U- 00000	ND 000004
992	0.020388	chemokine (C-X-C motif) ligand 3	NM_002090	Hs.89690	NP_002081
		(CXCL3), mRNA /cds=(78,398)		\$	
		/gb=NM_002090 /gi=4504156			
		/ug=Hs.89690 /len=1064	81.7		
993	0.012276	CREB binding protein (Rubinstein-Taybi	NM_004380	Hs.23598	NP_004371
		syndrome) (CREBBP), mRNA			
		/cds=(199,7527) /gb=NM_004380	Ú		
7.		/gi=4758055 /ug=Hs.23598 /len=8694	Y y		
1000	0.043799	bradykinin receptor B2 (BDKRB2),	NM_000623	Hs.250882	NP 000614
		mRNA /cds=(142,1317)			_
		/gb=NM_000623 /gi=17352499			
		/ug=Hs.250882 /len=4267			
1001	0.017288	RAD23 B (S. cerevisiae) (RAD23B),	NM 002874	Hs.404283	NP_002865
1001	0.017200	mRNA /cds=(352,1581)	14141_002074	113.404203	111 _002003
				,	
		/gb=NM_002874 /gi=19924138			
		/ug=Hs.404283 /len=2943	504 64 467	11. 100001	ND TOESOAO
1002	0.002893	NP220 nuclear protein (NP220), mRNA	NM_014497	Hs.169984	NP_055312
		/cds=(315,6251) /gb=NM_014497			
	1 .	/gi=21626467 /ug=Hs.169984	· •		
		/len=6570	44		
1003	0.002602	ribosomal protein S25 (RPS25), mRNA	NM_001028	Hs.409158	NP_001019
		/cds=(64,441) /gb=NM_001028		· ·	
	· · · · · · · · · · · · · · · · · ·	/gi=14591916 /ug=Hs.409158 /len=514.			
1004	0.001193	fibroblast growth factor receptor 2	NM 023028	Hs.278581	NP 075420
		(bacteria-expressed kinase,	1 - ,		
		keratinocyte growth factor receptor,			
		craniofacial dysostosis 1, Crouzon			
•		syndrome, Pfeiffer syndrome, Jackson-			
4		Weiss syndrome) (FGFR2), transcript			
				ļ.	
		variant 10, mRNA /cds=(594,2960)			
		/gb=NM_023028 /gi=13186268			
		/ug=Hs.278581 /len=4667	1		
				<u> </u>	
1011	0.032636	1	NM_002880	Hs.349650	NP_002871
		1	i.		
101,		1 (RAF1), mRNA /cds=(130,2076)			
		1 (RAF1), mRNA /cds=(130,2076)  /gb=NM_002880 /gi=4506400			

		nding To Differentially Expr ssed Gen			
Spot	p-value	D scription	Gene Accession No.	Unigene Accession	Protein Accession
				No.	No.
1015	0.006463	actinin, alpha 1 (ACTN1), mRNA /cds=(184,2862) /gb=NM_001102 /gi=12025669 /ug=Hs.119000 /len=3398	NM_001102	Hs.119000	NP_001093
1024	0.009388	5T4 oncofetal trophoblast glycoprotein	NM_006670	Hs.82128	NP_006661
024	0.00000	(5T4), mRNA /cds=(85,1347) /gb=NM_006670 /gi=5729717 /ug=Hs.82128 /len=2053	,	13.02120	
1030	0.007807	px19-like protein (PX19), mRNA	NM_013237	Hs.279529	NP_037369
		/cds=(177,836) /gb=NM_013237 /gi=7019508 /ug=Hs.279529 /len=1217			_
1031	0.03788	decorin (DCN), transcript variant A1,	NM_001920	Hs.433989	NP_598014
		mRNA /cds=(200,1279) /gb=NM_001920 /gi=19743844 /ug=Hs.433989 /len=1751			
1035	0.025911	NADH dehydrogenase (ubiquinone) 1	NM 002488	Hs.163867	NP 002479
1		alpha subcomplex, 2, 8kDa (NDUFA2), mRNA /cds≈(57,356) /gb=NM_002488 /gi=4505354 /ug=Hs.163867 /len=590			
1043	0.022106	mRNA for KIAA1376 protein, partial cds. /cds=(144,1457) /gb=AB037797 /gi=7243132 /ug=Hs.24684 /len=4131	AB037797	Hs.24684	
1054	0.025911	NADH dehydrogenase (ubiquinone) 1	NM_005000	Hs.83916	NP_004991
		alpha subcomplex, 5, 13kDa (NDUFA5), nuclear gene encoding mitochondrial protein, mRNA /cds=(110,460) /gb=NM_005000 /gi=13699821 /ug=Hs.83916 /len=1550			
1057	0.035177	mRNA for KIAA1609 protein, partial	AB046829	Hs.14449	
		cds. /cds=(1,1423) /gb=AB046829 /gi=15425661 /ug=Hs.14449 /len=4683			
1059	0.035177	clone IMAGE:4993796, mRNA /gb=BC040073 /gi=25455647 /ug=Hs.322437 /len=2265	BC040073	Hs.322437	
1061	9.43E-04	synaptosomal-associated protein, 25kDa (SNAP25), transcript variant 1, mRNA /cds=(213,833) /gb=NM 003081	NM_003081	Hs.84389	NP_570824
		/gi=18765732 /ug=Hs.84389 /len=2053			
1064		mitochondria solute carrier protein (MSCP)	AY032628		NP_061049
1081	0.01167	glutaredoxin (thioltransferase) (GLRX), mRNA /cds=(16,336) /gb=NM_002064 /gi=4504024 /ug=Hs.28988 /len=1328	NM_002064	Hs.28988	NP_002055

		nding To Differentially Express d Gen				
Spot	p-value	Description	Gen	Unigen	Protein	
- 1			Accession No.	Accession	Accession	
.′	]			No.	No.	
1090	0.014599	protein phosphatase methylesterase-1	NM 016147	Hs.63304	NP 057231	
1000	0.014000	(PME-1), mRNA /cds=(100,1260)			00, _0	
		1				
		/gb=NM_016147 /gi=7706644	,			
		/ug=Hs.63304 /len=2484			<u> </u>	
1093	0.025911	hypothetical gene AK023725	XM_048072			
		(LOC92923)				
1111	0.020388	hypothetical protein (HSPC016), mRNA	NM_015933	Hs.397853	NP_057017	
		/cds=(39,233) /gb=NM 015933				
~ ·		/gi=7705430 /ug=Hs 397853 /len=384				
		<i>g.</i>				
1113	0.043700	nischarin (NISCH), mRNA	NM 007184	Hs.26285	NP_009115	
1113	0.043733	/cds=(27,4541) /gb=NM 007184	007 104	113.20200		
15.00			4			
		/gi=6005787 /ug=Hs.26285 /len=5132		11 101007	ND 000000	
1115	0.043799	H3 histone, family 3A (H3F3A), mRNA	NM_002107	Hs.181307	NP_002098	
	1. 1. 1. 1.	/cds=(116,526) /gb=NM_002107				
		/gi=22027640 /ug=Hs.181307	aassa saasa saasa saasa saasa saasa saasa saasa saasa saasa saasa saasa saasa saasa saasa saasa saasa saasa s			
		/len=1047			÷ !	
1119	0.005325	pp9974 mRNA, complete cds	AF318382	Hs.251664		
		/cds=(2009,2350) /gb=AF318382				
		/gi=18027855 /ug=Hs.251664		*	i .	
		/len=2630				
1131	0.012204	actinin, alpha 1 (ACTN1), mRNA	NM_001102	Hs.119000	NP 001093	
1131	0.013394		14141_00   102	113.119000	145 00 1033	
		/cds=(184,2862) /gb=NM_001102				
		/gi=12025669 /ug=Hs 119000	e personal		1	
		/len=3398	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1		
1148	0.025911	CHLORIDE INTRACELLULAR	Q9Z1Q5			
		CHANNEL PROTEIN 1 (NUCLEAR			4.	
- i		CHLORIDE ION CHANNEL 27)				
	•	(NCC27) (P64 CLCP) (aa 2e-14 92%)				
1163	0.007807	reticulon 4 (RTN4), mRNA	NM_020532	Hs.65450	NP 722550	
	3.33, 33,	/cds=(245,3823) /gb=NM_020532				
	1	/gi=24638438 /ug=Hs.65450 /len=4166			1 5 5	
		//gi-24000400 /ug-i i3.00400 /icii-4 i00		•		
4477	0.005044	DNA EL 141720'60 plane	AK021901	He 201626	<del> </del>	
1177	Ų.025911	cDNA FLJ11739 fis, clone	AK021801	Hs.301626		
		HEMBA1005497. /gb=AK021801			1	
		/gi=10433061 /ug=Hs.301626				
		/len=2366				
1187	0.02801	serine (or cysteine) proteinase inhibitor,	NM_000295	Hs.297681	NP_000286	
		clade A (alpha-1 antiproteinase,	TT			
		antitrypsin), member 1 (SERPINA1),				
_		mRNA /cds=(233,1489)				
		/gb=NM_000295 /gi=21361197			<b>!</b> -	
	1					
40-5	0.000:55	/ug=Hs.297681 /len=1584	V44 000500	<del> </del>	ļ	
1200	0.006463	hypothetical gene supported by	XM_000590			
•	1	XM_000590 (LOC59176)		1		

		nding To Differentially Expr ssed Gen			
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1207	0.021	PTPRF interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1), mRNA /cds=(241,3258)	NM_003622	Hs.133207	NP_803193
		/gb=NM_003622 /gi=4505986 /ug=Hs.133207 /len=4028			
1210	0.007807	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase) (NDUFS1), mRNA /cds=(85,2268) /gb=NM_005006 /gi=28269700 /ug=Hs.8248 /len=2382	NM_005006	Hs.8248	NP_004997
1212	0.03788	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) (ST13), mRNA /cds=(144,1253) /gb=NM_003932 /gi=21237722 /ug=Hs.119222 /len=3214	NM_003932	Hs.119222	NP_003923
1222	0.047031	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9), mRNA /cds=(103,636) /gb=NM_003418 /gi=4827070 /ug=Hs.2110 /len=1500	_	Hs.2110	NP_003409
1236	0.035177	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) (MMP9), mRNA /cds=(20,2143) /gb=NM_004994 /gi=4826835 /ug=Hs.151738 /len=2334	NM_004994	Hs.151738	NP_004985
1244	0.011447	KIAA0625 protein (KIAA0625), mRNA /cds=(267,2753) /gb=NM_015046 /gi=7662211 /ug=Hs.154919 /len=3097	NM_015046	Hs.154919	NP_055861
1246	0.033876	mRNA; cDNA DKFZp686B2110 (from clone DKFZp686B2110) /gb=AL832120 /gi=21732663 /ug=Hs.432506 /len=4383	AL832120	Hs.432506	
1254	0.005325	DKFZp586I0923 (from clone DKFZp586I0923)	AL050218		•
1260		F-box only protein 2 (FBXO2), mRNA /cds=(343,1233) /gb=NM_012168 /gi=15812197 /ug=Hs.132753 /len=1551	NM_012168	Hs.132753	NP_036300
1261	0.002565	cDNA FLJ11971 fis, clone HEMBB1001208. /gb=AK022033 /gi=10433350 /ug=Hs.121806 /len=2355	AK022033	Hs.121806	

		nding To Diff r ntially Expressed Gen			The second second
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
1275	0.002337	gp25L2 protein (HSGP25L2G), mRNA	NM 017510	Hs.279929	NP 059980
		/cds=(76,720) /gb=NM_017510			
		/gi=24475637 /ug=Hs.279929			4
		/len=1420		,	
1327	0.035177	peptide transporter 3 (PHT2), mRNA	NM 016582	Hs.237856	NP 057666
1327	0.055177	/cds=(235,1980) /gb=NM 016582	10002	113.237630	NF_037000
		/gi=7706116 /ug=Hs.237856 /len=2113			
		/gi=//00110/ug=ns.23/630/len=2113			
1220	0.002562	mDNA for KIAAOQ41 protein modial	A D020648	Ho 7400	
1328	0.003563	mRNA for KIAA0841 protein, partial	AB020648	Hs.7426	
		cds. /cds=(1,1926) /gb=AB020648		,	
7277	2 22 122	/gi=4240170 /ug=Hs 7426 /len=4283			
1345	0.001193		NM_012477	Hs.7709	NP_036609
		mRNA /cds=(154,963) /gb=NM_012477			
		/gi=24430130 /ug=Hs:7709 /len=1183			
1348		col4A1 gene, 3'	X92395		
1360	0.025911	chromosome 15 open reading frame 15	NM_016304	Hs.284162	NP_057388
		(C15orf15), mRNA /cds=(144,635)			
. '		/gb=NM_016304 /gi=18491027			
		/ug=Hs.284162 /len=1487			
1376	0.013394	chaperonin containing TCP1, subunit 5	NM_012073	Hs.1600	NP_036205
		(epsilon) (CCT5), mRNA		:	
		/cds=(92,1717) /gb=NM_012073			
		/gi=24307938 /ug=Hs.1600 /len=1961			
1401	0.00587	prosaposin (variant Gaucher disease	NM 002778	Hs.406455	NP 002769
,		and variant metachromatic			
4.5	,	leukodystrophy) (PSAP), mRNA			
		/cds=(39,1613) /gb=NM_002778			
		/gi=11386146 /ug=Hs.406455			•
		/len=2767			
1406	0.004367	fibrillin 1 (Marfan syndrome) (FBN1),	NM_000138	Hs.750	NP_000129
1.100	0.00-007	mRNA /cds=(134,8749)	11111_000100	113.700	-000120
et a		/gb=NM_000138 /gi=24430140			
		/ug=Hs.750 /len=9749			e e
1407	3 05E 04	zinc finger protein 9 (a cellular retroviral	NM 003419	Hs.2110	NP_003409
140/	3.33 <b>⊆-</b> 04 	1		13.4   10 	
		nucleic acid binding protein) (ZNF9),			
		mRNA /cds=(103,636) /gb=NM_003418			
		/gi=4827070 /ug=Hs.2110 /len=1500			
1400	2 20 5 04	dibudrolingomido debudrocanos (F2	NM 000100	Ho 74625	ND 00000
1408	2.32E-04	dihydrolipoamide dehydrogenase (E3	NM_000108	Hs.74635	NP_000099
}	]	component of pyruvate dehydrogenase			1
	,	complex, 2-oxo-glutarate complex,		N.,	
		branched chain keto acid			
		dehydrogenase complex) (DLD),		:	
] .		mRNA /cds=(83,1612) /gb=NM_000108	1		
		/gi=5016092 /ug=Hs.74635 /len=2320		<u>.</u>	, ,
		<b>*</b> .	<u></u>	<u> </u>	

Genes	Correspoi	nding To Differentially Expr ssed Gen	s in Figure 20 -	RA	
		Description	Gen	Unigene	Protein
-			Accession No.	Accession	Accession
,			,	No.	No.
1409	0.014599	KDEL (Lys-Asp-Glu-Leu) endoplasmic	NM 006854	Hs.372755	NP 006845
		reticulum protein retention receptor 2			
		(KDELR2), mRNA /cds=(13,651)			
	1	/gb=NM_006854 /gi=8051609			· /
		/ug=Hs.372755 /len=1153			
1410	0.003947	fragile X mental retardation, autosomal	NM 005087	Hs.82712	NP 005078
		1 (FXR1), mRNA /cds=(13,1878)		,	
		/gb=NM_005087 /gi=4826735			1
		/ug=Hs.82712 /len=2132			
1413	9 43F-04	vacuolar protein sorting 29 (yeast)	NM 057180	Hs.69192	NP 476528
	0020	(VPS29) transcript variant 2, mRNA	1007.100	110.00102	1 17.0020
	2.5	/cds=(61,621) /gb=NM_057180			
		/gi=17402911 /ug=Hs.69192 /len=1107			
		7gi 17 1020 11 7dg 110.00 102 7icii 11 77			
1417	0.03788	phosphoglycerate mutase 1 (brain)	NM 002629	Hs.181013	NP 002620
	0.00700	(PGAM1), mRNA /cds=(32,796)	14141_002025	1113.101013	141 _002020
		/gb=NM_002629 /gi=4505752			
		/ug=Hs.181013 /len=1709			
1418	0.030249	voltage-dependent anion channel 2	NM 003375	Hs:78902	NP 003366
1710	0.000243	(VDAC2), mRNA /cds=(63,947)	14141_003573	113.70302	141 _000000
- 1		/gb=NM_003375 /gi=4507880			
		/ug=Hs.78902 /len=1404			
1419	n n3n249	CD74 antigen (invariant polypeptide of	NM 004355	Hs.84298	NP_004346
'-''	0.000240	major histocompatibility complex, class	14141_004333	113.04230	101 _004540
		II antigen-associated) (CD74), mRNA			
	•	/cds=(8,706) /gb=NM_004355			
-		/gi=10835070 /ug=Hs.84298 /len=1304			
		/gi=100000707dg=118.042907left=1004			
1426	0.033636	chemokine (C-C motif) ligand 13	NM_005408	Hs.11383	NP_005399
1720	0.002030	(CCL13), mRNA /cds=(76,372)	11111_003400	113.11303	141 _003399
		/gb=NM_005408 /gi=22538799			
		/ug=Hs.11383 /len=861			
1430	0.001330	synovial sarcoma, X breakpoint 2	NM_014021	Hs.22587	NP_054740
1750	0.001009	interacting protein (SSX2IP), mRNA	14111_014021	11.13.22.501	141004740
		/cds=(265,2109) /gb=NM_014021			
1.		/gi=7662381 /ug=Hs.22587 /len=5835			. ,
1442	6.56F-04	amyotrophic lateral sclerosis 2	NM 015049	Hs.154248	NP 055864
1772	0.000	(juvenile) chromosome region,	14101_013043	1113.104240	TAIF00000# .
		candidate 3 (ALS2CR3), mRNA			• '
	•	/cds=(382,3126) /gb=NM_015049			
		/gi=13027379 /ug=Hs.154248			
		/gi=130273797dg=115.134248  /len=6470			
1443	0.00169	cDNA FLJ13106 fis, clone	AK023168	Hs.12707	
'3	0.00100	NT2RP3002455, highly similar to		113.12/0/	
		mRNA for KIAA0678 protein.			
	'	/gb=AK023168 /gi=10434970		٠.	. ,
		/ug=Hs.12707 /len=3985			
L	L	//ug=ris.12/0/ /ieii=3900	l	<u> </u>	<u> </u>

Genes	Correspon	nding To Differentially Expressed Gen	es in Figure 20 -	RA 🗦	
	p-value	Description	Gene	Unigene	Protein
	<u> </u>		Accession No.	Accession	Accession (
	N			No.	No.
1445	6.35E-05	nuclear receptor coactivator 6	NM 014071	Hs.159613	NP 054790
•		(NCOA6), mRNA /cds=(2755,8760)	<del>-</del>		
		/gb=NM_014071 /gi=7661975			
		/ug=Hs.159613 /len=9301			
1449	0.047031	apoptosis related protein APR-3 (APR-	NM 016085	Hs.9527	NP_542159
	, , , , , , , , ,	3), transcript variant 1, mRNA			
		/cds=(336,851) /gb=NM 016085			
!		/gi=18105011 /ug=Hs.9527 /len=1086			
1453	0.030249	methyl-CpG binding domain protein 2	NM 015832	Hs.25674	NP 056647
		(MBD2), transcript variant testis-		:	
		specific, mRNA /cds=(230,1138)		· .	
ř · .		/gb=NM_015832 /gi=21464120			
		/ug=Hs.25674 /len=2792			
1458	0.032636	Williams-Beuren syndrome	NM 022170	Hs.180900	NP_114381
		chromosome region 1 (WBSCR1),			- · · · · · ·
		transcript variant 1, mRNA /cds=(9,755)		• **	
		/gb=NM_022170 /gi=11559922			
		/ug=Hs.180900 /len=2546		• •	
1459	0.023945	GABA(A) receptor-associated protein	NM_007278	Hs.7719	NP 009209
		(GABARAP), mRNA /cds=(105,458)			
		/gb=NM_007278 /gi=6005763			
		/ug=Hs.7719 /len=924			
1461	0.018784	phosphoglycerate kinase 1 (PGK1),	NM_000291	Hs.78771	NP 000282
		mRNA /cds=(70,1323) /gb=NM_000291			_
		/gi=22095338 /ug=Hs.78771 /len=2338	* * * * * * * * * * * * * * * * * * * *		
				÷ .	
1465	0.02801	splicing factor 3b, subunit 1, 155kDa	NM_012433	Hs.334826	NP_036565
	. 4	(SF3B1), mRNA /cds=(1,3915)			
		/gb=NM_012433 /gi=6912653			
	4.7	/ug=Hs.334826 /len=4259			
1475	2.32E-04	KIAA0193 gene product (KIAA0193),	NM_014766	Hs.75137	NP_055581
		mRNA /cds=(353,1393)		A P	
1		/gb=NM_014766 /gi=7661983			
		/ug=Hs.75137 /len=5076			
1478	0.018784	interferon induced transmembrane	NM_003641	Hs 366	
		protein 1 (9-27) (IFITM1), mRNA			
		/cds=(111,488) /gb=NM_003641	*		
		/gi=4504580 /ug=Hs.366 /len=647			
1490	0.047031	ARP3 actin-related protein 3 (yeast)	NM_005721	Hs.380096	NP_005712
		(ACTR3), mRNA /cds=(216,1472)			
		/gb=NM_005721 /gi=7262289			
		/ug=Hs.380096 /len=2189			
1494	0.032636	basic leucine zipper and W2 domains 2	NM_014038	Hs.5216	NP_054757
		(BZW2), mRNA /cds=(163,1422)			·
		/gb=NM_014038 /gi=7661743	* · · · · · · · · · · · · · · · · · · ·		
		/ug=Hs.5216 /len=1869			La de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la const

		nding To Differentially Expr ssed Gen	s in Figur 20 -	RA	
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
1498	0.016299	guanine nucleotide binding protein (G	NM_005274	Hs.424138	NP_005265
		protein), gamma 5 (GNG5), mRNA	and the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second s		
		/cds=(334,540) /gb=NM_005274			
ì	:	/gi=4885286./ug=Hs.424138./len=698			
1499	0.006463	ectonucleotide	NM_006208	Hs.11951	NP_006199
-		pyrophosphatase/phosphodiesterase 1			
		(ENPP1), mRNA /cds=(173,2794)	the second		
		/gb=NM_006208 /gi=13324676	· · · · · · · · · · · · · · · · · · ·		
. '-		/ug=Hs.11951 /len=3493	i.		
1502	0.040751	putative dimethyladenosine transferase	NM_014473	Hs.125819	NP_055288
	• .	(HSA9761), mRNA /cds=(79,1020)			
		/gb=NM_014473 /gi=7657197			
		/ug=Hs.125819 /len=1505	and the second of the		1 · · · · · · · · · · · · · · · · · · ·
4500	0.005050		A E 4 7000 E	11. 00740	The second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon
1506	0.005353	septin 2 (SEP2) mRNA, partial cds	AF179995	Hs.80712	
		/cds=(1,1528) /gb=AF179995			
4540	0.040700	/gi=9957543 /ug=Hs.80712 /len=4344	NIM OCCAO	11- 050554	ND 000440
1519	0.043799	step II splicing factor SLU7 (SLU7),	NM_006425	Hs.356551	NP_006416
		mRNA /cds=(82,1842) /gb=NM_006425			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
		/gi=27477110 /ug=Hs.356551			
1522	0.042700	/len=2030	NIM OOFTEC	Hs.184942	NP 005747
1522	0.043799	G protein-coupled receptor 64	NM_005756	HS. 164942	INP_005747
		(GPR64), mRNA /cds=(73,3117)			
		/gb=NM_005756 /gi=5031732 /ug=Hs.184942 /len=4665			
1524	0.001220	zinc finger protein 133 (clone pHZ-13)	NM 003434	Hs.78434	NP 003425 /
1324	0.001339	(ZNF133), mRNA /cds=(560,2521)	NIVI_003434	F15.70454	NP_003423 /
		/gb=NM_003434 /gi=27545331			
	·	/ug=Hs.78434 /len=2718	F.		
1525	0.011238	hypothetical protein FLJ10706	NM 018186	Hs.273193	NP_060656
1020	0.011200	(FLJ10706), mRNA /cds=(478,2634)	11111_010100	113.270100	_000000 ×
	*	/gb=NM_018186 /gi=8922604			
		/ug=Hs.273193 /len=2732			
1526		similar to rat myomegalin (LOC64182),	NM 022359	Hs.333512	NP_071754
		mRNA /cds=(336,1268)	· · · · · <del>-</del> ·		
		/gb=NM_022359 /gi=21314705	·		
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	/ug=Hs.333512 /len=1717			
1528	0.035177	tubulin, alpha, ubiquitous (K-ALPHA-1),	NM 006082	Hs.334842	NP_006073
	•	mRNA /cds=(68,1423) /gb=NM_006082			
		/gi=5174476 /ug=Hs.334842 /len=1596			
*					
1546	0.035177	Maternally expressed 3	AK092707.1	Hs.112844	
1553	0.003563	lymphocyte cytosolic protein 1 (L-	NM_002298	Hs.381099	NP_002289
		plastin) (LCP1), mRNA		· ,	ie :e
		/cds=(174,2057) /gb=NM_002298			
		/gi=7382490 /ug=Hs.381099 /len=3723			•
				<u> </u>	,

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene Accession No.	Unigene Accession	Protein Accession
1557	0.00587	MR2-CI0186-291100-010-a06 CI0186	BF814502	<b>No.</b> Hs.446594	No.
1007	0.00567	cDNA, mRNA sequence /gb=BF814502	DF014302	ITS.440094	
		/gi=12147047 /ug=Hs.446594 /len=530			
	. :	/gi=12147047/ug=H5.440594/lefi=550			
1558	0.007107	signal-induced proliferation-associated	NM_015556	Hs.172180	NP_056371
		1 like 1 (KIAA0440), mRNA	<del></del>	·	_
		/cds=(349,5763) /gb=NM_015556			
		/gi=7662125 /ug=Hs 172180 /len=6028	**************************************		
•	• .				
1559	0.003947	stromal cell derived factor receptor 1	NM_012428	Hs.389371	NP_059429
		(SDFR1), transcript variant beta, mRNA			
		/cds=(139,1335) /gb=NM_012428			
		/gi=6912645 /ug=Hs.389371 /len=2388		1	***
1565	0.003563	NADH dehydrogenase (ubiquinone)	NM_021075	Hs.59745	NP_066553
		flavoprotein 3, 10kDa (NDUFV3),			
		mRNA /cds=(575,1945)		<b>)</b>	
7		/gb=NM_021075 /gi=21361323	14.		
4507	0.005044	/ug=Hs.59745 /len=2023			
1567	0.025911	RAD21 (S. pombe) (RAD21), mRNA	NM_006265	Hs.81848	NP_006256
		/cds=(185,2080) /gb=NM_006265			100
4575	0.040004	/gi=5453993 /ug=Hs.81848 /len=3647	N. 1 10000 1		
1575	0.013394	WW domain-containing adapter with a	NM_100264	Hs.70333	NP_567823
		coiled-coil region (WAC), transcript			
	. •	variant 2, mRNA /cds=(332,2140)			
		/gb=NM_100264 /gi=18379329	1		
4577	0.047024	/ug=Hs.70333 /len=3088	NIN 470000	/ /	110 7 100 17
1577	0.047031	POM121 membrane glycoprotein (rat)	NM_172020	Hs.295112	NP_742017
4.5		(POM121), mRNA /cds=(978,3932) /gb=NM 172020 /gi=26051277	· · · · · · · · · · · ·		
214					
1613	0.011228	/ug=Hs.295112 /len=6014 IQ motif containing GTPase activating	NM 003870	Hs.1742	ND 002064
1015	0.011230	protein 1 (IQGAP1), mRNA	INIVI_003670	MS. 1742 	NP_003861
5		/cds=(468,5441) /gb=NM_003870			
		/gi=4506786 /ug=Hs.1742 /len=7573	* ·		
1614	0.001339	hypothetical protein FLJ10579	NM_018145	Hs.8055	NP 060615
	0.001000	(FLJ10579), mRNA /cds=(186,1598)	14101_010140	113.0000	
		/gb=NM 018145 /gi=8922531		. *	
		/ug=Hs.8055 /len=2251			
1628	0.03788	amyloid beta (A4) precursor-like protein	NM 001642	Hs.279518	NP_001633
		2 (APLP2), mRNA /cds=(73,2364)	,,_00 1072		-00,1000
		/gb=NM_001642 /gi=4502146			
	1	/ug=Hs.279518 /len=3727			
	-:	1.5, 1.5			
1647	4.50E-04	asporin (LRR class 1) (ASPN), mRNA	NM_017680	Hs.10760	NP_060150
		/cds=(228,1373) /gb=NM_017680			
		/gi=16596677 /ug=Hs.10760 /len=2466	•		
					i

Genes	Correspon	nding To Differentially Expressed Gen	es in Figur 20 -	RA	
	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
1648	0.018784	mRNA; cDNA DKFZp564E193 (from	AL049259	Hs.333141	
		clone DKFZp564E193) /gb=AL049259			
		/gi=4500005 /ug=Hs.333141 /len=1691		-	
					·
1667	0.017288	interleukin 1 receptor, type I (IL1R1),	NM_000877	Hs.82112	NP 000868
•		mRNA /cds=(83,1792) /gb=NM 000877	· <del>-</del> · ·		_
		/gi=27894331 /ug=Hs.82112 /len=4909			
1674	0.007107	calreticulin (CALR), mRNA	NM_004343	Hs.353170	NP_004334
		/cds=(69,1322) /gb=NM 004343	- <del>-</del>	. ,	_
		/gi=5921996 /ug=Hs.353170 /len=1899			
1684	0.03788	ubiquitin C (UBC), mRNA	NM_021009	Hs.183704	NP_066289
		/cds=(136,2193) /gb=NM_021009			
		/gi=20149305 /ug=Hs.183704			
		/len=2309		1 1 1 1	
1686	0.007807	CDC5 cell division cycle 5-like (S.	NM_001253	Hs.155174	NP_001244
		pombe) (CDC5L), mRNA			
		/cds=(260,2668) /gb=NM_001253			
		/gi=16357499 /ug=Hs.155174			
		/len=3012	, i		
1693	0.030249	JTV1 gene (JTV1), mRNA	NM_006303	Hs.301613	NP_006294
		/cds=(114,1076) /gb=NM_006303			1 17 1 1
		/gi=11125769 /ug=Hs.301613			
		/len=1221			
1705		KIAA0824	AB020631		NP_056969
1707	0.040751	tumor antigen SLP-8p (HCC8), mRNA	NM_016516	Hs.48499	NP_057600
		/cds=(21,2921) /gb=NM_016516			
		/gi=7705396 /ug=Hs.48499 /len=3480			
1708	0.030249	Hypothetical protein(cDNA FLJ13279	AK023341	11.0	NP_005737
		fis, clone OVARC1001055, moderately			
		similar to PRE-B CELL ENHANCING			
,		FACTOR PRECURSOR)			
	<u> </u>				
1709		KIAA0399	AB007859		NP_055928
1711	0.02801	KIAA0682 gene product (KIAA0682),	NM_014852	Hs.7482	NP_057280
		mRNA /cds=(80,2962) /gb=NM_014852			
		/gi=7662249 /ug=Hs.7482 /len=4422			
1722	0.014599	S100 calcium binding protein A11	NM_005620	Hs.417004	NP_005611
1		(calgizzarin) (S100A11), mRNA			,
	1.	/cds=(121,438) /gb=NM_005620			
		/gi=5032056 /ug=Hs.417004 /len=595		L	
1725	0.007807	ATPase, Ca transporting, cardiac	NM_170665	Hs.1526	NP_733765
		muscle, slow twitch 2 (ATP2A2),	<i>t</i>		
	1	transcript variant 1, mRNA		Į.	
		/cds=(164,3292) /gb=NM_170665	·		
[. ·		/gi=27886537 /ug=Hs.1526 /len=4205			·

	p-value	nding To Diff rentially Expressed Gen Description	Gene	Unigene	Protein	
Spot	p-value				1	
			Accession No.	Accession	Accession	
1734	0.004825	prefoldin 5 (PFDN5), transcript variant	NM 002624	No. Hs.288856	<b>No.</b> NP 665904	
	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1, mRNA /cds=(36,500)				
		/gb=NM 002624 /gi=22202632				
i i		/ug=Hs.288856 /len=661			4	
1736	0.012276	hypothetical protein FLJ21839	NM_021831	Hs.433334	NP_068603	
		(FLJ21839), mRNA /cds=(445,2619)				
		/gb=NM_021831 /gi=19923577				
		/ug=Hs.433334 /len=3252				
1737	0.004367	cytokine inducible SH2-containing	NM 007707.1		NP_031733.	
		protein 3 (Cish3)				
1740	0.033876	tumor necrosis factor receptor	NM 002546	Hs.81791	NP 002537	
		superfamily, member 11b				
		(osteoprotegerin) (TNFRSF11B),			<b>}</b>	
, -		mRNA /cds=(252,1457)				
		/gb=NM 002546 /gi=22547122				
		/ug=Hs.81791 /len=2291				
1757	0.014599	Similar to RIKEN cDNA 2310032N20	BC016142	Hs.6289		
	1	gene, clone MGC:9179				
		IMAGE:3909479, mRNA, complete cds				
		/cds=(43,873) /gb=BC016142				
		/gi=16507947 /ug=Hs.6289 /len=2161				
-		(=FLJ20886)				
1772	0.004825	hypothetical protein FLJ11011	NM 018299	Hs.21275	NP 060769	
	0.001020	(FLJ11011), mRNA /cds=(4,459)	11010200	110.21270	1000,00	
		/gb=NM 018299 /gi=8922821				
		/ug=Hs.21275 /len=2201	and the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of t			
1794	0.007807	cDNA FLJ13558 fis, clone	AK023620	Hs.86043	<b>-</b>	
.,,,,	0.007.007	PLACE1007743. /gb=AK023620	7111020020	1.10.00010		
		/gi=10435601 /ug=Hs.86043 /len=2271				
1796	0.011238	hypothetical protein MGC33901	NM_144987	Hs.423753	NP 659424	
	]	(MGC33901), mRNA /cds=(21,629)				
		/gb=NM_144987 /gi=21450690				
	1 P. 1	/ug=Hs.423753 /len=711				
1797	5 11F-04	cDNA FLJ14066 fis, clone	AK024128	Hs.306665	<del>                                     </del>	
., 07	0.112.04	HEMBB1001197. /gb=AK024128		1.15.555555		
,		/gi=10436433 /ug=Hs.306665		4,		
		/len=2086				
1798	0.03788	NADH dehydrogenase (ubiquinone)	NM_007103	Hs.7744	NP_009034	
1730	0.007,00	flavoprotein 1, 51kDa (NDUFV1),	1.4.4007.100	1.15.77.77	1.100000,4	
	·	mRNA /cds=(70,1464) /gb=NM 007103	<b>}</b>			
		/gi=20149567 /ug=Hs.7744 /len=1566				
		rgi-20 149007 /ug-115,7744 /leii- 1000		1		
1805	0.014500	matrilin 2 (MATN2), transcript variant 1,	NIM DOSSOO	Hs.19368	NP 085072	
1000	0.014599		114141_002300	119.19300	INF_0000/2	
* *		mRNA /cds=(126,2996)				
	· ·	/gb=NM_002380 /gi=13518036	<u>}</u>			
	<u>L</u>	/ug=Hs.19368 /len=3496		<u> </u>	<u> </u>	

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gen	Unigene	Protein
			Accession No.	Accession	Accession
			·	No.	No.
1810	0.012276	hypothetical protein FLJ12716	NM_021942	Hs.5354	NP_068761
		(FLJ12716), mRNA /cds=(66,2513)			
	*	/gb=NM_021942 /gi=21361577			
		/ug=Hs.5354 /len=3522			
1817	0.043799	mRNA; cDNA DKFZp761P18121 (from	AL834147	Hs.44198	:
		clone DKFZp761P18121)			
		/cds=(127,2289) /gb=AL834147	l e se		
	1.1	/gi=21739620 /ug=Hs.44198 /len=4286			
			· .		
1818	0.001339	candidate mediator of the p53-	NM_019845	Hs.100890	NP_062819
		dependent G2 arrest (REPRIMO),			Y .
		mRNA /cds=(244,573) /gb=NM_019845	4		
		/gi=9790192 /ug=Hs.100890 /len=1510			
1853	0.008677	hypothetical protein FLJ14153	NM_022736	Hs.7503	NP_073573
		(FLJ14153), mRNA /cds=(31,1428)			
		/gb=NM_022736 /gi=12232392			
•		/ug=Hs.7503 /len=2161			
1856	0.035177	hypothetical protein FLJ31121	NM_144723	Hs.350194	NP_653324
		(FLJ31121), mRNA /cds=(15,614)		* ,	
		/gb=NM_144723 /gi=21389510			
	1 % 4 % 1 % 1 % 1 % 1 % 1 % 1 % 1 % 1 %	/ug=Hs.350194 /len=1512	4		
1872	0.043799	suppressor of Ty 16 (S. cerevisiae)	NM_007192	Hs.14963	NP_009123
		(SUPT16H), mRNA /cds=(340,3483)			
· .		/gb=NM_007192 /gi=19924176			
		/ug=Hs.14963 /len=4696			
1878	0.047031	capping protein (actin filament), gelsolin	NM_001747	Hs.82422	NP_001738
		like (CAPG), mRNA /cds=(50,1096)			
		/gb=NM_001747 /gi=4502560			
		/ug=Hs.82422 /len=1221	L		
1880	0.032636	ubiquitin carboxyl-terminal esterase L1	NM_004181	Hs.76118	NP_004172
		(ubiquitin thiolesterase) (UCHL1),			
٠		mRNA /cds=(75,746) /gb=NM_004181			
		/gi=21361090 /ug=Hs.76118 /len=1119			
	:				
1889	0.001339	tyrosine 3-monooxygenase/tryptophan	NM_003405	Hs.349530	NP_003396
		5-monooxygenase activation protein,			ľ
		eta polypeptide (YWHAH), mRNA			
		/cds=(198,938) /gb=NM_003405			
		/gi=21464102 /ug=Hs.349530	f ·		
	]	/len=1775		]	ŀ
:	·				· .
1913	0.014599	small EDRK-rich factor 2 (SERF2),	NM_005770	Hs.380718	NP_005761
		mRNA /cds=(1023,1319)	.=		<del></del> .
		/gb=NM_005770 /gi=21361286			
		/ug=Hs.380718 /len=1408			

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene Accession No.	Unigen Accession	Protein Accession
				No.	No.
1923	0.018784	polymerase (DNA directed), delta 2,	NM_006230	Hs.74598	NP_006221
The second second	-: :	regulatory subunit 50kDa (POLD2),			
		mRNA /cds=(79,1488) /gb=NM_006230			
		/gi=5453923 /ug=Hs.74598 /len=1584			
1925	0.030249	ADP-ribosyltransferase (NAD; poly	NM 001618	Hs.177766	NP 001609
		(ADP-ribose) polymerase) (ADPRT),			
		mRNA /cds=(160,3204)			
. :		/gb=NM_001618 /gi=11496989			
		/ug=Hs 177766 /len=3859	n n		
1972	0.007107	mitochondrion, complete genome	NC 001807	3 13	
1973		keratin 8 (KRT8), mRNA	NM_002273	Hs.242463	NP 002264
		/cds=(60,1511) /gb=NM_002273			
		/gi=4504918 /ug=Hs.242463 /len=1752			
1995	0.025911	vacuolar protein sorting 28 (yeast)	NM_016208	Hs.339697	NP 057292
		(VPS28), mRNA /cds=(62,727)			
	1	/gb=NM_016208 /gi=7705884			
4,34		/ug=Hs.339697 /len=928	() ()		1
1999	0.032636	chromosome 20 open reading frame 40	NM 014054	Hs.105379	NP_054773
17.77		(C20orf40), mRNA /cds=(208,396)			
		/gb=NM 014054 /gi=7661709			
		/ug=Hs.105379 /len=417			
2039	0.03788	phosphatidyl inositol glycan class T	NM 015937	Hs.84038	NP 057021
	1 2	(PIGT), mRNA /cds=(20,1756)			
		/gb=NM_015937 /gi=23397652			
		/ug=Hs.84038 /len=2171	4. A		
2042	0.047031	ARF protein (LOC51326), mRNA	NM_016632	Hs.264509	NP_057716
		/cds=(88,489) /gb=NM_016632	· · · · <del>-</del> · · · · · · ·		
		/gi=7706177 /ug=Hs.264509 /len=826			
2052	0.022106	potassium large conductance calcium-	NM 002247	Hs.89463	NP_002238
		activated channel, subfamily M, alpha			
		member 1 (KCNMA1), mRNA			No. 1
. :		/cds=(178,3714) /gb=NM_002247			
		/gi=26638649 /ug=Hs.89463 /len=6103			
2066	0.022106	hypothetical protein FLJ35613	NM_173653	Hs.30022	NP 775924
		(FLJ35613), mRNA /cds=(126,2063)	<del></del>		<u> </u>
		/gb=NM_173653 /gi=27734934		1	
		/ug=Hs.30022 /len=3568		1	
2069	0.032636	zinc finger protein 36, C3H type-like 1	NM_004926	Hs.85155	NP_004917
		(ZFP36L1), mRNA /cds=(131,1147)	-	[·	<b> </b>
•		/gb=NM 004926 /gi=15812179			
		/ug=Hs.85155 /len=3022			
2070	0.047031	myotubular myopathy 1 (MTM1), mRNA	NM 000252	Hs.75302	NP 000243
		/cds=(55,1866) /gb=NM_000252			
		/gi=4557895 /ug=Hs.75302 /len=3411	4 °C		
			l · · · ·	1	l

		nding To Differentially Expr ssed G n			<u> </u>
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2083	0.023945	major histocompatibility complex, class I, B (HLA-B), mRNA /cds=(11,1099) /gb=NM_005514 /gi=21327676 /ug=Hs.77961 /len=1310	NM_005514	Hs.77961	NP_005505
,		•			
2090	0.020388	mitogen-activated protein kinase phosphatase x (MKPX), mRNA /cds=(449,1003) /gb=NM_020185 /gi=21314693 /ug=Hs.29106 /len=1520	NM_020185	Hs.29106	NP_064570
2093	0.022106	FYN binding protein (FYB-120/130) (FYB), mRNA /cds=(31,2382) /gb=NM_001465 /gi=4503820 /ug=Hs.58435 /len=2400	NM_001465	Hs.58435	NP_001456
2131	0.004825	tumor endothelial marker 8 (TEM8), transcript variant 1, mRNA /cds=(144,1838) /gb=NM_032208 /gi=14149903 /ug=Hs.8966 /len=5540	NM_032208	Hs.8966	NP_444262
2142	0.035177	KIAA0258 gene product (KIAA0258), mRNA /cds=(86,1261) /gb=NM_014785 /gi=7662029 /ug=Hs.47313 /len=6313	NM_014785	Hs.47313	NP_055600
2149	0.047031	phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA /cds=(207,4604) /gb=NM_007366 /gi=19923388 /ug=Hs.171945 /len=5633	NM_007366	Hs.171945	NP_031392
2150	0.023945	ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794 /ug=Hs.418650 /len=801	NM_002032	Hs.418650	NP_002023
2161	0.017288	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA /cds=(39,1613) /gb=NM_002778 /gi=11386146 /ug=Hs.406455 /len=2767	NM_002778	Hs.406455	NP_002769
2166	0.008566	nephroblastoma overexpressed gene (NOV), mRNA /cds=(73,1146) /gb=NM_002514 /gi=19923725 /ug=Hs.235935 /len=2389	NM_002514	Hs.235935	NP_002505
2179	0.043799	nuclear antigen Sp100 (SP100), mRNA /cds=(32,2671) /gb=NM_003113 /gi=19923235 /ug=Hs.77617 /len=3579	NM_003113	Hs.77617	NP_003104
2198	0.022106	ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794 /ug=Hs.418650 /len=801	NM_002032	Hs.418650	NP_002023

		nding To Differentially Express d Gen				
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.	
2209	0.002893	mRNA; cDNA DKFZp667O2119 (from clone DKFZp667O2119) /gb=AL832314	AL832314	Hs.180789		
		/gi=21732861 /ug=Hs.180789 /len=6868				
2230	0.018784	PMS1 postmeiotic segregation	NM 000534	Hs.111749	NP 000525	
		increased 1 (S. cerevisiae) (PMS1), mRNA /cds=(81,2879) /gb=NM_000534	1 <del>-3</del> -		<del>-</del>	
•		/gi=11496979 /ug=Hs.111749 /len=3121				
2231	0.006508	TTN gene for titin	AJ277892	<del>- ( ) :</del>		
2240		likely ortholog of mouse tumor	NM_020755	Hs.146668	NP_065806	
		differentially expressed 1, like (TDE1L), mRNA /cds=(76,1437) /gb=NM_020755	7			
		/gi=24308212 /ug=Hs.146668 /len=3149				
2242	0.007807	uncharacterized hypothalamus protein HT010 (HT010), mRNA	NM_018471	Hs.6375	NP_060941	
1 + + - ¹ 		/cds=(227,1420) /gb=NM_018471 /gi=8923807 /ug=Hs:6375 /len=2140				
2243	0.023945	KIAA0095 gene product (KIAA0095),	NM_014669	Hs.155314	NP_055484	
		mRNA /cds=(67,2526) /gb=NM_014669 /gi=7661901 /ug=Hs.155314 /len=2681				
2244	0.011238	F-box and leucine-rich repeat protein 5	NM_033535	Hs.5548	NP_277077	
		(FBXL5), transcript variant 2, mRNA				
		/cds=(586,2283) /gb=NM_033535				
2260	0.02801	/gi=21536439 /ug=Hs.5548 /len=3475 heterogeneous nuclear	NM 002140	Hs.129548	NP 112553	
2200	0.02001	ribonucleoprotein K (HNRPK), transcript variant 1, mRNA	WI_002140	113.123340	1112555	
se A	- F - F - F - F - F - F - F - F - F - F	/cds=(210,1604) /gb=NM_002140 /gi=14165438 /ug=Hs.129548 /len=2830				
2263	0.015895	cDNA FLJ32589 fis, clone SPLEN2000443. /gb=AK057151 /gi=16552741 /ug=Hs.21342 /len=2178	AK057151	Hs.21342		
2267	0.022106	frizzled 10 (Drosophila) (FZD10), mRNA /cds=(457,2202)	NM_007197	Hs.31664	NP_009128	
		/gb=NM_007197 /gi=22035684 /ug=Hs 31664 /len=3260		· · · · · · · · · · · · · · · · · · ·		
2273	0.00587	Pirin (PIR), mRNA /cds=(231,1103) /gb=NM_003662 /gi=4505822 /ug=Hs.424966 /len=1318	NM_003662	Hs.424966	NP_003653	
2296	0.023945	serine/threonine kinase 38 like (STK38L), mRNA /cds=(174,1568) /gb=NM_015000 /gi=24307970 /ug=Hs.184523 /len=4725	NM_015000	Hs.184523	NP_055815	

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
2306	0.010277	S100 calcium binding protein A4	NM_002961	Hs.81256	NP 062427
		(calcium protein, calvasculin,			
		metastasin, murine placental (S100A4),			
		transcript variant 1, mRNA			
-		/cds=(70,375) /gb=NM_002961		- 1	
	<b>.</b>	/gi=9845514 /ug=Hs.81256 /len=512			
2309	0.040751	GTPase-activating protein GAPIII	U20238		NP 033051
2315		metalloproteinase inhibitor TIMP-2	AF127803		
2331		RNA guanylyltransferase and 5'-	NM_003800	Hs.27345	NP 003791
	5.5.5.5	phosphatase (RNGTT), mRNA		1.0.2.0.0	_000701
		/cds=(289,2082) /gb=NM 003800		:	
		/gi=4506562 /ug=Hs.27345 /len=4546			·
2334	0.022106	androgen induced protein (AIG-1),	NM 016108	Hs.107528	NP_057192
2001	0.022100	mRNA /cds=(28,744) /gb=NM 016108	114141_010100	113.107320	_037 132
		/gi=7705269 /ug=Hs.107528 /len=1398			
* **					
2340	0.025011	mRNA, cDNA DKFZp434F2311 (from	AL137603	Hs.233890	
2540	0.020311	clone DKFZp434F2311) /gb=AL137603	AL 137003	H\$.233090	
		/gi=6808349 /ug=Hs.233890 /len=842			
		/g -0000349 /ug=Hs.233690 /lel1-642			
2342	0.020200	modifier 2 (M22) (=V12274 M22	V42074	<del> </del>	ND 024640
2342	0.020300	modifier 3 (M33) (=Y13274 M33	Y13274		NP_031649
0047	0.000040	polycomb-like protein)	NIM OCCOCO	11 000500	NE COCCE
2347	0.030249	nuclear RNA export factor 1 (NXF1),	NM_006362	Hs.323502	NP_006353
		mRNA /cds=(83,1942) /gb=NM_006362			:
		/gi=15487669 /ug=Hs.323502			
0000	0.007407	/len=2264			
2368	0.007107	capping protein (actin filament) muscle	NM_004930	Hs.333417	NP_004921
		Z-line, beta (CAPZB), mRNA			
		/cds=(1,819) /gb=NM_004930			
		/gi=4826658 /ug=Hs.333417 /len=1077			
2385	0.003213	Nedd4 binding protein 1 (N4BP1),	NM_014664	Hs.323712	NP_055479
1		mRNA /cds=(238,2928)			
		/gb=NM_014664 /gi=7662203			
		/ug=Hs.323712 /len=3319			
2395	0.018784	Purkinje cell protein 4 (PCP4), mRNA	NM_006198	Hs.80296	NP_006189
		/cds=(59,247) /gb=NM_006198			
-		/gi=5453857 /ug=Hs.80296 /len=540			
2398	0.040751	UDP-N-acetyl-alpha-D-	NM_022087	Hs.97056	NP_071370
		galactosamine:polypeptide N-			
		acetylgalactosaminyltransferase 11	. *		
		(GalNAc-T11) (GALNT11), mRNA			
		/cds=(84,1910)/gb=NM_022087	, ,		
		/gi=11545800 /ug=Hs.97056 /len=2591			
	].				
2404	0.03788	keratan sulfate proteoglycan	AF063301	<del>  -,</del>	NP 008966

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Acc ssion
: :				No	No.
2420	0.015895	zinc finger protein (LOC51042), mRNA	NM 015871	Hs.102419	NP 056955
0	0.01000	/cds=(115,465) /gb=NM_015871		113.102-110	-
1.				· .	
		/gi=21359908 /ug=Hs.102419 /len=649			
				·	
2421	- 0.03788	ribosomal protein S4, Y-linked	NM_001008	Hs.180911	NP_000999
		(RPS4Y), mRNA /cds=(13,804)			
		/gb=NM_001008 /gi=17981706		le se	,
•		/ug=Hs.180911 /len=931			
2442	0.032636	sushi-repeat-containing protein, X	NM 006307	Hs.15154	NP 006298
		chromosome (SRPX), mRNA			- 1.1 - <del>- 1</del> .1 - <del>- 1</del> .1
		/cds=(88,1482) /gb=NM 006307			
	7	/gi=21314639 /ug=Hs.15154 /len=1999			
	**	/gi=21514059 /dg=115.15154 /ieii=1999			
0440	0.00004	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	NINA 344400	U- 45540	LUD CEROS:
2446	0.02801	oxysterol binding protein-like 2	NM_144498	Hs.15519	NP_653081
	·	(OSBPL2), transcript variant 2, mRNA		1.	
	1	/cds=(203,1645) /gb=NM_144498		<u> </u>	
		/gi=21450852 /ug=Hs.15519 /len=3971			
. 1					<u> </u>
2452	0:039408	jun B proto-oncogene (JUNB), mRNA	NM_002229	Hs.400124	NP_002220
		/cds=(254,1297) /gb=NM 002229			
٠.		/gi=4504808 /ug=Hs.400124 /len=1797			
2469	0.014599	serine/threonine kinase 25 (STE20	NM 006374	Hs.155206	NP_006365
		yeast) (STK25), mRNA		(	
		/cds=(225,1505) /gb=NM 006374			
	1	/gi=21361357 /ug=Hs 155206			
0.470	0.000000	/len=2207	1114 000004	11. 5504	NO 000075
2476	0.020388	MAP kinase-interacting	NM_003684	Hs.5591	NP_003675
		serine/threonine kinase 1 (MKNK1),			1
		mRNA /cds=(174,1571)	No. 20 Per Control		
		/gb=NM_003684 /gi=21361100			
		/ug=Hs.5591 /len=2745			
2488	0.043799	likely ortholog of mouse hippocampus	NM_033055	Hs.21015	NP_149044
		abundant gene transcript 1 (HIAT1),			
	l	mRNA /cds=(6,1124) /gb=NM_033055			
		/gi=24308343 /ug=Hs.21015 /len=2230		the second	
2508	2 66F-04	sorting nexin 1 (SNX1), transcript	NM_003099	Hs.75283	NP_690039
_555	2.002.04	variant 1, mRNA /cds=(13,1581)	1000000	1.13.7 02.00	1
		/gb=NM 003099 /gi=23111033			
	1	, -			
2544	0.005044	/ug=Hs.75283 /len=1984	NIM 000000	11- 2025 44	NID 00000
2511	0.025911	ribosomal protein L35a (RPL35A),	NM_000996	Hs.288544	NP_000987
		mRNA /cds=(74,406) /gb=NM_000996			1.
		/gi=16117790 /ug=Hs.288544 /len=511			
2535	0.010277	thyroid receptor interactor trip15 mRNA,	AF100762		NP_004227
	1	complete cds	I 3	1	

Genes	Correspon	nding To Diff rentially Express d G n	s in Figur 20 -	RA	
Spot	p-value	Description	Gene Accession No.	Unigene Accession	Protein Accession
2536	0.017288	H3 histone, family 3B (H3.3B) (H3F3B),		<b>No.</b> Hs.180877	<b>No.</b> NP_005315
		mRNA /cds=(118,528) /gb=NM_005324 /gi=21264598 /ug=Hs.180877 /len=1662			
2538	0.040751	ETAA16 protein (ETAA16), mRNA /cds=(403,2925) /gb=NM_019002 /gi=9506580 /ug=Hs 82664 /len=3457	NM_019002	Hs.82664	NP_061875
2547	0.03788	B-cell CLL/lymphoma 3 (BCL3), mRNA /cds=(42,1382) /gb=NM_005178 /gi=20336471 /ug=Hs.31210 /len=1813	NM_005178	Hs.31210	NP_005169
2550	0.032636	uncharacterized bone marrow protein BM042 (BM042) (=cDNA sequence DKFZp761A1124)	NM_018458		
2553,	0.007107	transmembrane protein vezatin (VEZATIN), mRNA /cds=(177,1886) /gb=NM_017599 /gi=19923537 /ug=Hs.24135 /len=3949	NM_017599	Hs.24135	NP_060069
2567	0.017288	nuclear receptor Rev-ErbA-beta mRNA	U20796		
2568	0.00587	glycoprotein M6B (GPM6B), mRNA /cds=(255,1052) /gb=NM_005278 /gi=24307894 /ug=Hs.5422 /len=1642	NM_005278	Hs.5422	NP_005269
2569	0.025911	PEST-containing nuclear protein (PCNP), mRNA /cds=(19,555) /gb=NM_020357 /gi=9966826 /ug=Hs.71618 /len=2250	NM_020357	Hs.71618	NP_065090
2596	0.033876	malonyl-CoA decarboxylase (MLYCD), mRNA /cds=(96,1460) /gb=NM_012213 /gi=6912497 /ug=Hs.150748 /len=2136	NM_012213	Hs.150748	NP_036345
2600	0.002893	gene_id:F1D9.26~unknown protein [Arabidopsis thaliana]	AP002460		
2602	0.010277	fibrinogen-like 2 (FGL2), mRNA /cds=(34,1353) /gb=NM_006682 /gi=5730074 /ug=Hs.351808 /len=1496	NM_006682	Hs.351808	NP_006673
2624	0.012276	RAB27A, member RAS oncogene family (RAB27A), mRNA /cds=(246,911) /gb=NM_004580 /gi=19923263 /ug=Hs.50477 /len=2496	NM_004580	Hs.50477	NP_004571
2628	0.005325	methyltransferase reductase (MTRR), transcript variant 2, mRNA /cds=(31,2208) /gb=NM_024010 /gi=13325067 /ug=Hs.153792 /len=3291	NM_024010	Hs.153792	NP_076915

		nding To Diff rentially Expressed Gen	Gene		Protein
Spot	p-value	Description	Accession No.	Unigene Accession	Accession
	1.			No.	No.
2646	0.023945	EGF-containing fibulin-like extracellular	NM_004105	Hs.76224	NP_061489
	J	matrix protein 1 (EFEMP1), transcript			
,		variant 1, mRNA /cds=(150,1631)			l
1.7	1	/gb=NM_004105 /gi=9665261			
		/ug=Hs.76224 /len=2742			
		-	. ,		
2650	0.02801	fatty-acid-Coenzyme A ligase, long-	NM 021122	Hs.154890	NP 066945
		chain 2 (FACL2), mRNA	<del>-</del>		_ `
		/cds=(14,2110) /gb=NM_021122		1	
		/gi=12669906 /ug=Hs 154890			
		/len=3635			1.
2659	0.003947	mRNA for KIAA1373 protein, partial	AB037794	Hs.16229	
2000	3.0000-11	cds. /cds=(821,2212) /gb=AB037794	1		
		/gi=7243126 /ug=Hs.16229 /len=4052			
2660	0.047031	phosphoserine phosphatase-like	NM 003832	Hs.369508	NP 003823
2000	0.047031	(PSPHL), mRNA /cds=(162,380)	14IVI_003032	113.309300	NF_003023
•	N 3				
		/gb=NM_003832 /gi=4502934			
2074	0.000566	/ug=Hs.369508 /len=839	NM 014868	Hs.5094	NP 055683
2674	0.008366	ring finger protein 10 (RNF10), mRNA	NIVI_U 14000	IUS:2084	NP_000000
		/cds=(448,2883) /gb=NM_014868			
0070	0.005044	/gi=27544928 /ug=Hs.5094 /len=3129	NA 005000	11. 70407	ND 005000
2678	0.025911	protein-L-isoaspartate (D-aspartate) O-	NM_005389	Hs.79137	NP_005380
		methyltransferase (PCMT1), mRNA			•
	1.	/cds=(74,757) /gb=NM_005389			
		/gi=4885538 /ug=Hs.79137 /len=1599		<u> </u>	
2696	0.014599	cartilage linking protein 1 (CRTL1),	NM_001884	Hs.2799	NP_001875
		mRNA /cds=(316,1380)			
		/gb=NM_001884 /gi=4503052		1	1
		/ug=Hs.2799 /len=1492		4	
2698	0.022106	topoisomerase (DNA) II alpha 170kDa	NM_001067	Hs.156346	NP_001058
	1.	(TOP2A), mRNA /cds=(127,4722)			
		/gb=NM_001067 /gi=19913405	5 1		1
	<u> </u>	/ug=Hs.156346 /len=5698			
2709	0.005325	pleiotrophin (heparin binding growth	NM_002825	Hs.44	NP_002816
	<u>'</u>	factor 8, neurite growth-promoting	ļ		]
		factor 1) (PTN), mRNA /cds=(396,902)			
	]	/gb=NM_002825 /gi=27552761			
,		/ug=Hs.44 /len=1029			1
2712	9.43E-04	ash2 (absent, small, or homeotic)-like	NM_004674	Hs.6856	NP_004665
		(Drosophila) (ASH2L), mRNA			_
	·}.	/cds=(5,1891) /gb=NM_004674			
		/gi=4757789 /ug=Hs.6856 /len=2381		1,	
2716	9.43F-04	general transcription factor IIIC,	NM 012086	Hs.90847	NP 036218
<u></u> , 10	J. 15L-04	polypeptide 3, 102kDa (GTF3C3),	0 ,2000	1.5.555	
	-	mRNA /cds=(94,2754) /gb=NM_012086		1 .	1
		/gi=6912397 /ug=Hs.90847 /len=2961	1		1
		//gi-0312331 /ug-ms.30041 /igii-2301			

<u>Genes</u>	Correspoi	nding To Differentially Expressed Gen		RA	
Spot	p-value	Description	Gen	Unigene	Prot in
			Acc ssion No.	Accession No.	Accession No.
2720	0.035177	mitogen-activated protein kinase kinase	NM 006575	Hs.246970	NP 006566
		kinase kinase 5 (MAP4K5), mRNA	_		
•		/cds=(321,2861) /gb=NM_006575			
	1	/gi=14589908 /ug=Hs.246970	e e e		
		/len=3000			
2725	0.022106	hypothetical protein MGC29891	NM_144618	Hs.318393	NP_653219
		(MGC29891), mRNA /cds=(332,1678)			
		/gb=NM_144618 /gi=21389426			
		/ug=Hs.318393 /len=3356			
2738	0.018784	succinyl-CoA synthetase GTP-specific	AF171077		
· · · · · · · · · · · · · · · · · · ·		beta subunit			No. of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of
2746		putative serine-rich protein	AF246705		NP_060102
2747	0.006463	signal transducing adaptor molecule	NM_003473	1	NP_003464
		(SH3 domain and ITAM motif) 1			
:	1 2 2 2 2 2	(STAM)			
2755		ABL (M8604 Met) gene	U07561		
2756		KIAA0183 gene	D80005	-	NP_055427
2760		KVLQT1 gene	AJ006345	11: 40-044	115 000 10 1
2766	0.02801	sorting nexin 7 (SNX7), transcript	NM_015976	Hs.127241	NP_689424
		variant 1, mRNA /cds=(268,1431)			
		/gb=NM_015976 /gi=23111053		\$ 100	
2774	0.000040	/ug=Hs 127241 /len=1798	NIM OCCUPE	Un 75007	ND 002247
2774	0.003213	myristoylated alanine-rich protein kinase C substrate (MARCKS), mRNA	NM_002356	Hs.75607	NP_002347
		/cds=(370,1368) /gb=NM_002356			
		/gi=11125771 /ug=Hs.75607 /len=2589			
		/g =11123/71/ug=(15.73007/left=2309) 		1	\$
2779	0.001501	nuclear factor (erythroid-derived 2)-like	NM_006164	Hs.155396	NP 006155
21.70	0.001301	2 (NFE2L2), mRNA /cds=(114,1931)	11111 _000104	113.100000	
		/gb=NM_006164 /gi=20149575			
	1	/ug=Hs.155396 /len=2439			
2780	0.012276		X67534		
		surfeit 1 (SURF1), nuclear gene	NM 003172	Hs.423854	NP 003163
-		encoding mitochondrial protein, mRNA	_		1 - <del>-</del> -
		/cds=(33,935) /gb=NM 003172		٠.	
		/gi=19557683 /ug=Hs.423854			
		/len=1037			
2782	0.017288	high mobility group 2 protein (HMG-2)	M83665		
2791	0.01932	hypothetical protein FLJ10283	NM_018046	Hs.284216	NP_060516
× .		(FLJ10283), mRNA /cds=(218,1039)			
	,	/gb=NM_018046 /gi=8922325			
- :		/ug=Hs.284216 /len=1876			2,
2795	0.022106	nucleophosmin (nucleolar	NM_002520	Hs.355719	NP_002511
•		phosphoprotein B23, numatrin) /	i i		
		(NPM1), mRNA /cds=(100,984)		1	
		/gb=NM_002520 /gi=20070168			
		/ug=Hs.355719 /len=1347	1	1 .	

Genes	Correspo	nding To Differentially Expressed Gen	es in Figur 20 -	RA	
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
2797	0.02801	zinc finger homeobox 1b (ZFHX1B),	NM_014795	Hs.34871	NP 055610
	L	mRNA /cds=(445,4089)	- ,		
		/gb=NM_014795 /gi=7662183			
		/ug=Hs.34871 /len=5523			
2815	0.043799	proteasome (prosome, macropain)	NM 002791	Hs.410276	NP 002782
		subunit, alpha type, 6 (PSMA6), mRNA	7		<del>-</del>
		/cds=(110,850) /gb=NM 002791			
		/gi=23110943 /ug=Hs.410276			
		/len=1035	j'	$\sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^{n} \sum_{j$	
2826	0.035177	potassium voltage-gated channel,	NM 002252	Hs.47584	NP 002243
		delayed-rectifier, subfamily S, member			
24	<del>-</del>	3 (KCNS3), mRNA /cds=(381,1856)			
÷		/gb=NM_002252 /gi=25952107			
. 7		/ug=Hs 47584 /len=2344	, ,		
2833	6.56E-04	myotubularin related protein 6	AF072928		NP 004676
2837	0.030249		AF034237	1	
2839		synovial sarcoma translocation gene on		Hs.154429	NP 056373
		chromosome 18-like 1 (SS18L1),		110.101120	
	***	mRNA /cds=(61,1251) /gb=NM_015558			
	i i	/gi=27754185 /ug=Hs.154429			
•		/len=3723			
2847	0.007107	lysosomal-associated membrane	NM 013995	Hs.8262	NP 054701
	0.007 107	protein 2 (LAMP2), transcript variant	11111_010000	1113.0202	_054701
		LAMP2B, mRNA /cds=(138,1370)			
		/gb=NM_013995 /gi=7669502			
		/ug=Hs.8262 /len=4006			
2867	0.030249	mitogen-activated protein kinase kinase	NM 021970	Hs.6361	NP 068805
2001	0.0002-10	1 interacting protein 1 (MAP2K1IP1),	02 1370	113.0001	111 _000000
		mRNA /cds=(250,624) /gb=NM_021970			
		/gi=21614526 /ug=Hs.6361 /len=1416	·		
		7gi 210140207dg-113.00017icii-1410		1	
2889	0.02801	ubiquitous tetratricopeptide containing	NM 017590	Hs.25347	NP_060060
	5.5290 i	protein RoXaN (RoXaN), mRNA	1,4,01,7000	11.13.2007/	
		/cds=(217,3150) /gb=NM_017590			
<i>1</i> 1 1	!	/gi=27881483 /ug=Hs.25347 /len=5868		,	
		2100110014g 110.20041			
2890	0.047031	proteasome (prosome, macropain)	NM 002787	Hs.411773	NP 002778
	3.5 .7 00 1	subunit, alpha type, 2 (PSMA2), mRNA	002707	1,13.411773	_002/70
		/cds=(20,724) /gb=NM_002787			
		/gi=23110936 /ug=Hs.411773 /len=885		1	1
2896	0.023945	C-type lectin	BAA95671	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
2917		ADP-ribosylation factor-like 3 (ARL3),	NM_004311	Hs.182215	NP 004302
2011	J.010034	mRNA /cds=(16,564) /gb=NM_004311	14141_004311	11 13. 1022 13	INF_004302
1		/gi=4757773 /ug=Hs.182215 /len=900		1.	
25.0		1911911   19149-113. 1022   9 11 <del>6</del> 11-900		}	1.
			L	1,	L

Genes	Correspor	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
		Description	Gen	Unigene	Protein
•		· · · · · · · · · · · · · · · · · · ·	Accession No.	Accession	Accession
				No.	No.
2932	0.015895	cyclin D binding myb-like transcription	NM 021145	Hs.5671	NP 066968
2002	0.0.0000	factor 1 (DMTF1), mRNA	, , , , , , , , , , , , , , , , , , ,		
		/cds=(276,2558) /gb=NM_021145			<u> </u>
N			,		
00.47	0.040704	/gi=10863946 /ug=Hs.5671 /len=3767	NIM 000547	Un 247020	NE COOFOR
2947	0.018784	hemoglobin, alpha 2 (HBA2), mRNA	NM_000517	Hs.347939	NP_000508
	}	/cds=(38,466) /gb=NM_000517			
		/gi=14043068 /ug=Hs.347939 /len=575			
2961		line-1 protein ORF2 (=p150)	B28096		
2975	0.008677	actin related protein 2/3 complex,	NM_005719	Hs.293750	NP_005710
		subunit 3, 21kDa (ARPC3), mRNA			
		/cds=(94,630) /gb=NM_005719			
	1.	/gi=23397667 /ug=Hs.293750 /len=912			
		<b></b>			
2979	0.013394	hypothetical protein FLJ20574	NM 017886	Hs.99514	NP 060356
20,0	1 3.5 19554	(FLJ20574), mRNA /cds=(113,1741)	<u>,                                 </u>		
15 +					
7 . #	ł:.	/gb=NM_017886 /gi=8923538			
20-2	2 2 2 2 2 2	/ug=Hs 99514 /len=2581	1114 000070	11. 455045	NB 00000
2996	0.040751	ribosomal protein L12 (RPL12), mRNA	NM_000976	Hs.405042	NP_000967
	1	/cds=(89,586) /gb=NM_000976		}	
		/gi=15431291 /ug=Hs.405042 /len=632			
	·				<u></u>
3072	0.02801	trichorhinophalangeal syndrome I	NM_014112	Hs.26102	NP_054831
		(TRPS1), mRNA /cds=(639,4484)	'		
		/gb=NM_014112 /gi=7657658			
		/ug=Hs 26102 /len=10011	,		
3090	0.022106	Similar to kinesin family member C1,	BC000712	Hs.20830	NP 002254
		clone MGC:1202 IMAGE:3506669,			
	<b>.</b>	mRNA, complete cds /cds=(168,2189)			
		/gb=BC000712 /gi=12653842	-		
			·.		
	<b>∤</b> :	/ug=Hs.20830 /len=2400			
			104 005043	75075	ND 005000
3098	0.040751	malate dehydrogenase 1, NAD	NM_005917	Hs.75375	NP_005908
,	, .	(soluble) (MDH1), mRNA	Ì	ľ	
		/cds=(57,1061) /gb=NM_005917		J	]
		/gi=21735619 /ug=Hs.75375 /len=1268		]	
·	<u> </u>				
3109	0.030249	24-dehydrocholesterol reductase	NM_014762	Hs.75616	NP_055577
	i,	(DHCR24), mRNA /cds=(100,1650)		1	1
}		/gb=NM 014762 /gi=13375617	- '	ł	<b>1</b>
}		/ug=Hs.75616 /len=4248			
3116	0.023045	Hypothetical protein(cDNA FLJ11299	AK002161	T	NP_057295
2110	0.020040	fis, clone PLACE1009845, highly similar	1	1	].1, _00, 200
		_ · ·			$A = \frac{1}{2} \left( \frac{1}{2} - \frac{1}{2} \right)$
0715	0.00000	to KIAA0905 protein)	414004000	11- 000040	<del> </del>
3118	0.032636	cDNA: FLJ21243 fis, clone COL01164.	AK024896	Hs.268016	
		/gb=AK024896 /gi=10437310	1 -	1	ŀ
		/ug=Hs.268016 /len=1880			
I	J		j .	1	1 .

		nding To Differentially Expressed Gen			
Spot	p-value	Description	G ne	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
3123	0.043700	RNA processing factor 1 (RPF1),	NM 025065	Hs.287863	NP_079341
3123	0.043799		NIVI_U23003	IDS.207003	[NP_U/9341
	Part of the second	mRNA /cds=(8,1057) /gb=NM_025065	Programme of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Comp		
		/gi=18643386 /ug=Hs.287863			
		/len=1336			
3128	0.02801	mRNA for ras-related GTP-binding	Z29677	Hs.355976	NP_005605
	1	protein /cds=(24,578) /gb=Z29677			
		/gi≈453469 /ug=Hs.355976 /len=987			
2446	0.000000		NIM DOCOCO	11- 400000	ND COZOGA
3146	0.032636	aldo-keto reductase family 1, member	NM_006066	Hs.432896	NP_697021
5.5		A1 (aldehyde reductase) (AKR1A1),			
	)	transcript variant 1, mRNA			1. 1
		/cds=(465,1442) /gb=NM_006066	-		
		/gi=24497575 /ug=Hs.432896			1. 1
		/len=1556			
3148	0.035177		AVACCAC	Un 06067	<del></del>
3148	0.035177	cDNA: FLJ23155 fis, clone LNG09573.	AK026808	Hs.96867	
	[	/gb=AK026808 /gi=10439749			
	1	/ug=Hs.96867 /len=2089		1 7 7 1 1 1 1	
* *,		The first of the second of the			Language Company
3156	0.03788	golgi autoantigen, golgin subfamily b,	NM 004487	Hs.7844	NP 004478
		macrogolgin (with transmembrane			
		signal), 1 (GOLGB1), mRNA		1	}
		l =		**	
		/cds=(127,9906) /gb=NM_004487		<b>∤</b>	
		/gi=4758453 /ug=Hs.7844 /len=10300			
3180	0.013394	ferritin, heavy polypeptide 1 (FTH1),	NM_002032	Hs.418650	NP_002023
		mRNA /cds=(92,664) /gb=NM_002032			<b>.</b>
		/gi=4503794 /ug=Hs.418650 /len=801			
	}				-
3183	0.022045	Ciballes to bundth stiget install	DC000272	11- 250550	<b>{</b>
3103	0.023945	Similar to hypothetical protein	BC008373	Hs.356550	1.1
:		PRO1722, clone MGC:12239		<b>1</b>	
	1	IMAGE:3996377, mRNA, complete cds			
	100000	/cds=(1435,1635) /gb=BC008373			1.5
1 1	1	/gi=14249972 /ug=Hs.356550			1
1 M 1 M		/len=2470			
3219	0.005325	actin, alpha, cardiac muscle (ACTC),	NM 005159	Hs.118127	NP 005150
JZ 13	1 0.003323		14/41-002128	115.110121	INF_005150
	1	mRNA /cds=(1,1134) /gb=NM_005159			
٠.		/gi=10938011 /ug=Hs.118127			
•	<u> </u>	/len=1294		<u> </u>	
3220	8.37E-04	SHC (Src 2 domain containing)	NM_003029	Hs.81972	NP_003020
		transforming protein 1 (SHC1), mRNA	_	, :	·
		/cds=(195,1946) /gb=NM 003029			
	1	/gi=10835030 /ug=Hs.81972 /len=3664		1	
:		rgi- 10000000 rug-ms.61972 /leii-3004			
000	<del> </del>			<u> </u>	<b></b>
3230	0.035177	l ' '	AK000866	Hs.411490	
	1 .	HEMBA1000076./gb=AK000866			
	1	/gi=7021190 /ug=Hs.411490 /len=1974		1	
				}	
3235	0.030340	histone deacetylase 11 (HDAC11),	NM_024827	He 74290	ND 070102
JZJJ	0.030249		INIVI_UZ#0Z/	Hs.74280	NP_079103
	Į.	mRNA /cds=(25,1068) /gb=NM_024827			
	]	/gi=13376227 /ug=Hs.74280 /len=1755		1	1:
	1		l		1

Genes	Correspoi	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
Spot	p-value	Description	Gene Accession No.	Unigene Accession	Protein Accession
	<del>, , , , , , , , , , , , , , , , , , , </del>	k		No.	No.
3246	0.047031	UI-E-EJ0-ail-e-04-0-UI.r1 UI-E-EJ0	BM727687	Hs.446532	
		cDNA clone UI-E-EJ0-ail-e-04-0-UI 5',		·	
		mRNA sequence /clone=UI-E-EJ0-ail-e-			
		04-0-UI /clone_end=5' /gb=BM727687			
		/gi=19049020 /ug=Hs.446532			
	<del> </del>	/len=1103			
3280	0.014599	RETROVIRUS-RELATED POL	P11369 U	]	
لتببت	بنصمت	POLYPROTEIN			
3288	0.018784	cyclin G2 (CCNG2), mRNA	NM_004354	Hs.79069	NP_004345
	W 1	/cds=(136,1170) /gb=NM_004354			
		/gi=4757935 /ug=Hs.79069 /len=2044		l	
3294	0.018784	NCK adaptor protein 1 (NCK1), mRNA	NM_006153	Hs.54589	NP_006144
		/cds=(117,1250) /gb=NM_006153			
1 1		/gi=20070226 /ug=Hs.54589 /len=1947			
3296	0.00587	monocyte to macrophage differentiation	NM_012329	Hs.79889	NP_036461
με		associated (MMD), mRNA			
		/cds=(82,798) /gb=NM_012329			
		/gi=6912507 /ug=Hs.79889 /len=2533		1	
3299	2.32E-04	ADP-ribosylation factor 4 (ARF4),	NM_001660	Hs.75290	NP_001651
}		mRNA /cds=(211,753) /gb=NM_001660	A STATE OF THE STATE OF		
		/gi=6995998 /ug=Hs:75290 /len=1610			
·	*		1		
3303	0.022106	HSPC070 protein (HSPC070), mRNA	NM_014160	Hs.279474	NP_054879
		/cds=(332,1582) /gb=NM_014160			
}		/gi=8850222 /ug=Hs 279474 /len=3050			
				<del> </del>	<u> </u>
3326	0.017288	of yeast long chain polyunsaturated	NM_021814	Hs.250175	NP_068586
	- 1	fatty acid elongation enzyme 2			j
		(HELO1), mRNA /cds=(345,1244)		1	
•		/gb=NM_021814 /gi=21361903	Landa Control	1	
0007	5 445 54	/ug=Hs.250175 /len=3011	 		
3327	5.11E-04	goliath protein (GP), mRNA	NM_018434	Hs.155718	NP_060904
,		/cds=(428,1258) /gb=NM_018434			
	:	/gi=20127393 /ug=Hs.155718	9.0		
2200	0.000000	/len=1445	NIM OCCOOL	111-0047	ND 000504
3336	0.009388	stromal antigen 2 (STAG2), mRNA	NM_006603	Hs.8217	NP_006594
,		/cds=(405,3893) /gb=NM_006603	1	1	
3304	0.000000	/gi=27552767 /ug=Hs.8217 /len=4197	 	11- 055700	ND 00000
3361	0.020388	integrin, beta 8 (ITGB8), mRNA	NM_002214	Hs.355722	NP_002205
		/cds=(681,2990) /gb=NM_002214			} '
		/gi=4504778 /ug=Hs.355722 /len=3789		1	
2270	0.040754		A DO 40004		ND 000700
3378	0.040751	hypothetical protein KIAA1461 (ORF)	AB040894		NP_060798

Genes	Correspoi	nding To Differentially Expressed Gen	es in Figur 20 -	RA	
		Description	Gene	Unigene	Prot in
			Accession No.	Accession	Accession
:				No.	No.
3404	0.030249	protein tyrosine phosphatase, non-	NM 015466	Hs.25524	NP 056281
	0.0001	receptor type 23 (PTPN23), mRNA			
		/cds=(62,4972) /gb=NM_015466	ينفش مدادي		
		/gi=24308072 /ug=Hs.25524 /len=5248			
		/gi-243000/ 2 /dg-i is.23324 /ieii=3240 i			
3407	0.009388	BCL2/adenovirus E1B 19kD-interacting	XM 048077		
3-101	0.000000	protein 3-like (BNIP3L)	/0.10011		
3432	0.030249	polypyrimidine tract binding protein 1	NM 002819	Hs.172550	NP 787041
3 <del>4</del> 32	0.000240	(PTBP1), transcript variant 1, mRNA	1401_002013	110.172000	1
		/cds=(89,1762) /gb=NM_002819			
	11.54			t i di kacamatan	
		/gi=14165462 /ug=Hs.172550			
2422	0.040754	/len=3322 interferon induced transmembrane	NM 021034	Hs.381234	NP 066362
3433	0.040751		INIVI_UZ 1U34	1175.50 1254	INF_000302
		protein 3 (1-8U) (IFITM3), mRNA			<b> </b>
ش	{- ·	/cds=(238,639) /gb=NM_021034	the second	1	
		/gi=11995467 /ug=Hs.381234 /len=808			
* .			NIN'S 00000-	114045==	ND COCCO
3444	0.035177	laminin receptor 1 (ribosomal protein	NM_002295	Hs.181357	NP_002286
1		SA, 67kDa) (LAMR1), mRNA			
	(	/cds=(86,973) /gb= <b>NM_</b> 002295 \			
		/gi=9845501 /ug=Hs.181357 /len=1039		1.00	
				<u> </u>	1
3475	0.003947	hypothetical protein FLJ12389 similar to	NM_023928	Hs.239758	NP_076417
	·	acetoacetyl-CoA synthetase		1	
	1	(FLJ12389), mRNA /cds=(149,2167)			1
	ĺ	/gb=NM_023928 /gi=12965198			
	]	/ug=Hs.239758 /len=3253			
3476	0.03788	arginine-glutamic acid dipeptide (RE)	NM_012102	Hs.194369	NP 036234
		repeats (RERE), mRNA		1	1 -
	Ì	/cds=(637,5337) /gb=NM_012102			
		/gi=19923392 /ug=Hs.194369	in the second	1	
	<b>\</b>	/len=8035			
3485	0.047031	Saccharomyces cerevisiae	NC 001144	<del> </del>	
1,		chromosome XII, complete			
-		chromosome sequence		1	1
3495	0.03788	clone IMAGE:5212110, mRNA	BC028002	Hs.386507	
0-30	0.03700	/gb=BC028002 /gi=24081066	20020002	1.13.000007	
1	1	/ug=Hs.386507 /len=2415			1.
3506	0.035177		NM 018282	Hs.16364	NP_060752
āουρ	1 0.035177	paraspeckle protein 1 (PSP1), mRNA	114101_010202	JE15. 10304	NF_000/32
***		/cds=(294,1367) /gb=NM_018282	}		
0545	1001000	/gi=8922788 /ug=Hs.16364 /len=1709	A)A/OC4707	11- 407000	<del> </del>
3516	0.043799	PM1-DT0054-231299-002-a09 DT0054	AW364737	Hs.407368	
		cDNA, mRNA sequence	·		l
	}	/gb=AW364737 /gi=6869491	1		
		/ug=Hs.407368 /len=643		<u> </u>	<u> </u>
3520	0.032636	mRNA; cDNA DKFZp586F2423 (from	AL080209	Hs.13659	
		clone DKFZp586F2423) /gb=AL080209		1	
-		/gi=5262698 /ug=Hs.13659 /len=4254		1 .	t
	1	1 -	1	1	I

Genes Corresponding To Differentially Expressed Genes in Figure 20 - RA					
Spot	p-value	Description	Gene	Unigene	Prot in
			Accession No.	Acc ssion	Accession
				No.	No.
3524	0.045661	UI-H-DH1-awr-a-12-0-UI.s1	BQ001533	Hs. 194397	
		NCI_CGAP_DH1 cDNA clone			
		IMAGE:5893139 3', mRNA sequence	for the contract of		-
. • •		/clone=IMAGE:5893139 /clone_end=3'		,	
*		/gb=BQ001533 /gi=19726433			
		/ug=Hs.194397 /len=1039		,	
		749 119. 13 1007 Nen-1005			
3527	0.008566	UI-H-FL1-bge-c-14-0-UI.s1	CA430953	Hs.397680	
3321	0.000500			П5.397000	
		NCI_CGAP_FL1 cDNA clone UI-H-FL1-			
		bge-c-14-0-UI 3', mRNA sequence			
		/clone=UI-H-FL1-bge-c-14-0-UI			
		/clone_end=3' /gb=CA430953			
		/gi=24793679 /ug=Hs.397680			
		/len=1105		l	
3539	0.006463	ubiquitin C (UBC), mRNA	NM_021009	Hs.183704	NP_066289
		/cds=(136,2193) /gb=NM_021009			
	i .	/gi=20149305 /ug=Hs.183704			
		/len=2309		<b>.</b>	1.5
3540	0.032636	nucleoporin 155kDa (NUP155),	NM 153485	Hs.23255	NP 705618
00.0	0.002000	transcript variant 1, mRNA	1.1	110.20200	1111 = 100010
		/cds=(119,4294) /gb=NM_153485			
				,	
<i>;</i>	<b>.</b>	/gi=24430148 /ug=Hs.23255 /len=4355			
25.42	0.020240		NIM 004400	11- 2022	ND 004400
3542	0.030249	procollagen-proline, 2-oxoglutarate 4-	NM_004199	Hs.3622	NP_004190
		dioxygenase (proline 4-hydroxylase),			
	1	alpha polypeptide II (P4HA2), mRNA		Į.	
	<u>.</u>	/cds=(188,1795) /gb=NM_004199		1. 1	
		/gi=4758867 /ug=Hs.3622 /len=2194			
3560	0.040751	like mouse brain protein E46 (E46L),	NM_013236	Hs.13493	NP_037368
	ł	mRNA /cds=(199,1626)		1.	
	ł	/gb=NM_013236 /gi=7106298			
	ł.	/ug=Hs.13493 /len=1971			
3563	0:023945	hydroxyacyl-Coenzyme A	NM_000183	Hs.146812	NP 000174
		dehydrogenase/3-ketoacyl-Coenzyme			
		A thiolase/enoyl-Coenzyme A hydratase			
	=	(trifunctional protein), beta subunit			
		(thunctional protein), beta subunit ((HADHB), mRNA /cds=(47,1471)			
	1.1	/gb=NM_000183 /gi=4504326	<b> </b>		
	1	/ug=Hs.146812 /len=1991			
	L		L	<del> </del>	<del> </del>
3566	0.002893	Hypothetical protein(cDNA: FLJ23266	AK026919	1	}
		fis, clone COL06676, highly similar to		}	
·		HUMFRCCclone s153 mRNA)			
3570	0.001339	PTEN (PTEN) gene, exons 3 through 5	AF143314		
	1		Į.	1	

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Acc ssion	Accession
				No.	No.
3571	0.043799	proteasome (prosome, macropain) 26S	NM_002806	Hs.79357	NP_002797
		subunit, ATPase, 6 (PSMC6), mRNA			
		/cds=(21,1190) /gb=NM_002806			A CONTRACTOR OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF TH
		/gi=24430159 /ug=Hs.79357 /len=1590	r		
	ł* .				
3576	0.02801	osteoglycin (osteoinductive factor,	NM 033014	Hs.109439	NP 148935
		mimecan) (OGN), transcript variant 1,	· <del>-</del> · ·		
		mRNA /cds=(422,1318)			
		/gb=NM_033014 /gi=14916497			
		/ug=Hs.109439 /len=2976			
3578	0.010277	DKFZp586D2322 (from clone	AL049455	<del>                                     </del>	NP 001928
3370.	0.010277	DKFZp586D2322)	ALOHO-00		141 -00 1320
3587	0.047031	cAMP responsive element binding	NM 134442	Hs.79194	NP_604391
	0.047.031	protein 1 (CREB1), transcript variant B,	134442	1113.1.3 134	_004391
	[		÷ 1		
	]	mRNA /cds=(182,1207)	N 54	1	
	<b>\</b>	/gb=NM_134442 /gi=22219460			
0504	0.013001	/ug=Hs.79194 /len=3006			1,000
3591	0.04/031	hypothetical protein MGC4415	NM_031484	Hs.209614	NP_113672
		(MGC4415), mRNA /cds=(154,675)			
	le se	/gb=NM_031484 /gi=13899343		1.	
	<u> </u>	/ug=Hs.209614 /len=3243			
3599	0.011238	KDEL (Lys-Asp-Glu-Leu) endoplasmic	NM_006855	Hs.250696	NP_057839
,		reticulum protein retention receptor 3			
	*	(KDELR3), transcript variant 1, mRNA			
		/cds=(157,801) /gb=NM_006855			
	;	/gi=8051612 /ug=Hs 250696 /len=1705	art for the second	<b>1</b>	A
	l _{4.}			<b>\</b>	
3605	0.012276	KIAA0062 mRNA, partial cds	D31887	Hs.89868	
	1	/cds=(1,1598) /gb=D31887 /gi=505101	**		
	i	/ug=Hs.89868 /len=4573			
3606	0.012276	nucleolar protein family A, member 3	NM 018648	Hs.14317	NP 061118
		(H/ACA small nucleolar RNPs)	0.100.10		00 ; 0
	l	(NOLA3), mRNA /cds=(98,292)			Ì
	1	/gb=NM_018648 /gi=15011920	·		ľ
	1	/ug=Hs.14317 /len=556			<u> </u>
3617	0.018784	microtubule associated testis specific	NM_015112	Hs.101474	NP_055927
90 I I	0.010704	serine/threonine protein kinase	14141_010114	11 13. 10 14/4	INF_000927
		(MAST205), mRNA /cds=(284,5488)	. •	1	
: 1	1	/gb=NM_015112 /gi=14149670	} ·		
			<b>)</b>	1	Į.
2640	0.000500	/ug=Hs.101474 /len=5737	NIM 004007	115 00704	ND 004070
3618	0.008566	ATP synthase, H transporting,	NM_001687	Hs.89761	NP_001678
		mitochondrial F1 complex, delta subunit			
		(ATP5D), mRNA /cds=(84,590)	(		•
	<b>_</b>	/gb=NM_001687 /gi=4502296			<b>`</b>
		/ug=Hs.89761 /len=994			[
3640	0.010277	PTD015 protein (PTD015), mRNA	NM_014040	Hs.95870	NP_054759
		/cds=(148,504) /gb=NM_014040			]
		/gi=7662642 /ug=Hs.95870 /len=620			1

G nes	Correspo	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
	p-value	Description	Gene	Unigene	Protein
	,		Accession No.	Accession	Accession
				No.	No.
3653	0.030249	cDNA FLJ39355 fis, clone	AK096674	Hs.416902	
		PEBLM2003426. /gb=AK096674			ça e e
		/gi=21756218 /ug=Hs.416902			
		/len=2809		1.5	
3655	0.020388	oxysterol binding protein-like 7	NM 017731	Hs.274370	NP_665741
		(OSBPL7), transcript variant 2, mRNA			γ = -000,
		/cds=(257,2785) /gb=NM_017731			
		/gi=22035613 /ug=Hs.274370			
1		/len=3349	•		
3666	0.007807	DAZ associated protein 2 (DAZAP2),	NM 014764	Hs.75416	NP 055579
1 3000	0.007.007	mRNA /cds=(70,576) /gb=NM_014764	14141_014704	115.75410	141055579
		/gi=7661885 /ug=Hs.75416 /len=1897			
in the second		/gi=/001003/ug=H5./3410/left=109/			
3686	0.000566		NINA :045570	Us 22460	ND OFCOOL
3000	0.000000	autism susceptibility candidate 2	NM_015570	Hs.32168	NP_056385
	hi e ço	(AUTS2), mRNA /cds=(322,4101)			
	,	/gb=NM_015570 /gi=17864089			
0700	0.00507	/ug=Hs.32168 /len=5972	1111 000000		N.D. 000000
3702	0.00587	ferritin, heavy polypeptide 1 (FTH1),	NM_002032	Hs.418650	NP_002023
		mRNA /cds=(92,664) /gb=NM_002032		ļ.	
		/gi=4503794 /ug=Hs.418650 /len=801		. '	
3704	0.002602	LIM domain protein (RIL), mRNA	NM_003687	Hs.424312	NP_003678
		/cds=(42,1034) /gb=NM_003687		l · .	
		/gi=19923180 /ug=Hs.424312			
		/len=2256			
3715	0.007107	POP7 (processing of precursor, S.	NM_005837	Hs.416994	NP_005828
		cerevisiae) (RPP20), mRNA			
		/cds=(169,591) /gb=NM_005837			
	<u> </u>	/gi=5032046 /ug=Hs.416994 /len=878	<u> </u>		
3718	0.040751	dehydrogenase/reductase (SDR family)	NM_021004	Hs.418501	NP_066284
		member 4 (DHRS4), mRNA			,
		/cds=(80,862) /gb=NM_021004		<b>.</b>	
		/gi=10337604 /ug=Hs.418501	*.		ľ
		/len=1281			
3722	0.023945	clusterin (complement lysis inhibitor, SP	NM_001831	Hs.75106	NP_001822
1		40,40, sulfated glycoprotein 2,	] <del>-</del>		
		testosterone-repressed prostate			
	]	message 2, apolipoprotein J) (CLU),	<b> </b>		
		mRNA /cds=(48,1397) /gb=NM_001831		[ ·	
		/gi=4502904 /ug=Hs.75106 /len=1676		1	1
3731	0.012276	prosaposin (variant Gaucher disease	NM_002778	Hs.406455	NP_002769
		and variant metachromatic			
[	•	leukodystrophy) (PSAP), mRNA			,
<u> </u>		/cds=(39,1613) /gb=NM_002778	· · · · · · · · · · · · · · · · · · ·		
]		/gi=11386146 /ug=Hs.406455			1 4 4 T
] .		/len=2767	]		
	L	hou=5101	<u> </u>	L	L

Gen s Corresponding To Differentially Expressed Genes in Figure 20 - RA					
	p-value	Description	Gene Accession No.	Unigene Accession No.	Prot in Accession No.
3732	0.009388	hypothetical protein FLJ20718 (FLJ20718), mRNA /cds=(228,2012)	NM_017939	Hs.50579	NP_060409
		/gb=NM_017939 /gi=8923644 /ug=Hs.50579 /len=2658			
3750	0.023945	ferritin, light polypeptide (FTL), mRNA /cds=(189,716) /gb=NM_000146 /gi=20149497 /ug=Hs.430150 /len=878	NM_000146	Hs.430150	NP_000137
3751	0.043799	S100 calcium binding protein A11	NM 005620	Hs.417004	NP 005611
3/31	0.040739	(calgizzarin) (S100A11), mRNA /cds=(121,438) /gb=NM_005620 /gi=5032056 /ug=Hs.417004 /len=595	14W_003020	113.417004	_000011
3757	0.025911	tubulin, gamma complex associated protein 2 (TUBGCP2), mRNA /cds=(64,2772) /gb=NM_006659	NM_006659	Hs.13386	NP_006650
3760	0.035177	/gi=5729839 /ug=Hs.13386 /len=2846 cleavage and polyadenylation specific factor 3, 73kDa (CPSF3), mRNA	NM_016207	Hs.16251	NP_057291
		/cds=(36,2090) /gb=NM_016207 /gi=21314666 /ug=Hs.16251 /len=2286			
3787	0.011238	secretory leukocyte protease inhibitor (antileukoproteinase) (SLPI), mRNA /cds=(23,421) /gb=NM_003064 /gi=15834622 /ug=Hs.251754 /len=598	NM_003064	Ĥs.251754	NP_003055
3791	0.022106	TNF receptor-associated factor 4 (TRAF4), transcript variant 1, mRNA /cds=(86,1498) /gb=NM_004295 /gi=22027621 /ug=Hs.8375 /len=1999	NM_004295	Hs.8375	NP_665694
3793	0.013394	myosin, light polypeptide 5, regulatory (MYL5), mRNA /cds=(106,627) /gb=NM_002477 /gi=4505304 /ug=Hs.170482 /len=661	NM_002477	Hs.170482	NP_002468
3797	0.004367	KIAA0081 mRNA, partial cds /cds=(1,708) /gb=D42039 /gi=20521875 /ug=Hs.78871 /len=4174	D42039	Hs.78871	
3798	0.002602	chromodomain helicase DNA binding protein 4 (CHD4), mRNA /cds=(90,5828) /gb=NM_001273 /gi=4557452 /ug=Hs.74441 /len=6417	NM_001273	Hs.74441	NP_001264
3805	0.043799	hypothetical protein FLJ10350 (FLJ10350), mRNA /cds=(676,2340) /gb=NM_018067 /gi=21361780 /ug=Hs.177596 /len=2811	NM_018067	Hs.177596	NP_060537

		nding To Diff rentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		Accession No.	Accession	Accession
			·	No.	No.
3879	0.035177	DEAD/H (Asp-Glu-Ala-Asp/His) box	NM_004728	Hs.169531	NP_004719
		polypeptide 21 (DDX21), mRNA			
		/cds=(266,2413) /gb=NM_004728			
•		/gi=13787208 /ug=Hs.169531			
. :		/len=3319			
3891	0.018784	FLJ33146 fis, clone UTERU2000197,	AK057708	Hs.19500	
	0.0.0	moderately similar to Homo sapiens		, ,,,	
		nuclear localization signal containing			
: •	i.e	protein deleted in Velo-Cardio-Facial			
		syndrome (Nivcf) mRNA			
		/cds=UNKNOWN /gb=AK057708			
		/gi=16553625 /ug=Hs.19500 /len=3512			
		/gi= 10000020 /ug=i/i5. 19000 /ieii=3012	=		. '
2005	0.020200	paraneoplastic antigen MA1 (PNMA1),	NIM ODEO20	Hs.194709	ND 006020
3905	0.020368		NM_006029	ITS. 194709 	NP_006020
		mRNA /cds=(665,1726)			
100		/gb=NM_006029 /gi=14719429		i de la companya di sa	
		/ug=Hs.194709 /len=2530			115 11555
3937	0.02801	nuclear receptor binding factor-2	NM_030759	Hs.27181	NP_110386
		(NRBF-2), mRNA /cds=(180,1043)			
		/gb=NM_030759 /gi=13540514	,		
٠	14.	/ug=Hs.27181 /len=1866			
3958	0.012276	CGI-150 protein (CGI-150), mRNA	NM_016080	Hs.279061	NP_057164
		/cds=(202,1716) /gb=NM_016080		·	
		/gi=7705645 /ug=Hs.279061 /len=2580		* .	
	286.3				\$- 
3959	0.047031	actin-binding protein 22 kDa (SM22)	AF013711		
	i i	gene, complete cds			
3965	0.008566	serine (or cysteine) proteinase inhibitor,	NM_000295	Hs.297681	NP_000286
		clade A (alpha-1 antiproteinase,			<b>.</b> -
9		antitrypsin), member 1 (SERPINA1),			
51 TV		mRNA /cds=(233,1489)			
		/gb=NM_000295 /gi=21361197			
1.	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	/ug=Hs.297681 /len=1584		·	
3972	0.003563	chitinase 3-like 1 (cartilage glycoprotein-	NM 001276	Hs.75184	NP_001267
		39) (CHI3L1), mRNA /cds=(127,1278)			
		/gb=NM 001276 /gi=4557017			1
,		/ug=Hs.75184 /len=1925		[ .	
3997	0.022106	NADH dehydrogenase (ubiquinone)	NM 021074	Hs.51299	NP_066552
5557	0.022100	flavoprotein 2, 24kDa (NDUFV2),	10/1	1.13.01200	
	·	mRNA /cds=(19,768) /gb=NM_021074			
		l and the second second second second second second second second second second second second second second se			1
		/gi=10835024 /ug=Hs 51299 /len=827			
4000	0.00507		NINA ODDOOG	110 04040	ND 445000
4003	0.00587	methylmalonyl CoA epimerase (MCEE),	NM_032601	Hs.94949	NP_115990
		mRNA /cds=(11,541) /gb=NM_032601		· ·	
,		/gi=21314761 /ug=Hs.94949 /len=850		1.	1
·	<u> </u>		L	l	<u> </u>

Genes	Correspon	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
		Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
1005	0.004070		D14077004	No.	No.
4005	0.001878	UI-E-EJ0-aig-m-03-0-UI s1 UI-E-EJ0	BM677964	Hs.439607	
		cDNA clone UI-E-EJ0-aig-m-03-0-UI 3',			
	4	mRNA sequence /clone=UI-E-EJ0-aig-			lee septimories en installe Noord
·		m-03-0-UI /clone_end=3'	,		
		/gb=BM677964 /gi=18987860			1.
		/ug=Hs.439607 /len=1043		·	
4006	0.010277	protein kinase D2 (PRKD2), mRNA	NM_016457	Hs.91146	NP_057541
	45.4	/cds=(40,2676) /gb=NM_016457	,		
		/gi=19923467 /ug=Hs.91146 /len=2900	rayer		
4008	9.43E-04	jagged 1 (Alagille syndrome) (JAG1),	NM 000214	Hs.91143	NP_000205
		mRNA /cds=(414,4070)	<del>-</del>		
		/gb=NM 000214 /gi=4557678			
1		/ug=Hs.91143 /len=5896			
4025	0.014599	cytochrome c oxidase subunit Vb	NM 001862	Hs 1342	NP 001853
	]	(COX5B), nuclear gene encoding			
		mitochondrial protein, mRNA			
		/cds=(30,419) /gb=NM_001862			
		/gi=17017987 /ug=Hs 1342 /len=523			
4033	0.018784	protein tyrosine phosphatase, receptor	NM 002845	Hs 154151	NP 002836
4000	0.010704	type, M (PTPRM), mRNA /cds=(1,4359)		115.154151	NP_002030
		/gb=NM_002845 /gi=18860903			
	[	/ug=Hs.154151 /len=5065			
4046	0.000340	notionarias (DNA) II (DNA dispotad)	NA 022040	110 70400	ND 446550
4046	0.030249	polymerase (RNA) II (DNA directed)	NM_032940	Hs.79402	NP_116558
		polypeptide C, 33kDa (POLR2C),			
		transcript variant gamma, mRNA			
		/cds=(58,885) /gb=NM_032940			
		/gi=14702170 /ug=Hs.79402 /len=1782			
1001	0.00070		104 004000	10000	ND 077000
4064	0.012276	ubiquitin-like 5 (UBL5), mRNA	NM_024292	Hs.13836	NP_077268
		/cds=(66,287) /gb=NM_024292	'	la de la companya de la companya de la companya de la companya de la companya de la companya de la companya de	
1000		/gi=13236509 /ug=Hs.13836 /len=413			 
4078	0.035177	retinoblastoma binding protein 8	NM_002894	Hs.29287	NP_002885
·		(RBBP8), mRNA /cds=(299,2992)			
		/gb=NM_002894 /gi=4506440			
		/ug=Hs.29287 /len=3246			
4087	0.005843	TAF12 RNA polymerase II, TATA box	NM_005644	Hs.421646	NP_005635
		binding protein (TBP)-associated factor,			
		20kDa (TAF12), mRNA /cds=(167,652)		[	1
		/gb=NM_005644 /gi=9943840			
	!	/ug=Hs.421646 /len=1113	<b>(</b> .		1
· .				<u></u>	
4103	0.015895	protein kinase C, nu (PRKCN), mRNA	NM_005813	Hs.143460	NP_005804
	1	/cds=(556,3228) /gb=NM_005813	<b>1</b>		
		/gi=6563384 /ug=Hs.143460 /len=5792			
ļ.	1				

		nding To Differentially Expr ssed Gen			<u></u>
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
4118		HSPC154 protein (HSPC154), mRNA	NM_014177	Hs.7922	NP_054896
٠,٠.		/cds=(200,946) /gb=NM_014177			
		/gi=7661809 /ug=Hs.7922 /len=1343			
4121	0.018784	natural killer cell enhancing factor	L19184		NP_002565
, ,		(NKEFA)			-
4131	0.032636	thymosin, beta 4, X chromosome	NM_021109	Hs.75968	NP_066932
		(TMSB4X), mRNA /cds=(78,212)			_
	1	/gb=NM_021109 /gi=11056060			
1		/ug=Hs.75968 /len=556			The first transfer
4133	0.003947		NM 003380	Hs 297753	NP 000995
7.00	0.00001.	/gb=NM_003380 /gi=4507894		110.201700	-02000
		/ug=Hs.297753 /len=1851		]	]
		/ug=113.237700 /ieii=1001			
4134	0.040751	for P	X14897		NP 032062
4134		RAB10, member RAS oncogene family	NM_016131	Hs 236494	NP_057215
4 145	0.004825		NIVI_U 10131	IDS 230494	INP_05/215
		(RAB10), mRNA /cds=(91,693)			
	\$.	/gb=NM_016131 /gi=7705848			
· ·		/ug=Hs.236494 /len=3164			
4147	0.02801	GNAS complex locus (GNAS),	NM_080425	Hs.374523	NP_536351
		transcript variant 3, mRNA			
		/cds=(1,2730) /gb=NM_080425			
		/gi=18426897 /ug=Hs.374523			
		/len=3091		<u>                                     </u>	
4148	0.006463	FUSE binding protein 3 (FBP3) mRNA,	U69127	Hs.153636	
1 44 4		partial cds. /cds=(1,1803) /gb=U69127			
,		/gi=1575608 /ug=Hs.153636 /len=3131			
4152	0.022106	CG9469 gene product	AAF57414		
4153		KIAA0423 mRNA, partial cds.	AB007883	Hs.111373	1
	,	/cds=(206,5377) /gb=AB007883			
		/gi=20521046 /ug=Hs.111373			
		/len=6246		,	
4164	0.007107	translocated promoter region (to	NM 003292	Hs.169750	NP 003283
		activated MET oncogene) (TPR),			
		mRNA /cds=(298,7347)			
		/gb=NM_003292 /gi=4507658			1
	· .	/ug=Hs.169750 /len=7497			
4171	0.00587	AGENCOURT 7591767 NIH MGC 92	BO228526	Hs.282204	
41/I	0.00007	1		13.202204	
	1	cDNA clone IMAGE:6067123 5', mRNA			
		sequence /clone=IMAGE:6067123	1		
	· · ·	/clone_end=5' /gb=BQ228526		1	
		/gi=20409926 /ug=Hs.282204			1
	] _. :	/len=1263		·	
	<u> </u>				
4187	0.018784	serine protease inhibitor, Kunitz type, 2	NM_021102	Hs.31439	NP_066925
		(SPINT2), mRNA /cds=(301,1059)			1
		/gb=NM_021102 /gi=10863908		1	
_		/ug=Hs.31439 /len=1544			<u>L</u>
4192	0.040751	ribosomal 28S RNA	M11167		

		nding To Differentially Expressed Gen			ļ
Spot	p-value	Description	Gen	Unigene	Protein
			Acc ssion No.	Accession	Accession
				No.	No.
4209	0.009388	cDNA FLJ39491 fis, clone	AK096810	Hs.274170	NP 852480
1		PROST2015924, weakly similar to Opa-			
		interacting protein OIP2 mRNA.			·
•		/gb=AK096810 /gi=21756383	,		
,		/ug=Hs.274170 /len=2835	# 2 T	:	
4220	0.005325	ribosomal protein S2 (RPS2), mRNA	NM 002952	Hs.356360	NP 002943
,,,,,,	0.0000	/cds=(12,893) /gb=NM_002952			
		/gi=15055538 /ug=Hs.356360 /len=978		(	
1.					
4221	0.011238	ras inhibitor	M37190		NP 061866
4225		Parkinson disease (autosomal	NM 007262	Hs.10958	NP 009193
7223	0.002090	recessive, early onset) 7 (PARK7),	14141-001,202	113.10300	_009193
		mRNA /cds=(21,590) /gb=NM_007262		-	
ere ye	1.				1
17 1		/gi=6005748 /ug=Hs.10958 /len=842			
4244	0.047024	mDNA for KIAAAAAtiil	DE0011	Un 155504	<del> </del>
4244	0.04/031	mRNA for KIAA0121 protein, partial	D50911	Hs.155584	
		cds. /cds=(411,1301) /gb=D50911			
Mary E IA		/gi=6633996 /ug=Hs.155584 /len=3787	herennen ja versiere e		
10.					
4253	0.011745	cartilage associated protein (CRTAP),	NM_006371	Hs.155481	NP_006362
		mRNA /cds=(12,1217) /gb=NM_006371			
		/gi=21536278 /ug=Hs.155481			
		/len=2307			
4262	0.043799	peptidylprolyl isomerase B (cyclophilin	NM_000942	Hs.394389	NP_000933
		B) (PPIB), mRNA /cds=(150,800)		1 .	
		/gb=NM_000942 /gi=20149505			,
		/ug=Hs.394389 /len=1028			1
			1		
4264	0.004825	syntrophin, alpha 1 (dystrophin-	NM_003098	Hs.31121	NP_003089
٠.	  -	associated protein A1, 59kDa, acidic			
		component) (SNTA1), mRNA	}	1	
		/cds=(273,1790) /gb=NM_003098			
		/gi=18765742 /ug=Hs.31121 /len=2345			: .
			<u> </u>		
4268	0.001878	reticulon 3 (RTN3), mRNA	NM_006054	Hs.252831	NP_006045
		/cds=(125,835) /gb=NM_006054		1	_
		/gi=5174654 /ug=Hs.252831 /len=2524		1,	
			1	1	
4296	0.043799	splicing factor 3b, subunit 2, 145kD,	BC000401	Hs.406423	1:
		clone IMAGE:2822659, mRNA, partial			
	J			l	
		1CGS /CGS=(1 2696) /GD=BCOUU401	·/*	1	<b>I</b>
	:	cds /cds=(1,2696) /gb=BC000401  /gi=12653264 /ug=Hs.406423			<b>\</b> .

Genes	Correspor	nding To Diff rentially Expressed Gen	es in Figure 20 -	RA	
			Gen	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
4304	0.030249	1-acylglycerol-3-phosphate O-	NM_006411	Hs.240534	NP_116130
		acyltransferase 1 (lysophosphatidic acid	, <del></del>		-
1		acyltransferase, alpha) (AGPAT1),	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)		
		transcript variant 1, mRNA	4		
		/cds=(319,1170) /gb=NM_006411			
		/gi=26787964 /ug=Hs.240534			
		/len=2242			
4308	0.013304	Kruppel-like factor (LOC51713), mRNA	NM 016270	Hs.107740	NP_057354
4506	0.013394	/cds=(85,1152) /gb=NM_016270	14141_010270	1115.107740	00/304
. 4		/gi=7706468 /ug=Hs.107740 /len=1647			
		/gi=//00408/ug=H\$.10//40/leli=104/		• • •	
4200	0.042276		NM 006310	Hs.293007	NP 006301
4309	0.012276	aminopeptidase puromycin sensitive	14141_006310	IDS.293007	INP_000301
		(NPEPPS), mRNA /cds=(196,2823)			
		/gb=NM_006310 /gi=15451906			
4040	0.007007	/ug=Hs 293007 /len=4177	NIM COOFFO	11- 2002	NP 542166
4316	0.007807	UPF2 regulator of nonsense transcripts	  MM_080599	Hs.3862	INP_542100
, .	[	(yeast) (UPF2), transcript variant 1,		1	
	ļ·	mRNA /cds=(130,3948)			
		/gb=NM_080599 /gi=18375675			
L.,		/ug=Hs.3862 /len=5223			
4339	0.003539	lamin B receptor (LBR), mRNA	NM_002296	Hs.152931 ^{-/}	NP_002287
•	ļ	/cds=(76,1923) /gb=NM_002296			
	<b> </b>	/gi=4504960 /ug=Hs.152931 /len=3714			
4340	0.008566	heat shock 90kDa protein 1, beta	NM_007355	Hs.74335	NP_031381
ļ		(HSPCB), mRNA /cds=(85,2259)			
1		/gb=NM_007355 /gi=20149593			
		/ug=Hs.74335 /len=2567			<u> </u>
4341	0.014599	splicing factor, arginine/serine-rich 9	NM_003769	Hs.77608	NP_003760
	1 1 1 1 1 1 1	(SFRS9), mRNA /cds=(53,718)			
		/gb=NM_003769 /gi=4506902			
		/ug=Hs.77608 /len=1069	_		ļ.
4342	0.025911	RNA binding protein S1, serine-rich	NM_006711	Hs.75104	NP_542161
		domain (RNPS1), transcript variant 1,	]		
		mRNA /cds=(252,1169)	İ •		1
1	<b>∤</b> , '	/gb=NM_006711 /gi=18379335		•	
		/ug=Hs.75104 /len=2038			
4343	0.002893	lectin, galactoside-binding, soluble, 1	NM_002305	Hs.382367	NP_002296
	ŀ	(galectin 1) (LGALS1), mRNA			<b>{</b> .
		/cds=(69,476) /gb=NM_002305			
L	<u> </u>	/gi=6006015 /ug=Hs.382367 /len=526	<u> </u>	<u> </u>	
4345	0.007807	faciogenital dysplasia (Aarskog-Scott	NM_004463	Hs.1572	NP_004454
	1	syndrome) (FGD1), mRNA			
}	· ·	/cds=(735,3620) /gb=NM_004463		1	1
		/gi=24797152 /ug=Hs.1572 /len=4291		<u> </u>	<u> </u>
4349	0.004825	class I cytokine receptor (zcytor5)	AF178684		NP_004741

Genes	Correspon	nding To Differentially Expressed G n	es in Figure 20 -	RA	
Spot	p-value	Description	G ne	Unigen	Protein
			Accession No.	Accession	Accession
			. :-	No.	No.
4352	0.009388	zinc finger protein 38 (ZNF38), mRNA	NM_145914	Hs.20082	NP 666019
		/cds=(98,1519) /gb=NM_145914	_		<del></del>
	***	/gi=27544930 /ug=Hs.20082 /len=1960		[ i	
					·
4376	0.009388	KIAA0089 protein (KIAA0089), mRNA	NM 015141	Hs.82432	NP 055956
_		/cds=(66,1121) /gb=NM_015141	_		
-1		/gi=24307998 /ug=Hs.82432 /len=3959			
	1			]	]
4404	0.012276	KIAA1723 protein, partial cds	AB051510	Hs.8700	NP 006085
		/cds=UNKNOWN /gb=AB051510			
		/gi=12697990 /ug=Hs.8700 /len=7365			
4408	0.018784	mRNA for KIAA1165 protein, partial	AB032991	Hs.30340	1977 T. T.
	0.0.0.	cds. /cds=(1,855) /gb=AB032991	1,1002001	113.000.10	
in in		/gi=6330170 /ug=Hs.30340 /len=4415		le de la companya de la companya de la companya de la companya de la companya de la companya de la companya de	}
4415	0.030249	kinectin 1 (kinesin receptor) (KTN1),	NM 004986	Hs.418467	NP 004977
77.10	0.0002-10	mRNA /cds=(84,3986) /gb=NM_004986		1113.410407	141 _004977
,		/gi=4826813 /ug=Hs.418467 /len=4457			
		/gi==020010 /dg=113.410401 //c(i=4.51	]		
4423	0.035177	CD63 antigen (melanoma 1 antigen)	NM 001780	Hs.433996	NP 001771
7723	0.000177	(CD63), mRNA /cds=(95,811)		1115.433930	NINE_001771"
. T		/gb=NM_001780 /gi=21237758	- 1	- 1	
		/ug=Hs.433996 /len=925			
4428	0.020200	mRNA for KIAA1421 protein, partial	AB037842	Hs.117268	
4420	0.020300	cds. /cds=(1,4391) /gb=AB037842	AD037642	ПS.11/200	
	j, te ja		Jane 19 1 St. Control	10 y 3 y 3 y 3	
		/gi=7243222 /ug=Hs.117268 /len=4391			
4435	0.044220	clone IMAGE:3633225, mRNA	DC040750	U- 050077	
4433	0.011236		BC012758	Hs.356377	
		/gb=BC012758 /gi=15706478			
4440	0.000000	/ug=Hs.356377 /len=1914	NA 000074	11 70000	NE COCCO
4440	0.020388	alcohol dehydrogenase 5 (class III), chi	700007	Hs.78989	NP_000662
		polypeptide (ADH5), mRNA			
* .		/cds=(163,1287) /gb=NM_000671		No. 1	
		/gi=11496890 /ug=Hs.78989 /len=2496	<u>.</u>		
4450	0.0004	L	14 10774 10		ļ
4453	^0.02801	partial RAB18 gene for RAS-related	AJ277148	1.	
1.450	0.000500	small GTPase RAB18, exons 4-6	( <del> </del>	<b></b>	
4459		nonerythroid beta-spectrin	L02897	11. 50:0	NE 00000
4471	0.025911	proteasome (prosome, macropain) 26S	NM_002813	Hs.5648	NP_002804
		subunit, non-ATPase, 9 (PSMD9),			i ·
*		mRNA /cds=(96,767) /gb=NM_002813	}	1	}
		/gi=18543328 /ug=Hs.5648 /len=2338	)	}	ľ
4487	0.032636	alpha-2-macroglobulin (A2M), mRNA	NM_000014	Hs.74561	NP_000005
		/cds=(44,4468) /gb=NM_000014			
	·	/gi=6226959 /ug=Hs.74561 /len=4577		<u> </u>	L

Genes	Correspoi	nding To Differentially Expressed Gen	es in Figur 20 -	RA	
	p-value	Description	Gene	Unigene	Protein
•			Accession No.	Accession	Accession
				No.	No.
4492	0.017288	UI-E-CL1-afd-f-14-0-UI r1 UI-E-CL1	BM692513	Hs.446595	
	,	cDNA clone UI-E-CL1-afd-f-14-0-UI 5',			
		mRNA sequence /clone=UI-E-CL1-afd-f			ere e la la companya di series de la companya di series de la companya di series de la companya di series de l
		14-0-UI /clone_end=5' /gb=BM692513			
		/gi=19005771 /ug=Hs.446595 /len=624		1	
	}	<b>3</b>			
4496	0.013394	proteasome (prosome, macropain)	NM 002797	Hs.261927	NP_002788
		subunit, beta type, 5 (PSMB5), mRNA			<del>-</del>
Ì	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	/cds=(20,811) /gb=NM_002797			
		/gi=22538468 /ug=Hs.261927		•	
		/len=1050			
4499	0.013394	cDNA FLJ32300 fis, clone	AK056862	Hs.201676	NP 005782
'''	2.0,0004	PROST2002227, highly similar to M-	1,000,02	]	
		PHASE PHOSPHOPROTEIN 10.	lago esta esta en la constanta de la constanta de la constanta de la constanta de la constanta de la constanta		
2.2		/gb=AK056862 /gi=16552379		and a second second second second second second second second second second second second second second second	
		/ug=Hs.201676 /len=2334			
4508	2 03F-04	peptidyl-prolyl isomerase G (cyclophilin	NM 004792	Hs.77965	NP 004783
1000	2.000 04	G) (PPIG), mRNA /cds=(158,2422)	11111_00 1102	1113.77000	100 47 00
1		/gb=NM_004792 /gi=4758105			
		/ug=Hs.77965 /len=2695			
4514	0.043700	myeloid/lymphoid or mixed-lineage	NM_005935		NP 005926
1 4514	0.043133	leukemia (trithorax (Drosophila)	111111_0003303		111 _000020
		homolog); translocated to, 2 (MLLT2)			
		=L13773, AF-4 mRNA,			
4515	0.043700	cell recognition molecule CASPR3	NM 033655	Hs.212839	NP 387504
4515	0.043133	(CASPR3), transcript variant 1, mRNA	14141_033033	113.212033	147_307304
	- 10 ± 1, 1	/cds=(408,3872) /gb=NM_033655			
1.7		/gi=16306508 /ug=Hs.212839			
		/len=5017			
4522	0.00587	collagen, type IV, alpha 1 (COL4A1),	NM_001845	Hs.119129	NP 001836
4522	0.00567	mRNA /cds=(130,5139)	111111_001043	1113.113123	1111 _00 1000
		/gb=NM_001845 /gi=17017989			
		/ug=Hs.119129 /len=6447			
4531	0.001878	erythrocyte membrane protein band 4.1	NM 001431	Hs.7857	NP 001422
1001	0.001070	like 2 (EPB41L2), mRNA	11111_001401	,	
ļ		/cds=(45,3062) /gb=NM 001431			
ł · .	,	/gi=4503578 /ug=Hs.7857 /len=4336			*.
4532	0.047031	endonuclease/reverse transCRiptase	AAC53542		<del> </del>
عرب ا	0.047031	[Mus musculus]	, 01000042	-	
4554	0.012276	integral membrane protein 2B (ITM2B),	NM_021999	Hs.239625	NP 068839
7004	0.012270	mRNA /cds=(171,971) /gb=NM 021999		13.203020	
ł		//gi=11527401 /ug=Hs.239625	1	}	1
1	1	//len=1843			
4555	0.032636	P13-kinase associated p85 mRNA	M61906	<del> </del>	NP 852556
4556		phosphorylase, glycogen; liver (Hers	NM_002863	Hs.771	NP 002854
1 4000	0.014099	disease, glycogen storage disease type		113,111	_002004
4		VI) (PYGL), mRNA /cds=(52,2595)			
		/gb=NM_002863 /gi=4506352	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1		
1 .		/ug=Hs.771 /len=2643			
<u> </u>	<u> </u>	1/49-118.77 1 /1011-2043	1	<u> </u>	<del></del>

Snot	p-value	Description	es in Figure 20 - Gene	Unigene	Protein
Spot	p-value	Description	Accession No.	Accession	Accession
٠ -	,		Accession No.		
4568	0.040751	chaperonin containing TCP1, subunit 8	NM_006585	No. Hs.15071	NP 006576
4000	0.040751		14M_000000	1307 I	INF_000370
	ka estati e	(theta) (CCT8), mRNA /cds=(29,1675)			
		/gb=NM_006585 /gi=6005726			
4570	0.005477	/ug=Hs.15071 /len=1821	AD040204		ND OFCOAD
4570	0.035177	hypothetical protein KIAA0758 protein,	AB018301		NP_056049
		partial cds	104 004004	10.4040	ND 007007
4576	0.040751	E-1 enzyme (MASA), mRNA	NM_021204	Hs.18442	NP_067027
		/cds=(222,1007) /gb=NM_021204			1
		/gi=10864016 /ug=Hs.18442 /len=1992			
71 117 T				<u> </u>	100 22222
4578	0.017288	N-glycanase 1 (NGLY1), mRNA	NM_018297	Hs.63657	NP_060767
1.7		/cds=(42,2006) /gb=NM_018297			
		/gi=21314689 /ug=Hs 63657 /len=2182		. :	
				S	<u> </u>
4584	0.043799	Rho-associated, coiled-coil containing	NM_005406	Hs.17820	NP_005397
		protein kinase 1 (ROCK1), mRNA			1
	<b>1</b> ***	/cds=(1,4065) /gb=NM_005406			
		/gi=4885582 /ug=Hs:17820 /len=4065			
4600	0.010277	SEC24 related gene family, member D	NM_014822	Hs.19822	NP_055637
		(S. cerevisiae) (SEC24D), mRNA			
57 c		/cds=(201,3299) /gb=NM_014822			
		/gi=7662658 /ug=Hs.19822 /len=3988			
4604	0.013394	hypothetical protein FLJ21007	NM 030794	Hs.1975	NP 110421
		(FLJ21007), mRNA /cds=(258,2213)			
		/gb=NM_030794 /gi=13540575			
		/ug=Hs.1975 /len=2501			
4606	0.023945	cDNA FLJ33609 fis, clone	AK090928	Hs.433138	14
	0.020040	BRAMY2015890. /gb=AK090928	/ 11000020	119.100100	
		/gi=21749183 /ug=Hs.433138			
e egyr r		/len=2951			
4613	0.033636	cold shock domain protein A (CSDA),	NM_003651	Hs.198726	NP 003642
4013	0.032030		MNI_003033	113.130/20	INF_003042
		mRNA /cds=(195,1313)			
1		/gb=NM_003651 /gi=21359983		1,1	1
1611	0.007407	/ug=Hs.198726 /len=1931	ΛC107554		<del> </del>
4614		sperm antigen-36	AF187554	Un 100000	ND 057000
4617	0.025911	PTD008 protein (PTD008), mRNA	NM_016145	Hs.108969	NP_057229
		/cds=(234,554) /gb=NM_016145			1
		/gi=7706664 /ug=Hs.108969 /len=870	101 00 100	l	N. 6-00-
4622	0.009388	hypothetical protein FLJ11756	NM_024606	Hs.27497	NP_078882
	1	(FLJ11756), mRNA /cds=(375,2795)			
		/gb=NM_024606 /gi=24431999			
		/ug=Hs.27497 /len=3167		<u> </u>	
4627	0.005325	proteasome (prosome, macropain)	NM_002787	Hs.411773	NP_002778
		subunit, alpha type, 2 (PSMA2), mRNA		1	]
	1	/cds=(20,724) /gb=NM_002787	1		
		/gi=23110936 /ug=Hs.411773 /len=885	1		1
	1		1		

		nding To Differentially Expressed G n			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
	1. 5			No	No.
4629	0.020388	immediate early response 3 (IER3),	NM_052815	Hs.76095	NP_434702
		transcript variant long, mRNA			
		/cds=(30,611) /gb=NM_052815	11.5		i i i i i i i i i i i i i i i i i i i
		/gi=16554596 /ug=Hs.76095 /len=1345			
*		/gi: 1000-1000 /dg::113.70000 /iqii: 1040			
4632	0.006463	zinc finger protein (ZNF-U69274),	NM_014415	Hs.301956	NP 055230
7002	0.000,00	mRNA /cds=(162,3323)			[
		/gb=NM 014415 /gi=7657702		1	
		/ug=Hs.301956 /len=5052			
4633	0.002337	chromobox 3 (HP1 gamma Drosophila)	NM 016587	Hs.406384	NP 057671
4033	0.002337	(CBX3), transcript variant 2, mRNA	14141_010307	1113.400004	141 -00707
		/cds=(152,703) /gb=NM_016587	100		
	<b>,</b>	/gi=20544150 /ug=Hs.406384			
4004	0.005477	/len=1851	NIM 042220	No 45405	ND 027270
4634	0.035177	DNAJ domain-containing (MCJ), mRNA	NW_013238	Hs.45105	NP_037370
		/cds=(424,876) /gb=NM_013238			
-,	Kara Tagas	/gi=7019452 /ug=Hs.45105 /len=1074		1	ļ.,
	22222			1	ND 057440
4662	0.008566	CGI-128 protein (CGI-128), mRNA	NM_016062	Hs.9825	NP_057146
		/cds=(36,527) /gb=NM_016062			
		/gi=7706342 /ug=Hs.9825 /len=670		<u> </u>	
4664	0.032636	adaptor-related protein complex 3,	NM_001284	Hs.80917	NP_001275
		sigma 1 subunit (AP3S1), mRNA			ļ .
		/cds=(86,667) /gb=NM_001284			
	<u> </u>	/gi=4502860 /ug=Hs.80917 /len=1271	1		
4669	0.017288	adenylyl cyclase-associated protein	NM_006367	Hs.104125	NP_006358
		(CAP), mRNA /cds=(63,1490)	1. 17.37		,
:		/gb=NM_006367 /gi=10938021			
		/ug=Hs.104125 /len=2614			1
4670	0.003563	UI-E-DW0-agg-j-14-0-UI.r1 UI-E-DW0	BM706185	Hs.433563	
1.		cDNA clone UI-E-DW0-agg-j-14-0-UI			
		5', mRNA sequence /clone=UI-E-DW0-			
	<b>'</b>	agg-j-14-0-UI /clone_end=5'			
	1	/gb=BM706185 /gi=19019443			
•		/ug=Hs.433563 /len=949			
4673	0.020388	proteasome (prosome, macropain)	NM_002795	Hs.82793	NP_002786
		subunit, beta type, 3 (PSMB3), mRNA	<b>,</b> –		] -
		/cds=(79,696) /gb=NM_002795			
		/gi=22538464 /ug=Hs.82793 /len=784	1		
4		[		1	
4675	0.035177	proteasome (prosome, macropain)	NM_006263	Hs.75348	NP_788955
		activator subunit 1 (PA28 alpha)			1 7
		(PSME1), mRNA /cds=(93,842)			
•		/gb=NM_006263 /gi=5453989			T .
		/ug=Hs.75348 /len=985			
4676	0.045005	CDA14 (LOC51290), mRNA	NM 016570	Hs.26813	NP_057654
40/0	0.013693		[MNI_0 10370	113.20013	NF_05/054
	1 ' '	/cds=(89,1225) /gb=NM_016570		1	Ī
		/gi=7706104 /ug=Hs.26813 /len=1378	J		1

Genes	Correspor	nding To Diff rentially Expressed Gen		RA	<u> </u>
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
4684	0.00587	solute carrier family 25 (mitochondrial	NM 002635	Hs.78713	NP 005879
		carrier; phosphate carrier), member 3			<u> </u>
1		(SLC25A3), nuclear gene encoding		<u> </u>	
		mitochondrial protein, transcript variant	•	Į	
		1b, mRNA /cds=(49,1134)		1	
		/gb=NM_002635 /gi=4505774			
1.		/ug=Hs.78713 /len=1330		<b>1</b>	
ACOE	0.014500	calumenin (CALU), mRNA	NM 001219	Hs.7753	NP_001210
4685	0.014599	, ,,	111111_001219	IDS.7755	1NP_001210
		/cds=(63,1010) /gb=NM_001219			
} 1) 1	0.017000	/gi=6005991 /ug=Hs.7753 /len=3320	3114 007004	11 11000	115 00005
4700	0.017288	DnaJ (Hsp40) subfamily B, member 4	NM_007034	Hs.41693	NP_008965
		(DNAJB4), mRNA /cds=(160,1173)			
		/gb=NM_007034 /gi=24431959			! '
		/ug=Hs.41693 /len=2250			
4703	0.040751	leukotriene A4 hydrolase (LTA4H),	NM_000895	Hs.81118	NP_000886
		mRNA /cds=(69,1904) /gb=NM_000895			
		/gi=4505028 /ug=Hs.81118 /len=2060			
•					
4715	0.03788	hydroxysteroid (17-beta)	NM_016142	Hs.279617	NP_057226
		dehydrogenase 12 (HSD17B12),			
		mRNA /cds=(74,1012) /gb=NM_016142			·
		/gi=7705854 /ug=Hs.279617 /len=2393			
4	•	19 -770000474g			
4722	0.003563	S-phase kinase-associated protein 1A	NM 006930	Hs.171626	NP 733779
7122	0.00000	(p19A) (SKP1A), transcript variant 1,	111111_000000	113.171020	
		mRNA /cds=(140,622) /gb=NM_006930		1	1
		/gi=25777710 /ug=Hs.171626	•		
4700	0.00507	/len=2172	NINA OACOOO	11- 45004	ND 057297
4728	0.00587	pp21 (LOC51186), mRNA	NM_016303	Hs.15984	NP_057387
	}	/cds=(263,577) /gb=NM_016303	l e e		
		/gi=10047099 /ug=Hs.15984 /len=1038			
				<u> </u>	
4731	0.011238	tumor protein p53-binding protein	NM_005802	Hs.179982	NP_005793
		(TP53BPL), mRNA /cds=(541,2988)			
	1	/gb=NM_005802 /gi=5032190			İ
	·	/ug=Hs.179982 /len=3549			
4732	0.010277	MUF1 protein (MUF1), mRNA	NM_006369	Hs.172210	NP_006360
	<b>,</b> .	/cds=(1,1854) /gb=NM_006369	,		*
	i ·	/gi=5453747 /ug=Hs.172210 /len=2165			
					1
4735	0.011238	spectrin beta protein (pAZSP 3' end)	X91849		
4747		leucine zipper transcription factor-like 1	NM_020347	Hs.30824	NP 065080
1171	3.5.0000	(LZTFL1), mRNA /cds=(125,1024)			
		/gb=NM_020347 /gi=9966792			1
		/ug=Hs.30824 /len=3384	1		
ATEN	0.047200		BC022427	Hs.249247	<del>                                     </del>
4759	0.017288	clone IMAGE:4432159, mRNA	BC032437	I⊎2' <del>Č8</del> 2741	1
* * .		/gb=BC032437 /gi=21595543	1	1	
1	1	/ug=Hs.249247 /len=2309	I.	1	1

		nding To Differentially Expressed Gen	Company of the company of the		<b>.</b>
Spot	p-value	Description	Gene Accession No.	Unigene Accession	Prot in Accession
				No	No.
4766	0.009388	DnaJ (Hsp40) subfamily C, member 8	NM_014280	Hs.433540	NP 055095
		(DNAJC8), mRNA /cds=(8,802)	-		
·		/gb=NM_014280 /gi=7657610			
		/ug=Hs.433540 /len=1525			
4775	0.030249	glutathione-S-transferase like;	NM_004832	Hs.11465	NP 004823
4110	0.000243	glutathione transferase omega	141VI_004032	113.11405	147_004023
		(GSTTLp28), mRNA /cds=(10,735)	* 1		
1, 12			e e		(
•		/gb=NM_004832 /gi=4758483			(
4700	0.047024	/ug=Hs.11465 /len=793	NINA 004074	I I - 0000	NID 004000
4782	0.047031	CDC-like kinase1 (CLK1), mRNA	NM_004071	Hs.2083	NP_004062
	(a)	/cds=(156,1610) /gb=NM_004071			l land
		/gi=4758007 /ug=Hs.2083 /len=1834			
4789	J.U.U14599	tumor protein p53 binding protein, 2	NM_005426	Hs.44585	NP_005417
- 1 -		(TP53BP2), mRNA /cds=(757,3774)			·
		/gb=NM_005426 /gi=4885642			
		/ug=Hs.44585 /len=4534			
4796	0.03788	cofactor required for Sp1 transcriptional	NM_004229	Hs.407604	NP_004220
	Later of the Co	activation, subunit 2, 150kDa (CRSP2),			
		mRNA /cds=(120,4484)			
		/gb=NM_004229 /gi=4758101			
	:	/ug=Hs.407604 /len=7984		· .	
1, 1				1	1
4801	0.003947	growth hormone inducible	NM 014394	Hs.433957	NP 055209
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	transmembrane protein (GHITM),			<u> </u>
	ł	mRNA /cds=(130,1089)			}
	,	/gb=NM_014394 /gi=7657479		•	
	[ '	/ug=Hs.433957 /len=2374			İ
4804	0.035177	receptor-associated protein of the	NM 005055	Hs.81218	NP 116034
.00	0.000111	synapse, 43kD (RAPSN), transcript	11111_000000	113.012.10	114110001
	] .	variant 1, mRNA /cds=(215,1453)	}		<b>.</b>
	•	/gb=NM_005055 /gi=15619012			
4807	0.002047	/ug=Hs.81218 /len=1664	NIM COEZOS	115 440407	ND 005600
+00/	0.003947	glypican 6 (GPC6), mRNA	NM_005708	Hs.118407	NP_005699
	1	/cds=(616,2283) /gb=NM_005708			
	}	/gi=8051601 /ug=Hs.118407 /len=2760		1.	
4000	0.00001		NA 000070	UI- 4/50000	NE COSCE
4809	0.02801	matrilin 1, cartilage matrix protein	NM_002379	Hs.150366	NP_002370
		(MATN1), mRNA /cds=(490,1980)			
	i.	/gb=NM_002379 /gi=13518035			
		/ug=Hs.150366 /len=2414			<u> </u>
4832	0.035177	putative membrane protein	NM_019026	Hs.93832	NP_061899
	<u> </u>	(LOC54499), mRNA /cds≃(139,705)		, .	}
	]	/gb=NM_019026 /gi=24308132		-	
	<u></u>	/ug=Hs.93832 /len=1186		<u> </u>	
4838	0.043799	protein tyrosine phosphatase, receptor	NM_002844	Hs.79005	NP_002835
		type, K (PTPRK), mRNA	]		· -
	1	/cds=(221,4543) /gb=NM_002844	}	}	
		/gi=18860901 /ug=Hs.79005 /len=5982	ļ		
	Ì		· ·		

		nding To Differentially Express d Gen			
Spot	p-value	Description	Gen	Unigene	Protein
		C	Accession No.	Accession	Accession
	,			No.	No.
4846		thioredoxin related protein (MGC3178),	NM_030810	Hs 6101	NP_110437
		mRNA /cds=(82,1056) /gb=NM_030810			
		/gi=13540603 /ug=Hs.6101 /len=2712		ranger in a seco	
4882	0.043799	CGI-125 protein (CGI-125), mRNA	NM_016060	Hs.27289	NP_057144
		/cds=(79,474) /gb=NM_016060	_		1 7 1
		/gi=7705591 /ug=Hs.27289 /len=1196			
4885	0.003213	clone alpha_est218/52C1 mRNA	AF001542	Hs.356442	7 m 1 m 2 m 2 m 2 m 2 m 2 m 2 m 2 m 2 m 2
	į.	sequence /gb=AF001542 /gi=2529714			
o de la compansión de la compansión de la compansión de la compansión de la compansión de la compansión de la La compansión de la compansión de la compansión de la compansión de la compansión de la compansión de la compa		/ug=Hs:356442 /len=2992			
4904	0.035177	tj44d11.x1	Al470482	Hs.387691	
		Soares_NSF_F8_9W_OT_PA_P_S1		}	Ì
4 ,- 4		cDNA clone IMAGE:2144373 3' similar	1.0		
		to gb:Y00716 COMPLEMENT FACTOR			
		H PRECURSOR mRNA sequence			
	[	/clone=IMAGE:2144373 /clone_end=3'			
		/gb=Al470482 /gi=4332572			
		/ug=Hs.387691 /len=384			
4919	0.015895	KIAA0436 mRNA, partial cds.	AB007896	Hs.110	
4919	0.013033	/cds=(1,2070) /gb=AB007896	AD007030	[113.110	
		/gi=2662152 /ug=Hs.110 /len=4661			1.
4925	0.030340	tm68a09.x1 NCI_CGAP_Brn25 cDNA	Al498805	Hs.436349	
4923	0.030249	clone IMAGE:2163256 3', mRNA	A1430003	115.430343	<b>]</b>
* . * . *		sequence /clone=IMAGE:2163256			
10.			<b>[</b>		
		/clone_end=3' /gb=Al498805'			
4044	0.000045	/gi=4390787 /ug=Hs.436349 /len=460	AL 0222CE	11- 450474	-
4941	0.023945	mRNA; cDNA DKFZp451P176 (from	AL832365	Hs.159471	
		clone DKFZp451P176) /gb=AL832365			
, si		/gi=21732928 /ug=Hs.159471	•		1
45.4.4	0.005044	/len=5559	NIN 047000	054007	NE 000000
4944	0.025911	hypothetical protein FLJ20452	NM_017828	Hs.351327	NP_060298
		(FLJ20452), mRNA /cds=(15,614)	ļ		4.
		/gb=NM_017828 /gi=21361660			
		/ug=Hs.351327 /len=1948			118 -2 118
4946	0.02801	myosin, light polypeptide 6, alkali,	NM_079425	Hs.77385	NP_524149
		smooth muscle and non-muscle			
		(MYL6), transcript variant 3, mRNA	•		
		/cds=(41,514) /gb=NM_079425		1	
		/gi=17986263 /ug=Hs.77385 /len=717			
4950	0.010277	mRNA for KIAA1865 protein, partial	AB058768	Hs.179260	1
· . · · ·		cds. /cds=(622,2793) /gb=AB058768			
,		/gi=14017946 /ug=Hs.179260			1
		/len=3641		<u> </u>	
4951	0.020388	PAI-1 mRNA-binding protein (PAI-	NM_015640	Hs.165998	NP_056455
		RBP1), mRNA /cds=(86,1249)	1	}	1
	1	/gb=NM_015640 /gi=7661625	]		
		/ug=Hs.165998 /len=2201		[	<b>1</b>

Genes	Correspon	nding To Differentially Expressed Gen	es in Figure 20 -		
	p-value	Description	Gene	Unigene	Prot in
			Accession No.	Accession	Accession
				No.	No.
4962	0.018784	mRNA for KIAA1320 protein, partial	AB037741	Hs 117414	110.
4302	0.010104	cds. /cds=(2051,3754) /gb=AB037741	, iboolitati	11.3.777.414	
			A de la de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition de		}
	- 1	/gi=7243020 /ug=Hs.117414 /len≈5321			
			<del></del>		
4992	0.014599	tissue factor pathway inhibitor	NM_006287	Hs.170279	NP_006278
		(lipoprotein-associated coagulation			
		inhibitor) (TFPI), mRNA /cds=(1,915)		· · ·	
		/gb=NM_006287 /gi=6715569			
		/ug=Hs.170279 /len=915			
4999	0.04244	mRNA for KIAA0592 protein, partial	AB011164	Hs.439367	
	0.0.2	cds. /cds=(1,4062) /gb=AB011164			
		/gi=3043707 /ug=Hs.439367 /len=4623	:		
		/gi=3043707 /dg=[15.439307 /left=4025			
E000	0.000500	dinhtharia takin manatar (han-sir	NM 001945	Uo 700	ND 004026
5000	0.003563	diphtheria toxin receptor (heparin-	1945 	Hs.799	NP_001936
		binding epidermal growth factor-like			
		growth factor) (DTR), mRNA			
		/cds=(262,888) /gb=NM_001945			
		/gi=4503412 /ug=Hs.799 /len=2360			
5005	0.007107	ankyrin repeat and SOCS box-	NM_016114	Hs.153489	NP_057198
		containing 1 (ASB1), mRNA			*
		/cds=(87,1094) /gb=NM_016114			
. : ****		/gi=22208961 /ug=Hs 153489	e de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della comp		The state of the state of
1		/len=6798			
5012	0.006463	ATP synthase, H transporting,	NM 007100	Hs.85539	NP 009031
00 iz	1 0.000-00	mitochondrial F0 complex, subunit e	14111_007 100	113.00000	00000
,	l.	(ATP5I), mRNA /cds=(64,273)	the first stages		
		/gb=NM_007100 /gi=6005716			
		/ug=Hs.85539 /len=336			<u> </u>
5018	0.012276	mRNA; cDNA DKFZp762B195 (from	AL359585	Hs.356766	
		clone DKFZp762B195) /gb=AL359585			
1		/gi=8655645 /ug=Hs.356766 /len=2183			
	4				<u> </u>
5019	0.004367	desmin (DES), mRNA /cds=(81,1490)	NM_001927	Hs.279604	NP_001918
		/gb=NM_001927 /gi=18105049	_		
		/ug=Hs.279604 /len=2236			
5022	0.020388	ORM1-like 3 (S. cerevisiae) (ORMDL3),	NM 139280	Hs.374824	NP_644809
		mRNA /cds=(141,602) /gb=NM_139280	T .		
		/gi=27544926 /ug=Hs.374824			
-		/gi=273449267ug=⊓5.374624  /len=2109			
FOC 4	0.040704		NIM 002025	Ho 104605	ND 002020
5054	1.0.018784	topoisomerase (DNA) III beta (TOP3B),	โหเก_กกรลรอ	Hs.194685	NP_003926
	I	mRNA /cds=(445,3033)	·	!	· ,
	1		1	1	
•		/gb=NM_003935 /gi=20357524			
		/ug=Hs.194685 /len=3133		•	
5056	0.023945	,	NM_017728	Hs.15797	NP_060198
5056	0.023945	/ug=Hs.194685 /len=3133	NM_017728	Hs.15797	NP_060198
5056	0.023945	/ug=Hs.194685 /len=3133 hypothetical protein FLJ20255	NM_017728	Hs.15797	NP_060198

G nes	Correspoi	nding To Diff rentially Expr ssed Gen	es in Figure 20 -		
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5085	0.020388	paralemmin (PALM), mRNA /cds=(146,1309) /gb=NM_002579 /gi=4557041 /ug=Hs.78482 /len=2823	NM_002579	Hs.78482	NP_002570
5164	0.00587	nucleolar protein 5A (56kDa with KKE/D repeat) (NQL5A), mRNA /cds=(22,1830) /gb=NM_006392 /gi=5453793 /ug=Hs.296585 /len=1973	NM_006392	Hs.296585	NP_006383
5168	0.03788	nucleolar protein ANKT (ANKT), mRNA /cds=(713,1393) /gb=NM_016359 /gi=7705950 /ug=Hs.279905 /len=2268	NM_016359	Hs.279905	NP_060924
5170		glioblastoma amplified sequence (GBAS), mRNA /cds=(9,869) /gb=NM_001483 /gi≈4503936 /ug=Hs.152707 /len=1975	NM_001483	Hs.152707	NP_001474
5174 5176		plasminogen activator inhibitor-1 mRNA for KIAA0379 protein, partial cds. /cds=(1,3181) /gb=AB002377 /gi=6634024 /ug=Hs.32556 /len=4408	J03764 AB002377	Hs.32556	
5198	0.011238	platelet derived growth factor C (PDGFC), mRNA /cds=(492,1529) /gb=NM_016205 /gi=9994186 /ug=Hs.43080 /len=3007	NM_016205	Hs.43080	NP_057289
5203	0.032636	autocrine motility factor receptor (AMFR), transcript variant 1, mRNA /cds=(66,1997) /gb=NM_001144 /gi=21071000 /ug=Hs.80731 /len=3453	NM_001144	Hs.80731	NP_620408
5206	6.56E-04	CAAX box 1 (CXX1), mRNA /cds=(335,964) /gb=NM_003928 /gi=4503180 /ug=Hs.250708 /len=1209	NM_003928	Hs.250708	NP_003919
5213		H3 histone, family 3A (H3F3A), mRNA /cds=(116,526) /gb=NM_002107 /gi=22027640 /ug=Hs.181307 /len=1047	NM_002107	Hs.181307	NP_002098
5224		ubiquitously-expressed transcript (UXT), transcript variant 1, mRNA /cds=(155,664) /gb=NM_153477 /gi=24041017 /ug=Hs.172791 /len=734	NM_153477	Hs.172791	NP_705582
5236	0.030249	mitochondrial ribosomal protein L20 (MRPL20), nuclear gene encoding mitochondrial protein, mRNA /cds=(65,514) /gb=NM_017971 /gi=26638656 /ug=Hs.182698 /len=705	NM_017971	Hs.182698	NP_060441

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Acc ssion	Accession
. 1				No.	No.
5239	0.022106	zinc-finger protein AY163807	NM 014153	Hs.179898	NP_054872
<u></u>	0.022.00	(HSPC055), mRNA /cds=(199,3114)			<del>-</del>
		/gb=NM_014153 /gi=27414496	المراجع المحاجما		
					en en en en en en en en en en en en en e
		/ug=Hs.179898 /len=3859		11 110500	VD 00000
5240	0.014599	karyopherin (importin) beta 3 (KPNB3),	NM_002271	Hs.113503	NP_002262
		mRNA /cds=(139,3486)			
	[	/gb=NM_002271 /gi=24797085			
	Ì	/ug=Hs.113503 /len=5977			A
5242	0.005325	CDK2-associated protein 1	NM 004642	Hs.433201	NP 004633
		(CDK2AP1), mRNA /cds=(523,870)	-		
		/gb=NM_004642 /gi=17978492			
		/ug=Hs.433201 /len=1627	.*		
E0.40'	0.00004		NM 004894	Hs.109052	NP_004885
5243	0.02801	chromosome 14 open reading frame 2	19191_00409 <del>4</del>	15.10905Z	14E 704000
	1.	(C14orf2), mRNA /cds=(61,237)			
		/gb=NM_004894 /gi=4758939			
		/ug=Hs.109052 /len=627			
5250	0.017288	SFRS protein kinase 1 (SRPK1),	NM_003137	Hs.75761	NP_003128
722		mRNA /cds=(10,1974) /gb=NM_003137			
		/gi=15834623 /ug=Hs.75761 /len=4244			1-
		land			
5258	0.019794	testis derived transcript (3 LIM	NM 015641	Hs.165986	NP 690042
5230	0.010704		14141_013041	1113.100390	141 _030042
	{	domains) (TES), transcript variant 1,			•
2.4		mRNA /cds=(182,1447)			
		/gb=NM_015641 /gi=23238186			
te No. of		/ug=Hs.165986 /len=2766		1, 1	
5305	0.03788	cleavage and polyadenylation specific	NM_007007	Hs.64542	NP_008938
		factor 6, 68kDa (CPSF6), mRNA	•		
	· .	/cds=(35,1690) /gb=NM_007007		1 .	
	L	/gi=5901927 /ug=Hs.64542 /len=3426			
5309	0.005335	bone sialoprotein (BNSP) gene	L24759	<del></del>	
		mRNA; cDNA DKFZp564O0122 (from	AL049951	Hs.22370	4.1.4
5320	0.047031		ALU49951	HS.22370	
		clone DKFZp564O0122) /gb=AL049951			
;		/gi=4884198 /ug=Hs.22370 /len=1727			
5329	0.015895	dolichyl-diphosphooligosaccharide-	NM_005216	Hs.34789	NP_005207
		protein glycosyltransferase (DDOST),		<b>}</b>	
		mRNA /cds=(60,1430) /gb=NM_005216			
		/gi=20070196 /ug=Hs.34789 /len=2045			1
		.9. 250.0.00.49 .10.017.007.017 2040			
5348	0.006463	KIAA0066 mRNA, partial cds	D31886	Hs.227881	<del> </del>
JJ40	U.UUD403		U3 1000	113.22/001	
		/cds=(1,2948) /gb=D31886 /gi=505099			1
	<u> </u>	/ug=Hs.227881 /len=3635			
5365	0.005325	cDNA FLJ31667 fis, clone	AK056229	Hs.48692	
	1	NT2RI2004840. /gb=AK056229	I '		
		11172111200-10-10:195-7111000225	t .	1	1
		/gi=16551572 /ug=Hs.48692 /len=2052	[	1	

		nding To Differentially Express d Gen		KA	<u></u>
Spot	p-valu	Description	Gen	Unigene	Protein
			Acc ssion No.	Accession	Acc ssion
	<u> </u>		· · · · · · · · · · · · · · · · · · ·	No.	No.
5366	0.011238	glucagon (GCG), mRNA	NM_002054	Hs.423901	NP_002045
		/cds=(100,642) /gb=NM_002054			
		/gi=20302161 /ug=Hs.423901	li de e lieu e que :	h	en en en en en en en en en en en en en e
		/len=1128			
5374	0.023945	ribosomal protein L10 (RPL10), mRNA	NM_006013	Hs.412900	NP_006004
1		/cds=(42,686) /gb=NM_006013		1	
		/gi=15718685 /ug=Hs.412900	* · · · · · · · · · · · · · · · · · · ·		]
		/len=2188			
5388	0.006463	peroxiredoxin 1 (PRDX1), mRNA	NM 002574	Hs.180909	NP_002565
	i .	/cds=(61,660) /gb=NM_002574			
		/gi=4505590 /ug=Hs.180909 /len=937			
5392	0.030249	clone IMAGE:5398100, mRNA	BC035584	Hs.407477	
		/gb=BC035584 /gi=23273438			
	1	/ug=Hs.407477 /len=1570			
5393	0.020388	ubiquitination factor E4B (UFD2 yeast)	NM 006048	Hs.24594	NP_006039
		(UBE4B), mRNA /cds=(86,3994)	<del>-</del>		<b>1</b> → <del></del>
	HHS IT ST	/gb=NM 006048 /gi=5174482	* 1.00		
		/ug=Hs.24594 /len=5314			
5394	0.032636	hypothetical protein FLJ11294	NM_018383	Hs.107000	NP 060853
<b>,</b>		(FLJ11294), mRNA /cds=(160,4170)	, <u>-</u> 0		
		/gb=NM_018383 /gi=19923528	÷		
		/ug=Hs.107000 /len=4602			
5406	0.007107	autism susceptibility candidate 2	NM_015570	Hs.32168	NP 056385
0 100	0.007 107	(AUTS2), mRNA /cds=(322,4101)	00		-
	1	/gb=NM_015570/gi=17864089			
		/ug=Hs.32168 /len=5972			
5412	0.003947	SRY (sex determining region Y)-box 9	NM 000346	Hs.2316	NP_000337
V <del>4</del> 12	0.0055-7	(campomelic dysplasia, autosomal sex-	14141_000040	113.2010	
		reversal) (SOX9), mRNA		f .	
	with many are	/cds=(373,1902) /gb=NM_000346			
	Service of the service of	/gi=4557852 /ug=Hs.2316 /len=3936			
5414	0.010277	mRNA; cDNA DKFZp313L1834 (from	AL832699	Hs.336446	
J <del>4</del> 14	0.010277		175002033	113,000440	
		clone DKFZp313L1834) /gb=AL832699  /gi=21733278 /ug=Hs.336446		1	
	<b>1</b>	/g =21/332/6/ug=ns.336446  /len=2883	ļ. ·		
5417	0.040751	<del></del>	NM_018187	Hs.7187	NP_060657
041/	0.040751	(FLJ10707), mRNA /cds=(192,2966)	10101	115.7 107	TAF_00003/
	1			j	
		//gb=NM_018187 /gi=8922606			
F 404	0.04044	/ug=Hs.7187 /len=3334	AKOODECC	Ho 100051	<del> </del>
5421	0.04244	cDNA FLJ35247 fis, clone	AK092566	Hs.102951	]
		PROST2003517, weakly similar to zinc			
		finger protein dp mRNA. /gb=AK092566	, .		
	1.	/gi=21751188 /ug=Hs.102951	}	1	
		/len=2724	<u> </u>	_ ·	

Genes	Corr spor	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
	p-value	Description	G ne	Unigene	Prot in
			Accession No.	Accession	Acc ssion
				No.	No.
5422	0.003947	Finkel-Biskis-Reilly murine sarcoma	NM_001997	Hs.177415	NP_001988
		virus (FBR-MuSV) ubiquitously			
		expressed (fox derived); ribosomal			
		protein S30 (FAU), mRNA		,	Í.
		/cds=(106,507) /gb=NM_001997			
		/gi=17981709 /ug=Hs.177415 /len=574		j.	j . j
5428	0.043799	proteasome (prosome, macropain)	NM_002799	Hs.433434	NP_002790
		subunit, beta type, 7 (PSMB7), mRNA	<del>-</del>		-
		/cds=(18,851) /gb=NM_002799			
		/gi=23110926 /ug=Hs.433434			
ř	L 1	/len=1012	. 2 4		
5431	0.009388	thymine-DNA glycosylase (TDG),	NM 003211	Hs.173824	NP_003202
		mRNA /cds=(400,1632)			
i i		/gb=NM_003211 /gi=4507422			
	<b>)</b> ;	/ug=Hs.173824 /len=3410			
5433	0.032636	actin related protein 2/3 complex,	NM 005717	Hs.82425	NP_005708
0.00	0.002.000	subunit 5, 16kDa (ARPC5), mRNA			
		/cds=(192,647) /gb=NM_005717			
		/gi=23238212 /ug=Hs.82425 /len=2000			
					·
5435	0.002602	prolylcarboxypeptidase (angiotensinase	NM 005040	Hs.75693	NP_005031
0,00	0.002002	C) (PRCP), mRNA /cds=(30,1520)		[	
		/gb=NM_005040 /gi=4826939			
,		/ug=Hs.75693 /len=2060			
5448	0.040751	eukaryotic translation initiation factor	NM 001967	Hs.173912	NP 001958
,	0.010101	4A, isoform 2 (EIF4A2), mRNA		110:170012	
A		/cds=(16,1239) /gb=NM_001967		<u> </u>	
		/gi=9945313 /ug=Hs.173912 /len=1864			i :
		1			
5449	0.003947	mRNA; cDNA DKFZp667D2123 (from	AL832786	Hs.283643	
0110	0.0000	clone DKFZp667D2123) /gb=AL832786		110.200010	
**		/gi=21733368 /ug=Hs.283643			
		/len=3000		· ·	
5467	0.003213	DKFZp586L0218 (from clone	AL049383	<del> </del>	NP_004841
0.07	0.000210	DKFZp586L0218)	1,120,10000	* .	
5468	0.010277	Deleted in split-hand/split-foot 1 region	NM_006304	Hs.333495	NP 006295
0400	0.010277	(DSS1), mRNA /cds=(129,341)	11111_000001	110.000100	1000200
	Ì	/gb=NM 006304 /gi=5453639			1
٠.		/ug=Hs.333495 /len=509		,	1
5469	0.023045	hypothetical protein FLJ21432	NM_024551	Hs.334854	NP_078827
J-703	0.920340	(FLJ21432), mRNA /cds=(110,886)	]024001	1, 19,000,700,7	_07.0027
		/gb=NM_024551 /gi=13375714			
		/ug=Hs.334854 /len=3500			1
5472	0.047024	PR domain containing 10 (PRDM10),	NIM 020229	Hs.275086	NP_064613
541Z	0.04/031	_ `	NM_020228	115.273000	INF_004013
	<u> </u>	mRNA /cds=(217,3402)		The State of	
		/gb=NM_020228 /gi=9910503	[		
	<u></u>	/ug=Hs.275086 /len=6010	1	<u> </u>	

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No
5489	0.030249	DKFZP566H073 protein	NM_015528	Hs.7158	NP_056343
		(DKFZP566H073), mRNA			
		/cds=(450,1502) /gb=NM_015528	kan mala Maraya	1 :	
1.		/gi=14149701 /ug=Hs.7158 /len=1723		<b>)</b> .	. '
5499	0.007107	adaptor-related protein complex 2,	NM 004069	Hs.119591	NP 067586
1		sigma 1 subunit (AP2S1), transcript			
		variant AP17, mRNA /cds=(71,499)			
		/gb=NM 004069 /gi=11038644			
	3 1 7 1	/ug=Hs.119591 /len=781			
5502	0.003213	AGENCOURT 6626032	BM923381	Hs.437001	
330 <u>2</u>	0.000210	NIH_MGC_116 cDNA clone	Diviozogo i	11 13.437 001	
		IMAGE:5758987 5', mRNA sequence			
		/clone=IMAGE:5758987 /clone end=5'			
		/gb=BM923381 /gi=19373760	to the second		1
		_			
		/ug=Hs.437001 /len=1729			
5504	0.007007	F 100000	NIN	11 007050	NID 070000
5504	0.007807	hypothetical protein FLJ22329	NM_024656	Hs.367653	NP_078932
		(FLJ22329), mRNA /cds=(36,767)			
, i i i i		/gb=NM_024656 /gi=13375904			
		/ug=Hs.367653 /len=2501		<u> </u>	
5521	0.030249	papillomavirus L2 interacting nuclear	NM_052850	Hs.83135	NP_443082
		protein 1 (PLINP-1), mRNA			
100		/cds=(1,669) /gb=NM_052850			
<u> </u>		/gi=18959277 /ug=Hs.83135 /len=669	·		
5547	0.02801	hypothetical protein MGC31967	NM_174923	Hs.277026	NP_777583
		(MGC31967), mRNA /cds=(67,918)			
		/gb=NM_174923 /gi=28316809	•	3	
		/ug=Hs.277026 /len=936			
5578	0.001339	ATP synthase, H. transporting,	NM_001686	Hs.406510	NP_001677
•.		mitochondrial F1 complex, beta			
		polypeptide (ATP5B), nuclear gene			1.00
		encoding mitochondrial protein, mRNA			
		/cds=(46,1665) /gb=NM_001686	•		
	ary d	/gi=4502294 /ug=Hs.406510 /len=1807			
		3			
5580	0.047031	PTK9L protein tyrosine kinase 9-like	NM 007284	Hs.6780	NP_009215
	"	(A6-related protein) (PTK9L), mRNA	5,5.25		
	}	/cds=(105,1154) /gb=NM_007284			F 1
		/gi=6005845 /ug=Hs.6780 /len=1574	]		
5590	0.002337	eukaryotic translation initiation factor 4E	NM 004846	Hs.19122	NP 004837
2230	0.002337	like 3 (EIF4EL3), mRNA /cds=(15,752)	14141_004040	113.13122	141 _004037
			\$ 1 to		•
		/gb=NM_004846 /gi=4757701		1	
EEO4	0.044500	/ug=Hs.19122 /len=974	NIAA OO 4000	Un 42042	ND 440750
5591	0.014599	SEC22 vesicle trafficking protein-like 3	NM_004206	Hs.12942	NP_116752
		(S. cerevisiae) (SEC22L3), transcript		}	}
	[	variant 2, mRNA /cds=(119,871)			
	F	/gb=NM 004206 /gi=21536310	J ·	1	j
•	1 :	/ug=Hs.12942 /len=1519	· ·		** **

Spot   P-value   Description   Gene   Accession No.	Protein Acc ssion No. NP_001627  NP_037541  NP_620603
No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.	NP_001627  NP_037541  NP_620603
5620   0.020388   solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 (SLC25A6), nuclear gene encoding mitochondrial protein, mRNA /cds=(93,989) /gb=NM_001636 /gi=27764862 /ug=Hs.407372 /len=1455	NP_001627 NP_037541 NP_620603
5620   0.020388   solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 (SLC25A6), nuclear gene encoding mitochondrial protein, mRNA /cds=(93,989) /gb=NM_001636 /gi=27764862 /ug=Hs.407372 /len=1455	NP_001627 NP_037541 NP_620603
translocator), member 6 (SLC25A6), nuclear gene encoding mitochondrial protein, mRNA /cds=(93,989) /gb=NM_001636 /gi=27764862 /ug=Hs.407372 /len=1455  5629 0.017288 follistatin (FST), transcript variant FST317, mRNA /cds=(28,981) /gb=NM_006350 /gi=7242223 /ug=Hs.9914 /len=1386  5635 0.014599 mRNA for KIAA0251 gene, partial cds. /cds=(1,2464) /gb=D87438 /gi=2055294 /ug=Hs.343566 /len=3875  5639 5.79E-04 mitogen-activated protein kinase 7 (MAPK7), transcript variant 1, mRNA /cds=(355,2805) /gb=NM_139033 /gi=20986500 /ug=Hs.3080 /len=3113  5644 0.014599 integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700  5650 0.011238 small cytoplasmic Y RNA (Y4) L32608	NP_037541
translocator), member 6 (SLC25A6), nuclear gene encoding mitochondrial protein, mRNA /cds=(93,989) /gb=NM_001636 /gi=27764862 /ug=Hs.407372 /len=1455  5629 0.017288 follistatin (FST), transcript variant FST317, mRNA /cds=(28,981) /gb=NM_006350 /gi=7242223 /ug=Hs.9914 /len=1386  5635 0.014599 mRNA for KIAA0251 gene, partial cds. /cds=(1,2464) /gb=D87438 /gi=2055294 /ug=Hs.343566 /len=3875  5639 5.79E-04 mitogen-activated protein kinase 7 (MAPK7), transcript variant 1, mRNA /cds=(355,2805) /gb=NM_139033 /gi=20986500 /ug=Hs.3080 /len=3113  5644 0.014599 integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700  5650 0.011238 small cytoplasmic Y RNA (Y4) L32608	NP_620603
nuclear gene encoding mitochondrial protein, mRNA /cds=(93,989) /gb=NM_001636 /gi=27764862 /ug=Hs.407372 /len=1455  5629  0.017288 follistatin (FST), transcript variant FST317, mRNA /cds=(28,981) /gb=NM_006350 /gi=7242223 /ug=Hs.9914 /len=1386  5635  0.014599 mRNA for KIAA0251 gene, partial cds. /cds=(1,2464) /gb=D87438 /gi=2055294 /ug=Hs.343566 /len=3875  5639  5.79E-04 mitogen-activated protein kinase 7 (MAPK7), transcript variant 1, mRNA /cds=(355,2805) /gb=NM_139033 /gi=20986500 /ug=Hs.3080 /len=3113  5644  0.014599 integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700  5650  0.011238 small cytoplasmic Y RNA (Y4) L32608	NP_620603
protein, mRNA /cds=(93,989) /gb=NM_001636 /gi=27764862 /ug=Hs.407372 /len=1455  5629  0.017288  follistatin (FST), transcript variant     FST317, mRNA /cds=(28,981) /gb=NM_006350 /gi=7242223 /ug=Hs.9914 /len=1386  5635  0.014599  mRNA for KIAA0251 gene, partial cds. /cds=(1,2464) /gb=D87438 /gi=2055294 /ug=Hs.343566 /len=3875  5639  5.79E-04  mitogen-activated protein kinase 7     (MAPK7), transcript variant 1, mRNA /cds=(355,2805) /gb=NM_139033 /gi=20986500 /ug=Hs.3080 /len=3113  5644  0.014599  integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29     includes MDF2, MSK12) (ITGB1),     transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700  5650  0.011238  small cytoplasmic Y RNA (Y4) L32608	NP_620603
/gb=NM_001636 /gi=27764862 /ug=Hs.407372 /len=1455 5629  0.017288  follistatin (FST), transcript variant FST317, mRNA /cds=(28,981) /gb=NM_006350 /gi=7242223 /ug=Hs.9914 /len=1386 5635  0.014599  mRNA for KIAA0251 gene, partial cds. /cds=(1,2464) /gb=D87438 /gi=2055294 /ug=Hs.343566 /len=3875 5639  5.79E-04  mitogen-activated protein kinase 7 (MAPK7), transcript variant 1, mRNA /cds=(355,2805) /gb=NM_139033 /gi=20986500 /ug=Hs.3080 /len=3113 5644  0.014599  integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700 5650  0.011238  small cytoplasmic Y RNA (Y4) L32608	NP_620603
Jug=Hs.407372 /len=1455   Jug=Hs.407372 /len=1455   Jug=Hs.407372 /len=1455   Jug=Hs.9014   Jug=Hs.9914   Jug=Hs.9914 /len=1386   Jug=Hs.9914 /len=1386   Jug=Hs.9914 /len=1386   Jug=Hs.9914 /len=1386   Jug=Hs.9914 /len=1386   Jug=Hs.9914 /len=1386   Jug=Hs.9914 /len=1386   Jug=Hs.343566 /len=3875   Jug=Hs.343566 /len=3875   Jug=Hs.343566 /len=3875   Jug=Hs.343566 /len=3875   Jug=Hs.343566 /len=3875   Jug=Hs.343566 /len=3875   Jug=Hs.3080 /len=3113   Jug=19986500 /lug=Hs.3080 /len=3113   Jug=19986500 /lug=Hs.3080 /len=3113   Jug=19986500 /lug=Hs.3080 /len=3113   Jug=19986500 /lug=Hs.287797   Jug=19743812 /lug=Hs.287797   Jug=19743812 /lug=Hs.287797   Jug=19743812 /lug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=3700   Jug=Hs.287797   Jug=37	NP_620603
5629   0.017288   follistatin (FST), transcript variant   FST317, mRNA /cds=(28,981)   /gb=NM_006350 /gi=7242223   /ug=Hs.9914 /len=1386   D87438   Hs.343566   S635   0.014599   mRNA for KIAA0251 gene, partial cds.	NP_620603
FST317, mRNA /cds=(28,981) /gb=NM_006350 /gi=7242223 /ug=Hs.9914 /len=1386  5635	NP_620603
/gb=NM_006350 /gi=7242223 /ug=Hs.9914 /len=1386  5635	NP_620603
	NP_620603
5635 0.014599 mRNA for KIAA0251 gene, partial cds. /cds=(1,2464) /gb=D87438 /gi=2055294 /ug=Hs.343566 /len=3875  5639 5.79E-04 mitogen-activated protein kinase 7 (MAPK7), transcript variant 1, mRNA /cds=(355,2805) /gb=NM_139033 /gi=20986500 /ug=Hs.3080 /len=3113  5644 0.014599 integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700  5650 0.011238 small cytoplasmic Y RNA (Y4) L32608	NP_620603
/cds=(1,2464) /gb=D87438 /gi=2055294 //ug=Hs.343566 /len=3875  5639 5.79E-04 mitogen-activated protein kinase 7 (MAPK7), transcript variant 1, mRNA /cds=(355,2805) /gb=NM_139033 /gi=20986500 /ug=Hs.3080 /len=3113  5644 0.014599 integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700	NP_620603
/ug=Hs.343566 /len=3875  5639 5.79E-04 mitogen-activated protein kinase 7 (MAPK7), transcript variant 1, mRNA /cds=(355,2805) /gb=NM_139033 /gi=20986500 /ug=Hs.3080 /len=3113  5644 0.014599 integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700  5650 0.011238 small cytoplasmic Y RNA (Y4) L32608	
5639 5.79E-04 mitogen-activated protein kinase 7 (MAPK7), transcript variant 1, mRNA /cds=(355,2805) /gb=NM_139033 /gi=20986500 /ug=Hs.3080 /len=3113  5644 0.014599 integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700 L32608	
(MAPK7), transcript variant 1, mRNA //cds=(355,2805) /gb=NM_139033 /gi=20986500 /ug=Hs.3080 /len=3113  5644 0.014599 integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA //cds=(127,2523) /gb=NM_002211 //gi=19743812 /ug=Hs.287797 //len=3700  5650 0.011238 small cytoplasmic Y RNA (Y4)  L32608	
(MAPK7), transcript variant 1, mRNA //cds=(355,2805) /gb=NM_139033 /gi=20986500 /ug=Hs.3080 /len=3113  5644 0.014599 integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA //cds=(127,2523) /gb=NM_002211 //gi=19743812 /ug=Hs.287797 //len=3700  5650 0.011238 small cytoplasmic Y RNA (Y4)  L32608	
/cds=(355,2805) /gb=NM_139033 /gi=20986500 /ug=Hs.3080 /len=3113 5644 0.014599 integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700 L32608	NP_596867
/gi=20986500 /ug=Hs.3080 /len=3113  5644 0.014599 integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700  5650 0.011238 small cytoplasmic Y RNA (Y4) L32608	NP_596867
5644 0.014599 integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700 /s 5650 0.011238 small cytoplasmic Y RNA (Y4) L32608	NP_596867
beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700 5650 0.011238 small cytoplasmic Y RNA (Y4) L32608	NP_596867 
includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700 5650 0.011238 small cytoplasmic Y RNA (Y4) L32608	
transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700  5650 0.011238 small cytoplasmic Y RNA (Y4)  L32608	·#
/cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700 5650 0.011238 small cytoplasmic Y RNA (Y4) L32608	
/gi=19743812 /ug=Hs.287797 /len=3700 5650 0.011238 small cytoplasmic Y RNA (Y4) L32608	
/len=3700	
5650 0.011238 small cytoplasmic Y RNA (Y4) L32608	
(=X57566 hy4 Ro RNA (associated with)	
erythrocyte Ro RNP's))	<u> </u>
5653 0.011238 glypican 3 (GPC3), mRNA NM_004484 Hs.119651	NP_004475
/cds=(191,1933) /gb=NM_004484	
/gi=5360213 /ug=Hs.119651 /len=2382	
5656 0.047031 calcium channel, voltage-dependent, NM_000723 Hs.635	NP_000714
beta 1 subunit (CACNB1), mRNA	
/cds=(150,1940) /gb=NM_000723	
/gi=19923118 /ug=Hs.635 /len=3658	
5657 0.010277 ATPase, H transporting, lysosomal NM_005765 Hs.183434	NP_005756
(vacuolar proton pump) membrane	
sector associated protein M8-9	1.
(ATP6M8-9), mRNA /cds=(103,1155)	
/gb=NM_005765 /gi=15011917	
/ug=Hs.183434 /len=2044	
5665 0.010277 golgi associated, gamma adaptin ear NM_138619 Hs.87726	NP_619525
containing, ARF binding protein 3	
(GGA3), transcript variant long, mRNA	1.
/cds=(10,2181) /gb=NM_138619	
/gi=20336266 /ug=Hs 87726 /len=3860	

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Prot in
			Accession No.	Accession	Acc ssion
	(			No.	No.
5669	0.043799	membrane protein, palmitoylated 1,	NM 002436	Hs.1861	NP 002427
		55kDa (MPP1), mRNA /cds=(116,1516)			
	1	/gb=NM_002436 /gi=6006024		a ree ej	
	]	/ug=Hs.1861 /len=2001			
5670	0.042700	suppressor of cytokine signaling 1	NM 003745	Hs.50640	NP 003736
2010	0.043/99		14141_003743	TS.50040	line_onsvoo
		(SOCS1), mRNA /cds=(155,790)		]	
garan Ka		/gb=NM_003745 /gi=4507232			
<u> </u>	+	/ug=Hs.50640 /len=1216			
5674	0.003213	peroxisome biogenesis factor 1 (PEX1),	NM_000466	Hs.99847	NP_000457
T.		mRNA /cds=(61,3912) /gb=NM_000466		<b>\</b>	
		/gi=4505724 /ug=Hs 99847 /len=4343			
file.					
5675	0.018784	EST (aa17f08.r1 Soares NhHMPu S1	AA455618		
55.0	3.3,5,64	clone 813543 5')			
5697	0.00160	furin (paired basic amino acid cleaving	NM_002569	Hs.59242	NP_002560
2037	0.00100		 	1 13.00242	_002300
		enzyme) (FURIN), mRNA		1	
(d		/cds=(217,2601) /gb=NM_002569			
		/gi=20336193 /ug=Hs.59242 /len=4180			
5698	0.040751	serine (or cysteine) proteinase inhibitor,	NM_000295	Hs.297681	NP_000286
		clade A (alpha-1 antiproteinase,			
		antitrypsin), member 1 (SERPINA1),			-
. ;		mRNA /cds=(233,1489)			
		/gb=NM_000295 /gi=21361197			
		/ug=Hs.297681 /len=1584		1.	
5701	0.022045	mitochondrion, complete genome	NC 001807	<del> </del>	<del>                                     </del>
				No 222427	
5709	0.004367	clone IMAGE:4993796, mRNA	BC040073	Hs.322437	
		/gb=BC040073 /gi=25455647			
		/ug=Hs.322437 /len=2265			<u> </u>
5724	0.00168	proliferation-associated 2G4, 38kDa	NM_006191	Hs.374491	NP_006182
		(PA2G4), mRNA /cds=(98,1282)			
	1	/gb=NM_006191 /gi=5453841			
		/ug=Hs.374491 /len=1697	,	la contra	
5744	0.001339	DNA segment on chromosome X	NM 004699	Hs.54277	NP 004690
		(unique) 9928 expressed sequence		1	[ <del>-</del> ]
	]	(DXS9928E), mRNA /cds=(76,1095)			
		/gb=NM 004699 /gi=4758219			
		, -		* * · · · · · · · · · · · · · · · · · ·	
F740	0.000000	/ug=Hs.54277 /len=1311	NIM 000004	Hs.2699	ND 002072
5746	0.032636	glypican 1 (GPC1), mRNA	NM_002081	HS.Zoss	NP_002072
	1	/cds=(222,1898) /gb=NM_002081			ŀ
		/gi=4504080 /ug=Hs.2699 /len=3692			
5755	0.040751	paraoxonase 2 (PON2), mRNA	NM_000305	Hs.169857	NP_000296
		/cds=(33,1097) /gb=NM_000305			
		/gi=4505952 /ug=Hs.169857 /len=1600			
	1			1	[ · · · ·
5758	0.047031	STIP1 and U-Box containing protein 1	NM_005861	Hs.25197	NP_005852
0.00	1 3.5 77 55 1	(STUB1), mRNA /cds=(57,968)			
	1				1
		/gb≈NM_005861 /gi=5031962			
	1	/ug=Hs.25197 /len=1226	<u> </u>	<u> </u>	<u> </u>

Genes	Correspoi	nding To Differentially Express d Gen	es in Figure 20 -	RA	(A. 18 ) (18 ) (18 ) (18 ) (18 )
		D scription	Gene	Unig ne	Protein
, <del>.</del>			Accession No.	Accession	Accession
				No.	No.
5769	0.002096	cDNA: FLJ21561 fis, clone COL06415.	AK025214	Hs.96918	7 7 7 7 7 7
		/gb=AK025214 /gi=10437681			
	ter terminal	/ug=Hs.96918 /len=1641	::	ka sa hasa	
5777	0.020388	cathepsin L (CTSL), transcript variant 1,	NM 001912	Hs.78056	NP 666023
<b>J.</b>	0.02000	mRNA /cds=(345,1346)			-
		/gb=NM_001912 /gi=22202617			
		/ug=Hs.78056 /len=1632			
5781	0.002893	hect domain and RLD 3 (HERC3),	NM 014606	Hs.35804	NP_055421
3,01	0.002050	mRNA /cds=(167,3319)		110.00001	000 .2 .
		/gb=NM_014606 /gi=7657151			
	[ ·	/ug=Hs.35804 /len=4894			
5818	0.015805	CDC28 protein kinase regulatory	NM 001826	Hs.348669	NP 001817
JU 10	0.010090	subunit 1B (CKS1B), mRNA	14141_00 1020	13.040003	141, _00,1017
	yang termina	/cds=(10,249) /gb=NM_001826			
5004	0.02004	/gi=4502856 /ug=Hs.348669 /len=717	NM 000975	Hs.388664	NP 000966
5821	0.02801	ribosomal protein L11 (RPL11), mRNA	NIVI_000975	IUS:300004	INP_000900
		/cds=(21,557) /gb=NM_000975	ļ.		
÷ 2		/gi=15431289 /ug=Hs.388664 /len=609			
	2 2 2 2 2		1111 040400	11. 000005	ND COOFEE
5826	0.018784	ribosomal protein L13a (RPL13A),	NM_012423	Hs 389335	NP_036555
		mRNA /cds=(23,634) /gb=NM_012423	} ··	1	
÷ . •		/gi=14591905 /ug=Hs.389335	1 1		
		/len=1142		11 00054	110 001000
5834	0.035177	myosin IE (MYO1E), mRNA	NM_004998	Hs.82251	NP_004989
		/cds=(376,3705) /gb=NM_004998			
		/gi=4826843 /ug=Hs.82251 /len=4666			1.5.22.22
5837	0.02801	GK001 protein (GK001), mRNA	NM_020198	Hs.8207	NP_064583
	100	/cds=(185,1636) /gb=NM_020198			
		/gi=9910241 /ug=Hs.8207 /len=3294		<b>1</b>	<u> </u>
5844	0.007807	ATP synthase, H. transporting,	NM_007100	Hs.85539	NP_009031
		mitochondrial F0 complex, subunit e	1	1	
		(ATP5I), mRNA /cds=(64,273)			
		/gb=NM_007100 /gi=6005716			
		/ug=Hs.85539 /len=336	<b>1</b>		ļ
5868	0.043799	serine (or cysteine) proteinase inhibitor,	NM_000602	Hs.82085	NP_000593
		clade E (nexin, plasminogen activator			
	,	inhibitor type 1), member 1		]	
		(SERPINE1), mRNA /cds=(76,1284)			
		/gb=NM_000602 /gi=10835158			
	<u> </u>	/ug=Hs.82085 /len=2876		1	
5880	0.012276	amyloid beta precursor protein	NM_006380	Hs.84084	NP_006371
		(cytoplasmic tail) binding protein 2			
		(APPBP2), mRNA /cds=(289,2046)		1	
		/gb=NM_006380 /gi=18104961	*		
		/ug=Hs.84084 /len=6468		1	
5903	5.79F-04	dinucleotide miCRosatellite HUJII77	M96348	1	1

8						
L	Pot	p-value	nding To Differentially Express d Gen D scription	Gene	Unig ne	Protein
1				Accession No.	Accession No.	Accession No.
1.5	905	0.03788	protein phosphatase 2 (formerly 2A),	NM 002718	Hs.28219	NP 002709
	,500	0.007.00	regulatory subunit B", alpha	,,,,,_,,,,,		
			(PPP2R3A), mRNA /cds=(505,3957)			ent a compa
1			/gb=NM_002718 /gi=19923228			
	·	10	/ug=Hs.28219 /len=5217			}
-	912	0.043700	CGI-149 protein (CGI-149), mRNA	NM 016079	Hs.189658	NP_057163
١٢	1312	0.043733	/cds=(19,687) /gb=NM_016079	14141_010075	113.105050	141 _007 100
1			/gi=7706352 /ug=Hs.189658 /len=3064		]	
1		7 7 1	/gi=77003027ug=j is. 1090307ieii=3004			. ***
1	939	0.005335	BTAF1 RNA polymerase II, B-TFIID	NM_003972	Hs.180930	NP 003963
5	939	0.005325		NIVI_003972	Ins. 100930	NF_003903
İ	,		transcription factor-associated, 170kDa	ŕ		
1		er egati (Bai	(Mot1 S. cerevisiae) (BTAF1), mRNA		h and a second	[: :
	100	*	/cds=(118,5667) /gb=NM_003972	and the second section of		. , }
1.		·	/gi=27477069 /ug=Hs.180930			
-	-05-	0.00000	/len=6345	NIM 000450	115-4004	ND GOOD TO
5	5955	0.032636	glucan (1,4-alpha-), branching enzyme	NM_000158	Hs.1691	NP_000149
			1 (glycogen branching enzyme,		1	
1			Andersen disease, glycogen storage			
			disease type IV) (GBE1), mRNA			
-			/cds=(79,2187) /gb=NM_000158			
1	. (		/gi=4557618 /ug=Hs.1691 /len=2913		}	
L						
{	5974	0.043799	KIAA0266 gene product (KIAA0266),	NM_021645	Hs.127376	NP_067677
ļ	,		mRNA /cds=(734,3034)			
(	4		/gb=NM_021645 /gi=11063982			, , ,
.[.			/ug=Hs.127376 /len=5585			
[ (	5976	0.007807	ox06a01.s1	AI033469	Hs.386279	
1		· V	Soares_fetal_liver_spleen_1NFLS_S1	•		]
1.		!	cDNA clone IMAGE:1655496 3' similar	<u></u>		
			to gb:M86849 GAP JUNCTION BETA-2			
1	•	1 + 55	PROTEIN mRNA sequence	}		1
			/clone=IMAGE:1655496 /clone_end=3'			
			/gb=AI033469 /gi=3254422		1.	
			/ug=Hs.386279 /len=551	<u> </u>		
T:	5980	0.015895	MCM6 minichromosome maintenance	NM_005915	Hs.155462	NP_005906
			deficient 6 (MIS5 S. pombe) (S.			
			cerevisiae) (MCM6), mRNA		1	
-	ř.		/cds=(56,2521) /gb=NM_005915			
	:		/gi=24431964 /ug=Hs.155462			1.
1			/len=3744			1
1	5982	0.047031	neuron navigator 1 (NAV1), mRNA	NM 020443	Hs.6298	NP_065176
	•	]	/cds=(348,5972) /gb=NM_020443	-		1 .
			/gi=27262621 /ug=Hs.6298 /len=11365	ļ		
1	5986	0.040751	zinc finger and BTB domain containing	NM 014950	Hs.372699	NP_055765
Τ`			1 (ZBTB1), mRNA /cds=(263,2197)		1	
1			/gb=NM 014950/gi=7662437			<u>.</u>
			/ug=Hs.372699 /len=3990			1
			, ag 110.01 2000 11011 0000	·		

	7	nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
·				No.	No.
5988	0.001193	aldehyde dehydrogenase 1 family,	NM_000693	Hs.75746	NP_000684
		member A3 (ALDH1A3), mRNA			
		/cds=(53,1591) /gb=NM_000693			i garage
		/gi=4502040 /ug=Hs.75746 /len=3442		ľ	
5991	0.030249	coagulation factor V (proaccelerin,	NM 000130	Hs.30054	NP 000121
		labile factor) (F5), mRNA			-
		/cds=(98,6772) /gb=NM_000130	•		
		/gi=10518500 /ug=Hs.30054 /len=6914		[	
		3			
6006	0.049079	ribosomal protein L23a (RPL23A),	NM 000984	Hs.419463	NP 000975
00.00	)	mRNA /cds=(22,492) /gb=NM_000984			
. : -		/gi=17105393 /ug=Hs.419463 /len=546	•		
ş '		791-17 100000 749 113.4 10400 71011 040			
6015	0.023045	KIAA0373 gene product (KIAA0373),	NM 014684	Hs.150444	NP 055499
0013	0.023343	mRNA /cds=(1181,5800)	14101_014004	1113.130444	141 _000439
		/gb=NM_014684 /gi=7662079			
		/ug=Hs.150444 /len=5967			
6020	0.020240	high-glucose-regulated protein 8	NM 016258	Hs.20993	NP 057342
6029	0.030249		NNI_U 10230	IUS.50999	JNP_057542
- ; .		(HGRG8), mRNA /cds=(151,1863)			
		/gb=NM_016258 /gi=7705410			
20.10		/ug=Hs.20993 /len=2730		=====	
6049	0.035177	chromobox 1 (HP1 beta Drosophila )	NM_006807	Hs.77254	NP_006798
i		(CBX1), mRNA /cds=(292,849)		· ·	1
		/gb=NM_006807 /gi=21359877		}	
		/ug=Hs.77254 /len=2242			
6052	0.007107	thioredoxin (TXN), mRNA	NM_003329	Hs.432922	NP_003320
		/cds=(64,381) /gb=NM_003329			
<u> </u>		/gi=4507744 /ug=Hs.432922 /len=501			
6058	0.003213	mRNA for KIAA0276 gene, partial cds.	D87466	Hs.240112	
1		/cds=(1,932) /gb=D87466 /gi=1665816			
1.		/ug=Hs:240112 /len=4185		į .	
6062		zinc finger protein (ZNF141)	L15309	<u> </u>	NP_003432
6064	0.004825	actin related protein 2/3 complex,	NM_005719	Hs.293750	NP_005710
	<b>[</b>	subunit 3, 21kDa (ARPC3), mRNA		1	1
		/cds=(94,630) /gb=NM_005719		<b>.</b>	
	·	/gi=23397667 /ug=Hs.293750 /len=912			1
6069	0.040751	stress-associated endoplasmic	NM 014445	Hs.76698	NP_055260
		reticulum protein 1; ribosome	-		<u> </u>
		associated membrane protein 4	1	3	1
	ŀ	(SERP1), mRNA /cds=(316,516)	)		1
.+		/gb=NM_014445 /gi=19923408		Ì	1
		/ug=Hs.76698 /len=2488	ĺ	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	
6079	0.015895	extracellular matrix protein 2, female	NM_001393	Hs.35094	NP_001384
5013	0.010030	lorgan and adipocyte specific (ECM2),	114111_001090	1.13.00004	1.11 _001004
	1	mRNA /cds=(74,2173) /gb=NM_001393	]	}	}
	1	hituriate long-frage trailian-talation 1989	1.	1	· ·
	1′	/gi=4557542 /ug=Hs.35094 /len=3171		ł .	i

Accession No.   Acc   Saion   Access   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   N			nding To Differentially Expressed Gen			
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6092   0.002893   mypothetical protein (KIAA0128)   D50918   NP   668   6112   0.009388   gp25L2 protein   X90872   NP   005   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP   058   NP	1	,		Accession No.	Acc ssion	Accession
6112         0.009388 gp25L2 protein         X90872         NP_056           6128         0.006463 Rab acceptor 1 (prenylated) (RABAC1), MM_006423 / gi=5453959 /ug=Hs.11417 /len=770         NM_006423 / gi=5453959 /ug=Hs.11417 /len=770         NM_006423 / gi=5453959 /ug=Hs.11417 /len=770         NM_006423 / gi=5453959 /ug=Hs.11417 /len=770         NM_001316 / gi=4503072 /ug=Hs.19073 / gi=3147         NM_001316 / gi=4503072 /ug=Hs.90073 / gi=3147         NM_001316 / gi=303072 /ug=Hs.90073 / gi=3147         NM_002914 / gi=306486 / gi=3147         NM_002914 / gi=306486 / gi=3147         NM_002914 / gi=306486 / gi=3147         NM_002914 / gi=306486 / gi=3147         NM_002914 / gi=306486 / gi=3147         NM_002914 / gi=306486 / gi=3147         NM_002914 / gi=306486 / gi=3147         NM_002914 / gi=306486 / gi=3147         NM_002914 / gi=306486 / gi=3147         NM_002914 / gi=306486 / gi=3147         NM_002914 / gi=306486 / gi=3147         NM_002914 / gi=306486 / gi=3147         NM_002914 / gi=306486 / gi=3147         NM_002914 / gi=306486 / gi=3147         NM_006013 / gi=314900 / gi=3147         NM_006013 / gi=314900 / gi=3147         NM_006013 / gi=314900 / gi=3147         NM_006013 / gi=314900 / gi=3147         NM_006013 / gi=314900 / gi=314900 / gi=31447         NM_006013 / gi=314900 / gi=31447         NM_006013 / gi=31447         NM_006013 / gi=31447         NM_006013 / gi=31447         NM_006013 / gi=31447         NM_006013 / gi=31447         NM_006013 / gi=31447         NM_006013 / gi=31447         NM_006013 / gi=31447         NM_006013 / gi=31447         NM_006013 / gi=31447         NM_006013 / gi	- 1				No.	No.
6128         0.006463         Rab acceptor 1 (prenylated) (RABAC1), mRNA /cds=(31,588) /gb=NM_006423         Hs.11417         NP_006           6144         0.018784         CSE1 chromosome segregation 1-like (yeast) (CSE1L), mRNA /cds=(124,3039) /gb=NM_001316 /gi=4503072 /ug=Hs.90073 /len=3147         NM_001316         Hs.90073         NP_803           6145         0.009388 replication factor C (activator 1) 2, 40kDa (RFC2), mRNA /cds=(208,1272) /gb=NM_002914 /gi=4506486 /ug=Hs.139226 /len=1709         NM_002914         Hs.139226         NP_002 /mm_002914 /gi=4506486 /ug=Hs.139226 /len=1709           6155         0.008566 lamin A /cds=(2686) /gb=NM_006013 /gi=15718685 /ug=Hs.412900 /len=2188         M13452         NP_733 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm_006013 /mm	6092	0.002893	hypothetical protein (KIAA0128)	D50918		NP_665801
6128   0.006463   Rab acceptor 1 (prenylated) (RABAC1), NM_006423   Ms.11417   NP_006   NRNA /cds=(31,588) /gb=NM_006423   /gi=5453959 /ug=Hs.11417 /len=770   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_0001316   NM_00001316   NM_00001316   NM_00001316   NM_00001316   NM_00001316   NM_000001316   NM_000001316   NM_000001316   NM_000001316   NM_000001316   NM_000001316   NM_00	6112			X90872		NP 059980
mRNA /cds=(31,588) /gb=NM_ 006423 /gi=5453959 /ug=Hs.11417 /len=770  6144				NM 006423	Hs.11417	NP 006414
Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interest   Image: Interes				<b>.</b>		
6144   0.018784   CSE1 chromosome segregation 1-like (yeast) (CSE1L), mRNA (/ds=(124,3039) /gb=NM_001316 (gi=4503072 /ug=Hs.90073 /len=3147 (gi=4503072 /ug=Hs.90073 /len=3147 (gi=4503072 /ug=Hs.90073 /len=3147 (gi=4503072 /ug=Hs.90073 /len=3147 (gi=4503072 /ug=Hs.90073 /len=3147 (gi=4503072 /ug=Hs.90073 /len=3147 (gi=4508186 /ug=Hs.139226 /len=1709 /len=218 /ug=Hs.139226 /len=1709 /len=2188 (gi=4508186 /ug=Hs.412900 /len=2188 (gi=4508186 /ug=Hs.412900 /len=2188 (gi=4508186 /ug=Hs.412900 /len=2188 (gi=4508186 /ug=Hs.412900 /len=2188 (gi=4508186 /ug=Hs.28707 /len=3061 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3061 /len=1520 /ug=Hs.28707 /len=3062 /ug=Hs.28707 /len=3062 /ug=Hs.28707 /len=3062 /ug=Hs.28707 /len=3062 /ug=Hs.28707 /len=3062 /ug=Hs.28707 /len=3062 /ug=Hs.28707 /len=3062 /ug=Hs.28707 /len=3062 /ug=Hs.28707 /len=3062 /ug=Hs.28707 /ug=Hs.28707 /ug=Hs.28707 /ug=Hs.28707 /ug=Hs.28707 /ug=Hs.28707 /ug=Hs.28707 /ug=Hs.28707 /ug=Hs.28707 /ug=Hs.28707 /ug=Hs.28707	2	1 -5				
(yeast) (CSE1L), mRNA /cds=(124,3039) /gb=NM_001316 /gi=4503072 /ug=Hs_90073 /len=3147    6145						
(yeast) (CSE1L), mRNA /cds=(124,3039) /gb=NM_001316 /gi=4503072 /ug=Hs_90073 /len=3147    6145	6144	0.018784	CSE1 chromosome segregation 1-like	NM 001316	Hs.90073	NP 803185
International Content						
dj=4503072 /ug=Hs.90073 /len=3147						
February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February	. 1772 A					
40kDa (RFC2), mRNA /cds=(208,1272)   /gb=NM_002914 /gi=4506486   /ug=Hs.139226 /len=1709     M13452   NP_733   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006	6145	0.009388		NM 002914	Hs 139226	NP: 002905
/gb=NM_002914 /gi=4506486 /ug=Hs.139226 /len=1709	0140	0.000000		/ · · · · _ · · · · · · · · · · · · · ·	110,100220	002000
Aug=Hs.139226 /len=1709		1				
6158	1.5					
6166   0.035177   ribosomal protein L10 (RPL10), mRNA   NM_006013   Hs.412900   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP	J. 1.		rug-115, 139220 /1611-1703			
6166   0.035177   ribosomal protein L10 (RPL10), mRNA   NM_006013   Hs.412900   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP_006   NP	6150	0.000566	lamin Λ	M12452	<del>                                     </del>	ND 733833
/cds=(42,686) /gb=NM_006013 //gi=15718685 /ug=Hs.412900 //len=2188 6182					He 412000	
/gi=15718685 /ug=Hs.412900   /len=2188	0100	1 0.035177,				NF_000004 
Inn=2188						
6182   0.043799   signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), mRNA /cds=(57,614) /gb=NM_007107 /gi=6005883 /ug=Hs.28707 /len=3061   NM_005720   Hs.433506   NP_008			10			
(translocon-associated protein gamma) (SSR3), mRNA /cds=(57,614) //gb=NM_007107 /gi=6005883 //ug=Hs.28707 /len=3061  6183	0.400	0.040700	<u> </u>	NNA 007407	11- 00707	ND 00000
(SSR3), mRNA /cds=(57,614) /gb=NM_007107 /gi=6005883 /ug=Hs.28707 /len=3061  6183	6182	0.043799		NM_00/10/	HS.28707	MP_009038
/gb=NM_007107 /gi=6005883 /ug=Hs.28707 /len=3061  6183				}	}	
Nug=Hs.28707 /len=3061					]	
6183						
subunit 1B, 41kDa (ARPC1B), mRNA //cds=(90,1208) /gb=NM_005720 /gi=22907055 /ug=Hs.433506 //len=1520  6214  0.005325 adenylosuccinate lyase(ADSL)						
/cds=(90,1208) /gb=NM_005720 /gi=22907055 /ug=Hs.433506 //len=1520  6214  0.005325 adenylosuccinate lyase(ADSL)	6183	0.043799		NM_005720	Hs.433506	NP_005711
/gi=22907055 /ug=Hs.433506   /len=1520   NM_000026   NP_000     6214						
I/Ien=1520						ر فسار مو
6214         0.005325         adenylosuccinate lyase(ADSL)         NM_000026         NP_000           6223         0.018784         proteasome (prosome, macropain) subunit, alpha type, 4 (PSMA4), mRNA /cds=(137,922) /gb=NM_002789 /gi=23110940 /ug=Hs.251531 /len=1189         NM_002789         Hs.251531         NP_000           6236         0.035177         Similar to deleted in lymphocytic leukemia, 2, clone IMAGE:4044244, mRNA /gb=BC006995 /gi=14711944 /ug=Hs.383241 /len=1150         BC006995         Hs.383241           6260         0.004367         catenin (cadherin-associated protein), beta 1, 88kDa (CTNNB1), mRNA /cds=(215,2560) /gb=NM_001904 /gi=4503130 /ug=Hs.171271 /len=3362         NM_0014503         Hs.178614         NP_05           6263         0.040751         down-regulated in metastasis (DRIM), NM_014503         Hs.178614         NP_05						* 1 .3
6223 0.018784 proteasome (prosome, macropain) subunit, alpha type, 4 (PSMA4), mRNA /cds=(137,922) /gb=NM_002789 /gi=23110940 /ug=Hs.251531 /len=1189 6236 0.035177 Similar to deleted in lymphocytic leukemia, 2, clone IMAGE:4044244, mRNA /gb=BC006995 /gi=14711944 /ug=Hs.383241 /len=1150 6260 0.004367 catenin (cadherin-associated protein), beta 1, 88kDa (CTNNB1), mRNA /cds=(215,2560) /gb=NM_001904 /gi=4503130 /ug=Hs.171271 /len=3362 6263 0.040751 down-regulated in metastasis (DRIM), NM_014503 Hs.178614 NP_05						
subunit, alpha type, 4 (PSMA4), mRNA /cds=(137,922) /gb=NM_002789 /gi=23110940 /ug=Hs.251531 /len=1189  6236  0.035177  Similar to deleted in lymphocytic leukemia, 2, clone IMAGE:4044244, mRNA /gb=BC006995 /gi=14711944 /ug=Hs.383241 /len=1150  6260  0.004367  catenin (cadherin-associated protein), beta 1, 88kDa (CTNNB1), mRNA /cds=(215,2560) /gb=NM_001904 /gi=4503130 /ug=Hs.171271 /len=3362  6263  0.040751  down-regulated in metastasis (DRIM), NM_014503  Hs.178614  NP_05						NP_000017 34
/cds=(137,922) /gb=NM_002789 /gi=23110940 /ug=Hs.251531 /len=1189  6236	6223	0.018784		NM_002789	JHs.251531	NP_002780
/gi=23110940 /ug=Hs.251531 /len=1189  6236	4.1					
/len=1189 6236 0.035177 Similar to deleted in lymphocytic leukemia, 2, clone IMAGE:4044244, mRNA /gb=BC006995 /gi=14711944 /ug=Hs.383241 /len=1150 6260 0.004367 catenin (cadherin-associated protein), beta 1, 88kDa (CTNNB1), mRNA /cds=(215,2560) /gb=NM_001904 /gi=4503130 /ug=Hs.171271 /len=3362 6263 0.040751 down-regulated in metastasis (DRIM), NM_014503 Hs.178614 NP_05			/cds=(137,922) /gb=NM_002789			
6236 0.035177 Similar to deleted in lymphocytic leukemia, 2, clone IMAGE:4044244, mRNA /gb=BC006995 /gi=14711944 /ug=Hs.383241 /len=1150 6260 0.004367 catenin (cadherin-associated protein), beta 1, 88kDa (CTNNB1), mRNA /cds=(215,2560) /gb=NM_001904 /gi=4503130 /ug=Hs.171271 /len=3362 6263 0.040751 down-regulated in metastasis (DRIM), NM_014503 Hs.178614 NP_05			/gi=23110940 /ug=Hs.251531			
leukemia, 2, clone IMAGE:4044244, mRNA /gb=BC006995 /gi=14711944 /ug=Hs.383241 /len=1150  6260 0.004367 catenin (cadherin-associated protein), beta 1, 88kDa (CTNNB1), mRNA /cds=(215,2560) /gb=NM_001904 /gi=4503130 /ug=Hs.171271 /len=3362  6263 0.040751 down-regulated in metastasis (DRIM), NM_014503 Hs.178614 NP_05						
mRNA /gb=BC006995 /gi=14711944 /ug=Hs.383241 /len=1150  6260 0.004367 catenin (cadherin-associated protein), beta 1, 88kDa (CTNNB1), mRNA /cds=(215,2560) /gb=NM_001904 /gi=4503130 /ug=Hs.171271 /len=3362  6263 0.040751 down-regulated in metastasis (DRIM), NM_014503 Hs.178614 NP_05	6236	0.035177		BC006995	Hs.383241	
mRNA /gb=BC006995 /gi=14711944 /ug=Hs.383241 /len=1150  6260 0.004367 catenin (cadherin-associated protein), beta 1, 88kDa (CTNNB1), mRNA /cds=(215,2560) /gb=NM_001904 /gi=4503130 /ug=Hs.171271 /len=3362  6263 0.040751 down-regulated in metastasis (DRIM), NM_014503 Hs.178614 NP_05			leukemia, 2, clone IMAGE:4044244,	<b>]</b>		]
6260 0.004367 catenin (cadherin-associated protein), beta 1, 88kDa (CTNNB1), mRNA /cds=(215,2560) /gb=NM_001904 /gi=4503130 /ug=Hs.171271 /len=3362 Hs.178614 NP_05			mRNA /gb=BC006995 /gi=14711944	100		
6260 0.004367 catenin (cadherin-associated protein), beta 1, 88kDa (CTNNB1), mRNA /cds=(215,2560) /gb=NM_001904 /gi=4503130 /ug=Hs.171271 /len=3362 Hs.178614 NP_05			/ug=Hs.383241 /len=1150			<u> </u>
/cds=(215,2560) /gb=NM_001904 /gi=4503130 /ug=Hs.171271 /len=3362 6263 0.040751 down-regulated in metastasis (DRIM), NM_014503 Hs.178614 NP_05	6260	0.004367		NM_001904	Hs.171271	NP_001895
/gi=4503130 /ug=Hs.171271 /len=3362 6263 0.040751 down-regulated in metastasis (DRIM), NM_014503 Hs.178614 NP_05			beta 1, 88kDa (CTNNB1), mRNA		1	
/gi=4503130 /ug=Hs.171271 /len=3362 6263 0.040751 down-regulated in metastasis (DRIM), NM_014503 Hs.178614 NP_05		}	/cds=(215,2560) /gb=NM_001904		$\frac{1}{2}i$	] .
6263 0.040751 down-regulated in metastasis (DRIM), NM_014503 Hs.178614 NP_05	1					
1				1	·	
	6263	0.040751	down-regulated in metastasis (DRIM).	NM 014503	Hs.178614	NP_055318
	]		mRNA /cds=(145,8502)	_		] -
/gb=NM 014503 /gi=7657040						
/ug=Hs.178614 /len=9017	[	1.	,			[ * · · .

Genes	Correspor	nding To Differentially Expressed Gen		RA	
Spot	p-value	Description	Gene	Unig n	Protein
· ·	, ,		Accession No.	Accession	Accession
				No.	No.
6264	0.023945	BNIP3H (BNIP3H) nuclear gene for	AF255051	· · · · · · · · · · · · · · · · · · ·	
		mitochondrial product			
6311		peptidylprolyl isomerase A (cyclophilin	NM 021130	Hs.401787	NP 066953
		A) (PPIA), mRNA /cds=(45,542)		, '''	
		/gb=NM 021130 /gi=10863926		·	
		/ug=Hs.401787 /len=753	- *,		
4.					
6316	0.039408	KIAA1046 protein (KIAA1046)	NM 014928		
6322		ubiquitin specific protease 9 (USP9Y)	XM 000563		
6326		mitochondrial ribosomal protein S31	NM 005830	Hs.154655	NP 005821
0020	0.010277	(MRPS31), nuclear gene encoding	11111_000000	113.10-1000	-0000
		mitochondrial protein, mRNA			
		/cds=(22,1209) /gb=NM_005830			
*.		/gi=16950599 /ug=Hs.154655			
•		1 T			
6220	0.014220	/len=1284	NM 006022	Hs.114360	NP 006013
6329	0.011238	transforming growth factor beta-	NIVI_000022	Ins. 114300	INF_000013
1. 1.	1.4	stimulated protein TSC-22 (TSC22),	et a traditional expension		
		mRNA /cds=(192,626) /gb=NM_006022			
,	1 5-	/gi=5174728 /ug=Hs 114360 /len=1725			
					NB COSES
6331	0.02801	decay accelerating factor for	NM_000574	Hs.1369	NP_000565
		complement (CD55, Cromer blood		1	
		group system) (DAF), mRNA			
		/cds=(66,1211) /gb=NM_000574			
		/gi=10835142 /ug=Hs.1369 /len=2102			
6342	0.003213	oxidoreductase UCPA (LOC56898),	NM_020139	Hs.124696	NP_064524
		mRNA /cds=(70,807) /gb=NM_020139			
		/gi=10047131 /ug=Hs.124696			
		/len=1048			
6343	0.032636	inhibitor of Bruton's tyrsoine kinase	NM_015525	Hs 306425	NP_056340
	- 35 T	(IBTK), mRNA /cds=(420,1031)		ļ	
		/gb=NM_015525 /gi=24308082			
		/ug=Hs.306425 /len=2240			
6347	0.011238	mitochondrion, complete genome	NC_001807		
6348		major histocompatibility complex, class	NM_018950	Hs.110309	NP_061823
{		I, F (HLA-F), mRNA /cds=(1,1089)			
ļ		/gb=NM_018950 /gi=9665231			
		/ug=Hs.110309 /len=1188	100		
1			1		* * * * * * * * * * * * * * * * * * * *
6354	0.026797	N-myristoyltransferase 1 (NMT1),	NM 021079	Hs.111039	NP 066565
		mRNA /cds=(28,1518) /gb=NM_021079			\ \frac{1}{3}
		/gi=20070182 /ug=Hs.111039	(		
l		/len=4912		4.	
6363	0.006508	RAS, dexamethasone-induced 1	NM_016084	Hs.25829	NP_057168
5555	0.00000	(RASD1), mRNA /cds=(213,1058)	1510004	1.0.20020	
		/gb=NM_016084 /gi=22027484			
		/ug=Hs.25829 /len=1758			
L	ــــــــــــــــــــــــــــــــــــــ	//uy-118.20029 /IEII-1700	<u> </u>	1	1

		nding To Differentially Expressed G n	E 217 .		<u> </u>	
Spot	p-value	Description	Gene	Unigene	Protein	
ĺ			Accession No.	Accession	Accession	
				No.	No.	
6367	0.002096	growth arrest-specific 1 (GAS1), mRNA	NM 002048	Hs 65029	NP 002039	
-		/cds=(411,1448) /gb=NM_002048	er e <del>e e</del> e e e e e e e e e e e e e e e e		_	
** .**	- T	/gi=4503918 /ug=Hs.65029 /len=2828			ere je karaji da	
		/gi- 10000 10 14g   10.00020 /ioi1 12020				
6383	0.025911	S100 calcium binding protein A6	NM_014624	Hs.275243	NP_055439	
5000	0.020011	(calcyclin) (S100A6), mRNA	11111_01-102-1	113.270240	111 _000403	
		/cds=(103,375) /gb=NM 014624			·	
	و سيه ه	/gi=9845517 /ug=Hs.275243 /len=470				
6403	0.002047		NM 014236	Uo 10490	ND OFFOE	
0403	0.003947	glyceronephosphate O-acyltransferase	NIVI_U 14230	Hs.12482	NP_055051	
	ÿa. ∮	(GNPAT), mRNA /cds=(158,2200)				
		/gb=NM_014236 /gi=7657133				
245=	0.00=00=	/ug=Hs.12482 /len=2470	 			
6405	0.007807	cyclic AMP-regulated phosphoprotein	AF112220		NP_057384	
		(90% match)		<u> </u>		
6406	0.015895	cleavage stimulation factor, 3' pre-RNA,	NM_001326	Hs.180034	NP_001317	
		subunit 3, 77kDa (CSTF3), mRNA				
		/cds=(132,2285) /gb=NM_001326			,	
		/gi=4557494 /ug=Hs.180034 /len=2766				
6407	0.005325	hypothetical protein LOC51244	NM_016474	Hs.158006	NP_057558	
* -		(LOC51244), mRNA /cds=(340,1233)			-	
		/gb=NM_016474 /gi=24475969				
		/ug=Hs.158006 /len=1614				
6411	0.00587	tubulin, gamma complex associated	NM 006322	Hs.9884	NP 006313	
J	0.000	protein 3 (TUBGCP3), mRNA	/····			
1.1		/cds=(85,2808) /gb=NM_006322				
	87	/gi=5453659 /ug=Hs.9884 /len=3795				
6412	0.003047	KIAA0716 gene product (KIAA0716),	NM_014705	Hs.118140	NP_055520	
0412	0.003947		NIVI_014703	I   10 14 U	INP_055520	
	and of the	mRNA /cds=(192,2489)	Bara Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah S	}		
	2.	/gb=NM_014705 /gi=7662263				
0440		/ug=Hs.118140 /len=4652		11. 10005	ND 000040	
6419		RNA helicase family (RNAH), mRNA	NM_006828	Hs 48295	NP_006819	
		/cds=(39,6647) /gb=NM_006828		• • •		
		/gi=24307916 /ug=Hs.48295 /len=7315				
0.4.0						
6443	0.025911	Mlx interactor (MONDOA), mRNA	NM_014938	Hs.52081	NP_055753	
		/cds=(153,1733) /gb=NM_014938				
		/gi=7662347 /ug=Hs.52081 /len=4339			<u> </u>	
6480	0.002602	cysteine-rich motor neuron 1 (CRIM1),	NM_016441	Hs.19280	NP_057525	
		mRNA /cds=(40,3150) /gb=NM_016441		1		
		/gi=10092638 /ug=Hs.19280 /len=5601			l	
					<u> </u>	
6485	0.020388	serologically defined colon cancer	NM_006642	Hs.300642	NP_006633	
		antigen 8 (SDCCAG8), mRNA	<del>-</del>		<u> </u>	
		/cds=(1,2142) /gb=NM_006642		J	j	
			I .	1	1	
- '-		/gi=28269671 /ug=Hs.300642			1	

		nding To Differentially Express d Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
			<u> </u>	No.	No.
6515	0.014599	defensin, beta 1 (DEFB1), mRNA	NM 005218	Hs.32949	NP 005209
	117	/cds=(72,278) /gb=NM_005218			_
	e e e l'e equipale de la constant	/gi=13124884 /ug=Hs.32949 /len=366	in the second of the second		
6519	0.006463	eukaryotic translation initiation factor	NM 015636	Hs.169474	NP 056451
0319	0.000403		14141_013030	1113.103474	111 _030401
•		2B, subunit 4 delta, 67kDa (EIF2B4),			
		transcript variant 1, mRNA		i	
		/cds=(20,1588) /gb=NM_015636			}
		/gi=26986531 /ug=Hs 169474			
		/len=1643			
6531	0.040751	development and differentiation	NM_003887	Hs.12802	NP_003878
•		enhancing factor 2 (DDEF2), mRNA	No. of the second		
		/cds=(341,3361) /gb=NM_003887			
		/gi=4502248 /ug=Hs 12802 /len=5711			
6536	0.03788	synaptophysin-like protein (SYPL),	NM_006754	Hs.80919	NP_006745
		mRNA /cds=(34,813) /gb=NM_006754			
		/gi=5803184 /ug=Hs.80919 /len=2130	e de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de l		
1	[	igi -0000 104 /ug-113.000 13 /icii=2 100			
6544	0.040754	matrix metalloproteinase 11	NM 005940	Hs.155324	NP 005931
6544	0.040751		1005940	IDS. 100324	INP_005931
	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	(stromelysin 3) (MMP11), mRNA			
		/cds=(23,1489) /gb=NM_005940			<b>{</b>
		/gi=13027795 /ug=Hs 155324		.,	
		/len=2260			
6545	0.040751	low molecular mass ubiquinone-binding	NM_014402	Hs.3709	NP_055217
,		protein (9.5kD) (QP-C), nuclear gene			
		encoding mitochondrial protein, mRNA			
-		/cds=(37,318) /gb=NM_014402			ļ
		/gi=27894387 /ug=Hs 3709 /len=388			
2				1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
6547	0.030249	sorting nexin 6 (SNX6), transcript	NM 021249	Hs.284291	NP 689419
<b>0</b>	0.0002.0	variant 1, mRNA /cds=(498,1370)			
		/gb=NM 021249 /gi=23111048		<u> </u>	14.
121		/ug=Hs.284291 /len=3041	19 19 19 19 19 19 19 19 19 19 19 19 19 1		
6540	0.003563		NM 001903	Hs.177556	NP 001894
6549	0.003563	catenin (cadherin-associated protein),	LAM TOO 1903	1113, 177,000	_001094
	]	alpha 1, 102kDa (CTNNA1), mRNA	la de la la la la la la la la la la la la la	,	
		/cds=(5,2728) /gb=NM_001903			
	<b>1</b> .	/gi=4503126 /ug=Hs 177556 /len=3454			
	<u></u>			<u> </u>	 
6559	0.002893	kinesin-associated protein 3 (KIFAP3),	NM_014970	Hs.171374	NP_055785
		mRNA /cds=(272,2650)			
		/gb=NM_014970 /gi=18105053		1	`
		/ug=Hs.171374 /len=2997		1	
6569	0.011238	tuberous sclerosis 2 (TSC2), transcript	NM 000548	Hs.90303	NP_066400
		variant 1, mRNA /cds=(19,5442)	_	•	_
		/gb=NM 000548 /gi=10938006		1	4
	}	/ug=Hs.90303 /len=5543	,	1	1
		1 13.00000 /1011-0040		]	
CE74	0.005335	KIAAAA22 protoin (KIAAA422) mDNA	NIM 015016	Hs.26179	NP_056031
6571	0.005325	KIAA0433 protein (KIAA0433), mRNA	NM_015216	IDS.201/9	INF_00003.1
	· .	/cds=(510,4241) /gb=NM_015216		1 .	
	1	/gi=7662117 /ug=Hs.26179 /len=5814		٠.,	1

Genes	Correspoi	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
Spot	p-value	Description	G ne	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
6575	0.030249	epidermal growth factor receptor	NM 004447	Hs.2132	NP_004438
		pathway substrate 8 (EPS8), mRNA	-		=
		/cds=(210,2678) /gb=NM_004447	and the second	[;] .	(
		/gi=4758295 /ug=Hs.2132 /len=3832			
6578	0.017288	tumor protein p53 (Li-Fraumeni	NM 000546	Hs.1846	NP 000537
		syndrome) (TP53), mRNA			
	1	/cds=(252,1433) /gb=NM_000546			
		/gi=8400737 /ug=Hs.1846 /len=2629			
6589	0.003213	cytochrome c, somatic (CYCS), mRNA	NM 018947	Hs.169248	NP 061820
0000	0.000213	/cds=(61,378) /gb=NM_018947	114101_010347	1113.103240	1111 _00 1020
		· · · · · · · · · · · · · · · · · · ·			
		/gi=21361707 /ug=Hs:169248			
0040	0.00000	/len=3990	NIM 000400	11- 40522	ND 000474
6646	0.020388	protein phosphatase 1, regulatory	NM_002480	Hs.16533	NP_002471
		(inhibitor) subunit 12A (PPP1R12A),			
		mRNA /cds=(1,3093) /gb=NM_002480			
:		/gi=4505316 /ug=Hs.16533 /len=4613			
6653	0.004825	ribosomal protein S27	NM_001030	Hs.195453	NP_001021
	}	(metallopanstimulin 1) (RPS27), mRNA			
		/cds=(36,290) /gb=NM_001030			
		/gi=15011937 /ug=Hs.195453 /len=344		<u>.</u>	
					<u> </u>
6654	0:010277	pM5 protein (PM5), mRNA	NM_014287	Hs.439182	NP_055102
		/cds=(1,3669) /gb=NM_014287			
		/gi=10947030 /ug=Hs.439182			
		/len=4182			:
6663	0.020388	PRO0461 protein (PRO0461), mRNA	NM 031268	Hs.25063	
		/gb=NM_031268 /gi=20588827	-		
		/ug=Hs.25063 /len=1100		1	
6678	0.03788		NM 003761	Hs.172684	NP 003752
7,7.		(endobrevin) (VAMP8), mRNA			
		/cds=(54,356) /gb=NM_003761		1.5	
7.5	1 11 4	/gi=14043025 /ug=Hs.172684 /len=702			
6682	0.035177	hypothetical protein FLJ12442	NM_022908	Hs.84753	NP_075059
0002	0.000111	(FLJ12442), mRNA /cds=(412,1974)	522500	1.15.5-7.55	
		/gb=NM_022908 /gi=12597652			
		/ug=Hs.84753 /len=2057		ļ	· , 2,
6695	0.042700	histidine triad nucleotide binding protein	NIM 005340	Hs.256697	NP_005331
0093	0.043799		WIVI_UUDS4U	16.200097	NF_005551
·		1 (HINT1), mRNA /cds=(108,488)			
		/gb=NM_005340 /gi=4885412	<b>}</b>		
0704	0.005055	/ug=Hs.256697 /len=641	\	<del>                                     </del>	
6701	0.005325	inositol 1,4,5-triphosphate receptor,	NM_002223		<b>1</b>
		type 2 (ITPR2)		l	
6702	J 0.006463	mRNA for KIAA0310 protein, partial	AB002308	Hs.5716	1
		cds. /cds=(1,5287) /gb=AB002308			
		/gi=20520992 /ug=Hs.5716 /len=6941	1	1	

		nding To Diff rentially Expressed Gen			<u></u>
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
- 1				No.	No
6703	8.37E-04	nuclear phosphoprotein similar to S.	NM 007062	Hs.172589	NP 008993
		cerevisiae PWP1 (PWP1), mRNA	_		
		/cds=(88,1593) /gb=NM_007062		ere i de la la i i i	
		/gi=5902033 /ug=Hs.172589 /len=1853			
		/gi-5902055 /ug=ns. 1/2569 /ieii=1655		,	
1					
6706	0.023945	adaptor-related protein complex 3,	NM_001284	Hs.80917	NP_001275
	* .	sigma 1 subunit (AP3S1), mRNA			
	- "	/cds=(86,667) /gb=NM_001284			
5 E 4		/gi=4502860 /ug=Hs.80917 /len=1271			
6710	0.001339	clone 23611 mRNA sequence	AF035311	Hs.365646	
		/gb=AF035311 /gi=2661073			
•		/ug=Hs.365646 /len=2146			
6713	0.025911	cDNA FLJ23648 fis, clone COL04718.	AK074228	Hs.375782	
	3.520	/gb=AK074228 /gi=18676772	,		
• 10 11		/ug=Hs.375782 /len=2295		1	
6715	0.00000		NM 014780	Hs.51039	NP 055595
0/15	0.020300	KIAA0076 gene product (KIAA0076),	I == '	I	[MF_022282
	}	mRNA /cds=(87,5183) /gb=NM_014780	-, -, -, -, -, -, -, -, -, -, -, -, -, -	1	
,		/gi=7661893 /ug=Hs.51039 /len=5253		İ	
			<u> </u>	<u> </u>	
6716	0.014599	ribosomal protein L21 (RPL21), mRNA	NM_000982	Hs.431927	NP_000973
	. ;	/cds=(30,512) /gb=NM_000982			
	S 11.	/gi=18104947 /ug=Hs.431927 /len=568			,
6718	9.43E-04	nucleoporin 210 (NUP210), mRNA	NM 024923	Hs.270404	NP_079199
Ÿ	{	/cds=(84,5747) /gb=NM_024923	<del>-</del> -	1 T T T T T T T T T T T T T T T T T T T	
	]	/gi=27477133 /ug=Hs.270404			
	]	/len=7191			
6742	0.002337	septin 6 (SEPT6), transcript variant II,	NM 015129	Hs.90998	NP 665801
0/42	0.002337		14141_012129	Lu2'a0àa0	INF_000001
	• 1	mRNA /cds=(257,1561)			the second of
		/gb=NM_015129 /gi=22035575			
		/ug=Hs.90998 /len=2686			
6744	0.003213	ribosomal protein, large, P0 (RPLP0),	NM_053275	Hs.406511	NP_444505
		transcript variant 2, mRNA	]	ļ	
		/cds=(111,1064) /gb=NM_053275		ļ ·	
		/gi=16933545 /ug=Hs.406511		1	
		/len=1148		ļ	
6749	0.020388	histidyl-tRNA synthetase 2 (HARS2),	NM 080820	Hs.352419	NP_543010
		mRNA /cds=(111,752) /gb=NM_080820			
		/gi=21361784 /ug=Hs.352419		1	
		//en=2396		'	
6750	0.000000		NINA CACCOO	Un 402504	ND 004404
6750	U.U32636	ADP-ribosylation-like factor 6	NM_016638	Hs.103561	NP_061164
		interacting protein 4 (ARL6IP4), mRNA			-
		/cds=(63,719) /gb=NM_016638			
		/gi=7706183 /ug=Hs.103561 /len=952	j	} '	
					<u> </u>
6756	0.008566	KIAA1197 protein, partial cds	AB033023		NP 060493

Genes	Correspon	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
		Description	Gene	Unigene	Protein
•			Accession No.	Accession	Accession
:				No.	No.
6770	0.018784	FK506 binding protein 1A, 12kDa	NM 000801	Hs.380080	NP 463460
		(FKBP1A), transcript variant 12B,			
		mRNA /cds=(104,430) /gb=NM 000801		ļ	
<b>,</b>		/gi=17149837 /ug=Hs.380080			
		/len=1578			
6771	0.007107	surfeit 6 (SURF6), mRNA	NM_006753	Hs.274430	NP 006744
0,,,	0.007 107	/cds=(56,1141) /gb=NM_006753	14111_000733	113.274400	141 _000744
		/gi=19557701 /ug=Hs.274430			1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1
		/len=2329			
6816	0.014500		AF185705		La estada de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la compa
0010	0.014399		AF 103703 		
		gene, exons 13 and 14, and complete			
6925	0.040754	cds	NIM 020070	H- 420004	ND 440000
6825	0.040751	hypothetical protein MGC4400	NM_032679	Hs.130891	NP_116068
		(MGC4400), mRNA /cds=(381,1817)			
L		/gb=NM_032679 /gi=14249251			
0040	0.005044	/ug=Hs.130891 /len=3067			
6846	0.025911	mitogen-activated protein kinase kinase	NM_003188	Hs.7510	NP_663306
		kinase 7 (MAP3K7), transcript variant			
		A, mRNA /cds=(306,2045)			
		/gb=NM_003188 /gi=21735560			
		/ug=Hs.7510 /len=2912			
6847	0.012276	tropomodulin 3 (ubiquitous) (TMOD3),	NM_014547	Hs 22826	NP_055362
,		mRNA /cds=(66,1124) /gb=NM_014547			
		/gi=7657648 /ug=Hs.22826 /len=2072			
6854	7.41E-04	mRNA; cDNA DKFZp434H1235 (from	AL122071	Hs.238927	
		clone DKFZp434H1235); partial cds			
		/cds=(1,476) /gb=AL122071			
		/gi=6102868 /ug=Hs 238927 /len=2499			
6862	0.003563	golgi apparatus protein 1 (GLG1),	NM_012201	Hs.78979	NP_036333
		mRNA /cds=(27,3560) /gb=NM_012201			_
[		/gi=6912389 /ug=Hs.78979 /len=3909		1 .	,
				1	
6875	0.040751	cDNA FLJ12924 fis, clone	AK022986	Hs.38034	
{		NT2RP2004709. /gb=AK022986	}	l	
		/gi=10434694 /ug=Hs 38034 /len=2667			
					1.0
6877	0.001339	hypothetical protein FLJ22625	NM_024715	Hs.106534	NP 078991
		(FLJ22625), mRNA /cds≈(694,1776)			
		/gb=NM 024715 /gi=21362011		d	
]		/ug=Hs.106534 /len=2747		Production in	
6897	0.035177	FLJ14613 fis, clone NT2RP1001113,	AK027519	Hs.105509	NP_065161
] 555,	0.000177	highly similar to Homo sapiens CTL2	, "(0£1 0 10	1.13.100000	-000101
		gene /cds=UNKNOWN /gb=AK027519			[
1		/gi=14042254 /ug=Hs:105509			
J :		/len=3310		<u> </u>	]
لــــــــــــــــــــــــــــــــــــــ		/ICII-00 U	L	L	L

		nding To Differentially Expressed Gen				
Spot	p-value	Description	Gene	Unigene	Protein	
			Accession No.	Accession	Accession	
				No.	No.	
6916	0.040751	cDNA FLJ11174 fis, clone	AK002036	Hs.24359		
		PLACE1007367./gb=AK002036		ļ , , , , , , , , , , , , , , , , , , ,	,	
		/gi=7023674 /ug=Hs.24359 /len=2285				
6920	0.006463	thioredoxin (TXN), mRNA	NM_003329	Hs.432922	NP_003320	
		/cds=(64,381) /gb=NM_003329				
		/gi=4507744 /ug=Hs.432922 /len=501				
6921	0.007807	drebrin 1 (DBN1), transcript variant 2,	NM 080881	Hs.89434	NP 543157	
		mRNA /cds=(611,2566)			7.	
		/gb=NM_080881 /gi=18426912				
		/ug=Hs.89434 /len=3383				
6931	0.009388	Mov10, Moloney leukemia virus 10,	NM 020963	Hs.20725	NP 066014	
- <del></del> -		(mouse) (MOV10), mRNA			_	
		/cds=(71,3082) /gb=NM_020963				
	,	/gi=14211539 /ug=Hs.20725 /len=3328				
*						
6941	0.032636	SWI/SNF related, matrix associated,	NM 003075	Hs.236030	NP 620706	
00-11	0.002000	actin dependent regulator of chromatin,	1,111,_0000.0	1.10.20000		
		subfamily c; member 2 (SMARCC2),				
		transcript variant 1, mRNA				
	]	/cds=(33,3677) /gb=NM_003075				
		/gi=21237804 /ug=Hs.236030				
		/len=4039	202	<b>)</b>		
6942	0.002227	eukaryotic translation elongation factor	NM 001402	Hs.422118	NP 001393	
0942	0.002337		NN _00 1402	NS.422110	INF_001393	
		1 alpha 1 (EEF1A1), mRNA				
		/cds=(63,1451) /gb=NM_001402		J		
		/gi=25453469 /ug=Hs.422118				
0054	0.047004	/len=1837	NIA OAFCAA	U- 255020	ND DECAED	
6951	0.047031	DKFZP434B103 protein	NM_015644	Hs.355920	NP_056459	
		(DKFZP434B103), mRNA				
		/cds=(892,1950) /gb=NM_015644				
, i.i.,		/gi=7661563 /ug=Hs.355920 /len=2553	for the			
000	0.00000	15 H2 12 11 10 15 11 10 15 15 15 15 15 15 15 15 15 15 15 15 15	NA 005000	111- 400007	ND OCEOE	
6984	0.032636	follistatin-like 3 (secreted glycoprotein)	MM_002860	Hs.433827	NP_005851	
		(FSTL3), mRNA /cds=(8,799)			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
		/gb=NM_005860 /gi=5031700				
	1. 1	/ug=Hs.433827 /len=2500				
			<del> </del>		hip of the	
6989	0.032636	transmembrane 9 superfamily member	NM_006405	Hs.91586	NP_006396	
. ,		1 (TM9SF1), mRNA /cds=(35,1855)			1	
		/gb=NM_006405 /gi=21361314		J .	J	
V*		/ug=Hs.91586 /len=2138				
					<u> </u>	
7010	0.002565	hypothetical protein MGC32043	NM_144582	Hs.226138	NP_653183	
		(MGC32043), mRNA /cds=(8,457)	(			
	<b>]</b> , ,	/gb=NM_144582 /gi=21389354				
	1	/ug=Hs.226138 /len=3131		1 '	Į.	

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
	,		Accession No.	Accession	Accession
	İ			No.	No.
7022	0.004367	ribosomal protein S29 (RPS29), mRNA	NM 001032	Hs.539	NP 001023
		/cds=(31,201) /gb=NM_001032			_
		/gi=13904868 /ug=Hs.539 /len=346		la de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición dela composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición de la composición dela composición de la composición del composición de la composición de la composición de la composición de la composición dela composición de la composición dela composición dela composició	
. •		/gi-15504000 /dg-115,555 /icji-540			
7020	0.040754	tubulis alaba ubiquitaua (K ALDLIA 1)	NM 006092	110 224942	NP 006073
7038	0.040751	tubulin, alpha, ubiquitous (K-ALPHA-1),		Hs.334842	INP_000073
		mRNA /cds=(68,1423) /gb=NM_006082	Martin Communication (Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communication Communi		
		/gi=5174476 /ug=Hs.334842 /len=1596			
			l .		<u> </u>
7040	0.006463	PAK2 mRNA, complete cds	AF092132	Hs.284275	
		/cds=(218,1840) /gb=AF092132			
		/gi=5138913 /ug=Hs.284275 /len=4137			
i .	}				
7041	0.032636	oxysterol binding protein-like 1A	NM_080597	Hs.252716	NP 579802
		(OSBPL1A), transcript variant	_		
		OSBPL1B, mRNA /cds=(175,3027)			
15 295		/gb=NM_080597 /gi=19718740			
		/ug=Hs.252716 /len=4165			
7046	0.040754		AB023230	Ha 06427	
7046	0.040751	mRNA for KIAA1013 protein, partial	AB023230	Hs.96427	
		cds. /cds=(1,3189) /gb=AB023230	}		
		/gi=4589675 /ug=Hs.96427 /len=4783			
7052	0.030249	SUMO-1-specific protease (SUSP1),	NM_015571	Hs.27197	NP_056386
		mRNA /cds=(1,3339) /gb=NM_015571			
	}	/gi=7662311 /ug=Hs.27197 /len=4210			1
•					
7083	0.018784	chromosome 14 open reading frame 11	NM_018453	Hs.433269	NP_060923
		(C14orf11), mRNA /cds=(96,797)			
		/gb=NM 018453 /gi=8922092			1
* **		/ug=Hs.433269 /len=1264			
7092	0.022106	chromosome condensation 1 (CHC1),	NM 001269	Hs.84746	NP 001260
1002	0.022100	mRNA /cds=(287,1552)	14141_001203	113.0-11-0	141 -00 1200
		/gb=NM 001269 /gi=20149512	ggatam in a si	<b>;</b>	
7444	0.040070	/ug=Hs.84746 /len=2559	NINA 040454	Hs 250905	ND OFTER
7111	0.012276	hypothetical protein LOC51234	NM_016454	HS.250905	NP_057538
٠.		(LOC51234), mRNA /cds=(72,623)	4		
		/gb=NM_016454 /gi=24475963			
	<u></u>	/ug=Hs.250905 /len=1013	·		P.
7115	0.012276	microtubule-actin crosslinking factor 1	NM_012090	Hs.108258	NP_149033
		(MACF1), transcript variant 1, mRNA		1	
		/cds=(52,16344) /gb=NM_012090		1.	
	1	/gi=15011903 /ug=Hs.108258	[ -	<i>t</i> -	}
	1	/len=17532			
7142	0.011238	eukaryotic translation elongation factor	NM 001402	Hs.422118	NP_001393
., I <del>.,</del> ∠	0.011230	1 alpha 1 (EEF1A1), mRNA	1.111_00 1702	10.722110	1.41 =00 (000)
-	1		la service de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya della companya della companya de la companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della companya della comp	1	
		/cds=(63,1451) /gb=NM_001402			
	1.	//gi=25453469 /ug=Hs.422118	·	1	ŀ
		/len=1837	<u> </u>	1	L

7154		Description	Gene Accession No.	Unig n Acc ssion	Protein Accession
7154			Accession No.		Accession
7154					
7154				No.	No.
	⊩ 0.03788I	hypothetical protein FLJ22169	NM 024085	Hs.323363	NP 076990
	0.007,90	(FLJ22169), mRNA /cds=(380,1720)		1	
		/gb=NM_024085 /gi=13129081		l izana di	
*					
7450	0.007007	/ug=Hs.323363 /len=3509	NINA 000470	11- 472004	NP 002461
7159	0.007807	myosin, heavy polypeptide 3, skeletal	NM_002470	Hs.173084	NP_002461
-		muscle, embryonic (MYH3), mRNA		-	
		/cds=(85,5907) /gb=NM_002470		1	
		/gi=11342671 /ug=Hs.173084		'	
		/len=6032			
7163	0.013394	KIAA0652 gene product (KIAA0652),	NM_014741	Hs.79672	NP_055556
		mRNA /cds=(309,1862)	2	100	
		/gb=NM_014741 /gi=7662225			
		/ug=Hs.79672 /len=4040			
7170	0.003213	ribosomal protein L27 (RPL27), mRNA	NM 000988	Hs.405528	NP 000979
		/cds=(45,455) /gb=NM_000988			
		/gi=17017972 /ug=Hs.405528 /len=513			
7175	0.02700	AGENCOURT 6853421 NIH MGC 99	BQ064669	Hs.380699	
/ 1/3	0.03766		DQ004009	118.300099	
		cDNA clone IMAGE:5926418 5', mRNA			
1		sequence /clone=IMAGE:5926418			
		/clone_end=5' /gb=BQ064669			
		/gi=19893520 /ug=Hs.380699 /len=969			
		[일본 기계 문항 전략 (1442 147 원)			
1 -				L	
7176	0.023945	tumor protein, translationally-controlled	NM_003295	Hs.401448	NP_003286
		1 (TPT1), mRNA /cds=(95,613)			
		/gb=NM_003295 /gi=4507668			
		/ug=Hs.401448 /len=830			
7177	0.032636	aminomethyltransferase (glycine	NM_000481	Hs.102	NP 000472
		cleavage system protein T) (AMT),			_
i s v	1	mRNA /cds=(146,1357)		•	
		/gb=NM_000481 /gi=4502082			
		/ug=Hs.102 /len=2119			
7193	0.022106	heterogeneous nuclear	NM 031157	Hs.376844	NP 112420
1193	0.022100	ribonucleoprotein A1 (HNRPA1),	1917   197	113.370044	
		transcript variant 2, mRNA	1.7		
j-	i .	/cds=(105,1223) /gb=NM_031157			
(		/gi=14043069 /ug=Hs.376844			
		/len=1925		<u> </u>	
7209	0.007807	ribosomal protein L37a (RPL37A),	NM_000998	Hs.296290	NP_000989
		mRNA /cds=(36,314) /gb=NM_000998			
		/gi=16306561 /ug=Hs.296290 /len=392	`	· , .	
			1 1 1 1 1 1 1 1 1	<u>1</u>	<u> </u>
7210	0.047031	dodecenoyl-Coenzyme A delta	NM_001919	Hs.403436	NP_001910
		isomerase (3,2 trans-enoyl-Coenzyme	-		1 - ·
			I .	1	1
		IA isomerase) (DCI) mRNA		1	1
		A isomerase) (DCI), mRNA /cds=(9.917) /db=NM_001919			/
	,	A isomerase) (DCI), mRNA /cds=(9,917) /gb=NM_001919 /gi=4503266 /ug=Hs.403436 /len=1017			1

		nding To Differentially Express d Gen			to-to-	
Spot	p-value	Description	Gene	Unigene	Protein	
			Accession No.	Accession	Accession	
7222	0.032636	REV3-like, catalytic subunit of DNA	NM_002912	No. Hs.115521	No. NP 002903	
1 222	0.032030	polymerase zeta (yeast) (REV3L),		110.110021		
		mRNA /cds=(823,9981)		e german e a g		
		/gb=NM_002912 /gi=4506482				
		/ug=Hs.115521 /len=10919				
7227	0.015895	cytidine monophosphate kinase CMP	AF259961		NP_057392	
		mRNA, (≃UMP-CMP kinase				
		(LOC51727))				
7237	0.018784	protein disulfide isomerase-related	NM_005742	Hs.182429	NP_005733	
		protein (P5), mRNA /cds=(95,1417)				
		/gb=NM_005742 /gi=5031972				
		/ug=Hs.182429 /len=1882				
7238	9.43E-04	pp11741 mRNA, complete cds	AF318323	Hs.382867		
		/cds=(1126,2058) /gb=AF318323			,	
	· ·	/gi=18027737 /ug=Hs.382867		. ,	ĺ	
7020	0.02700	/len=3222 HNC58-1-D7.R cDNA /gb=BG928970	BG928970	Hs.133898	NP 694953	
7239	0.03788	/gi=14323493 /ug=Hs.133898 /len=683	BG926970	IUS. 133090	INP_094955	
	t de la company	/g = 14323493 /ug=Hs. 133696 /ieii=063 				
7241	0.00587	likely ortholog of mouse guanine	NM 018049	Hs.173739	NP 060519	
12-1	0.00507	nucleotide releasing protein x	14101_010043	1113.170700	111 _000010	
		(GNRPX), mRNA /cds=(82,531)				
		/gb=NM_018049 /gi=8922332			ļ	
	1	/ug=Hs.173739 /len=1215				
7245	0.00587	cDNA FLJ90297 fis, clone	AK074778	Hs.405809		
		NT2RP2000447, moderately similar to				
		GOLGIN-95. /cds=(333,728)				
	1.	/gb=AK074778 /gi=22760446		1		
		/ug=Hs.405809 /len=2520		<u> </u>	<u> </u>	
7246	9.43E-04	mRNA for FLJ00012 protein, partial	AK024423	Hs.21051		
	, ,	cds. /cds=(2618,3166) /gb=AK024423			}	
• • • •		/gi=10440354 /ug=Hs.21051 /len=4577				
70.4=	0.00507	100400400	NIA 420242	115 46000	ND COOFEE	
7247	0.00587	hypothetical gene LOC128439	NM_139016	Hs.16936	NP_620585	
•		(LOC128439), mRNA /cds=(109,360)				
		/gb=NM_139016 /gi=20502979 /ug=Hs.16936 /len=1526				
7262	0.001102	LIM and senescent cell antigen-like	NM 004987	Hs.112378	NP 004978	
1202	0.001193	domains 1 (LIMS1), mRNA	1.4141_00-1001	110.112070		
•		/cds=(120,1097) /gb=NM 004987			* *	
		/gi=13518025 /ug=Hs.112378				
		/len=1236				
7293	0.008566	cDNA: FLJ21895 fis, clone HEP03439.	AK025548	Hs.99532	<del>                                      </del>	
		/gb=AK025548 /gi=10438097			* * * * * * * * * * * * * * * * * * * *	
	1	/ug=Hs.99532 /len=2049	1			
	1 .					

Gen's Corresponding To Differentially Expressed Genes in Figure 20 - RA					
Spot	p-value	Description	Gene	Unigen	Protein
	1		Accession No.	Accession	Accession
				No.	No.
7307	0.014599	myeloid/lymphoid or mixed-lineage	NM 018682	Hs.333300	NP 061152
7.		leukemia 5 (trithorax Drosophila)	<del>-</del>		
	1	(MLL5), mRNA /cds=(202,5778)	e an er grote e e		
		/gb=NM_018682 /gi=23503326			
		/ug=Hs.333300 /len=6543		1	
7222	0.004005	BM-017 (=ALEX3)	AF208859		NP 808817
7322				He 12210	
7327	0.014599	tumor endothelial marker 6 (TEM6),	NM_022748	Hs.12210	NP_073585
		mRNA /cds=(93,3710) /gb=NM_022748	*** ***		
		/gi=17511208 /ug=Hs.12210 /len=6702			
			\ <u>\</u>		
7328	0.014599	basic leucine zipper and W2 domains 1	NM_014670	Hs.155291	NP_055485
		(BZW1), mRNA /cds=(81,1340)			
		/gb=NM_014670 /gi=7661849		ļ	
	i i	/ug=Hs 155291 /len=2998			
7343	0.043799	hypothetical protein FLJ12619	NM 030939	Hs.7779	NP_112201
		(FLJ12619), mRNA /cds=(539,1228)			-
		/gb=NM 030939 /gi=21359961			
7 .		/ug=Hs.7779 /len=2444	ing and the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the seco		
7344	0.018784	phosphoprotein regulated by mitogenic	NM 025195	Hs.7837	NP 079471
7544	0.010704	pathways (C8FW), mRNA	14101_025155	113.7007	141 _073471
		/cds=(274,1392) /gb=NM_025195			[
7004	0.00700	/gi=13399327 /ug=Hs.7837 /len=3317	NA 000070	11- 70000	ND 000000
7361	0.03788	SWI/SNF related, matrix associated,	NM_003072	Hs.78202	NP_003063
	2 4 4	actin dependent regulator of chromatin,		est e	
		subfamily a, member 4 (SMARCA4),			
	·	mRNA /cds=(277,5220)			
		/gb=NM_003072 /gi=21071055	* •		
		/ug=Hs.78202 /len=5681			
7368	0.035177	NADH-ubiquinone oxidoreductase	NM_175614	Hs.406062	NP_783313
		subunit B14.7 (NDUFA11), mRNA			
		/cds=(1,426) /gb=NM_175614			
]		/gi=28269680 /ug=Hs.406062 /len=426			
		<b>3</b>			
7376	0.03788	KIAA1805 protein (KIAA1805), mRNA	NM 032434	Hs.294122	NP 115810
ا ا	, 0.00700	/cds=(55,1758) /gb=NM_032434	11111_002101	110.20 1122	
		/gi=24308327 /ug=Hs.294122			ļ
		//len=2873		,	
727	7 0 040704	Abl-philin 2 (APH2), mRNA	NM 032327	Hs.76662	NP_115703
7377	0.018/84		U32321	ITIS. / 000Z	NF_113/03
}		/cds=(159,1049) /gb=NM_032327		,	
l ·		/gi=14150105 /ug=Hs.76662 /len=1545			Ì
			72-12-1		
7386	6   0.012276	mRNA for KIAA1013 protein, partial	AB023230	Hs.96427	
].	1	cds: /cds=(1,3189) /gb=AB023230			1
		/gi=4589675 /ug=Hs.96427 /len=4783			
7387	7 0.002565	ribosomal protein L4 (RPL4), mRNA	NM_000968	Hs.286	NP_000959
ľ		/cds=(57,1340) /gb=NM_000968			
		• • • • • • • • • • • • • • • • • • •	1	1	1

Genes	Correspoi	nding To Differ ntially Expressed Gen	es in Figur 20 -	RA	
		Description	Gene	Unigene	Protein
-	. 1		Accession No.	Accession	Accession
				No	No.
7398	0.013394	laminin, alpha 2 (merosin, congenital	NM_000426	Hs.75279	NP 000417
		muscular dystrophy) (LAMA2), mRNA			<u>,                                    </u>
		/cds=(50,9382) /gb=NM 000426		'	• • • • • • • • • • • • • • • • • • • •
	- ".	/gi=4557708 /ug=Hs.75279 /len=9534		,	
7403	0.006463	ubiquitin-conjugating enzyme E2, J1	NM_016021	Hs.184325	NP_057420
* *		(UBC6 yeast) (UBE2J1), mRNA			
		/cds=(118,1095) /gb=NM_016021			
		/gi=7706311 /ug=Hs.184325 /len=1786			lia i
			<u> </u>	<u></u>	
7404	0.035177	hypothetical protein MGC2827	NM_023940	Hs.8035	NP_076429
		(MGC2827), mRNA /cds=(190,936)			1
		/gb=NM_023940 /gi=13027611			
		/ug=Hs.8035 /len=1988			
7415	0.035177	hypothetical protein FLJ12619	NM_030939	Hs.7779	NP_112201
		(FLJ12619), mRNA /cds=(539,1228)			
		/gb=NM_030939 /gi=21359961			
		/ug=Hs.7779 /len=2444			
7463	0.002337	early growth response 1 (EGR1),	NM_001964	Hs.326035	NP_001955
		mRNA /cds=(271,1902)			
		/gb=NM_001964 /gi=4503492			
		/ug=Hs.326035 /len=3132			<u> </u>
7468	0.018784	hypothetical protein MGC5576	NM_024056	Hs.103834	NP_076961
		(MGC5576), mRNA /cds=(52,804)			
		/gb=NM_024056 /gi=13129025			
7404	0.047000	/ug=Hs.103834 /len=1472	1111 005005		ND 070044
7484	0.017288	RNA processing factor 1 (RPF1),	NM_025065	Hs.287863	NP_079341
		mRNA /cds=(8,1057) /gb=NM_025065			
•		/gi=18643386 /ug=Hs.287863 /len=1336			
7488	0.007803	UI-E-CI1-afw-c-22-0-UI.r1 UI-E-CI1	BM708589	Hs.433343	
7400	0.007093	cDNA clone UI-E-CI1-afw-c-22-0-UI 5',		1115.455545	
	*	mRNA sequence /clone=UI-E-CI1-afw-			
		c-22-0-UI /clone_end=5'			
		/gb=BM708589 /gi=19021847			
•		/ug=Hs.433343 /len=901			
7507	0.043799	KIAA0581 protein, partial cds	AB011153	Hs.41143	NP_056007
, , , ,		/cds=UNKNOWN /gb=AB011153			
		/gi=3043685 /ug=Hs.41143 /len=5147	A	<b> </b> -	
7514	0.040751	cDNA FLJ35055 fis, clone	AK092374	Hs.349303	
		OCBBF2018563./gb=AK092374			
		/gi=21750952 /ug=Hs.349303			
		/len=3817			
7515	0.009388	FLJ11708 fis, clone HEMBA1005123	AK021770		NP_803882
7517		deoxyguanosine kinase (DGUOK),	NM_080916	Hs.432811	NP_550440
		transcript variant 1, nuclear gene	1	1	<u> </u>
		encoding mitochondrial protein, mRNA			
		/cds=(86,919) /gb=NM_080916			
		/gi=18426966 /ug=Hs.432811			
		/len=1144	1	1	1

Genes	Correspoi	nding To Differentially Expressed G n	es in Figure 20 -		
	p-value	Description	G ne	Unigene	Protein
			Accession No.	Accession	Accession
1.				No	No.
7518	0.001878	FLJ21950 fis, clone HEP04949	AK025603		NP 054900
7519		myotubularin related protein 3	NM 021090	Hs.63302	NP 694691
		(MTMR3), transcript variant 3, mRNA			± . ₹
		/cds=(288,3884) /gb=NM_021090		]	
		/gi=23510385 /ug=Hs.63302 /len=5963			
1	}	/g/			
7522	0.004825	TH1-like (Drosophila) (TH1L), mRNA	NM_016397	Hs.5184	NP 057481
1022	0.004020	/cds=(8,1429) /gb=NM_016397	1111_010001	110.0104	111 _001401
		/gi=7705462 /ug=Hs.5184 /len=2130			
7536	0.001330	inhibitor of growth family, member 1	NM 005537	Hs.46700	NP 005528
7330	0.001339	(ING1), mRNA /cds=(433,1701)	14W_000007	1115.40700	141:_003320
		/gb=NM_005537 /gi=19923770			
7544	0.007000	/ug=Hs.46700 /len=2886	NIM 047704	He 201000	ND 060054
7544	0.007,500	oxysterol binding protein-like 10	NM_017784	Hs.321622	NP_060254
		(OSBPL10), mRNA /cds=(382,2676)	•		1
. e. e: L		/gb=NM_017784 /gi=23111057			
		/ug=Hs.321622 /len=3938	11/20/2025		
7549	0.00168	cDNA: FLJ21552 fis, clone COL06322.	AK025205	Hs.6634	
		/gb=AK025205 /gi=10437670			
<u> </u>		/ug=Hs.6634 /len=2045			
7550	7.41E-04	hypothetical protein FLJ20343	NM_017775	Hs.252692	NP_060245
	*	(FLJ20343), mRNA /cds=(19,1524)			
		/gb=NM_017775 /gi=22547158			
		/ug=Hs.252692 /len=2784			
7551	0.017288	hypothetical protein FLJ11021 similar to	NM_023012	Hs.81648	NP_075388
	100	splicing factor, arginine/serine-rich 4			
*.		(FLJ11021), mRNA /cds=(767,1375)			
		/gb=NM_023012 /gi=20127619			
	1	/ug=Hs.81648 /len=1878			
7552	0.013394	interferon, alpha-inducible protein	NM_005101	Hs.432233	NP_005092
		(clone IFI-15K) (G1P2), mRNA			
		/cds=(76,573) /gb=NM_005101	,	1.	
		/gi=4826773 /ug=Hs.432233 /len=634	· '		
7554	0.018784	mRNA IRO40627 full length insert	AL109779		NP_075379
		cDNA clone EUROIMAGE 40627			
7562	0.035177	snail zinc finger protein (SNAI1) gene,	AF155233		
		complete cds			
7567	0.030249	cDNA FLJ34889 fis, clone	AK092208	Hs.125294	
	2.3002.10	NT2NE2017397, weakly similar to			
	· ·	Rattus norvegicus beta-catenin binding	{		
		protein mRNA. /cds=(274,2188)			
	,	/gb=AK092208 /gi=21750743	1		
-		/ug=Hs.125294 /len=2188		•	]. · · · · · · ·
,		749-115, 123254 /ICH-2100		1	
7570	0.022045	Inclu(A) apocific sibopustaces	NIM 002592	Ho 43445	ND 002572
7572	0.023945	poly(A)-specific ribonuclease	NM_002582	Hs.43445	NP_002573
		(deadenylation nuclease) (PARN),	1	· <b> </b> .	5.
		mRNA /cds=(58,1977) /gb=NM_002582		[.	
		/gi=4505610 /ug=Hs.43445 /len=2984		1	
	<u> </u>	<u> </u>	<u> </u>	L	

		nding To Differentially Expressed Gen			<u> </u>
Spot	p-value	Description	Gene	Unigene	Protein
		· · · · · · · · · · · · · · · · · · ·	Accession No.	Accession	Accession
				No.	No.
7573	0.047031	galactokinase 2 (GALK2), mRNA	NM 002044	Hs.129228	NP 002035
		/cds=(21,1397) /gb=NM_002044	· · · · · <u> </u>		
	1.0	/gi=4503896 /ug=Hs 129228 /len=1510	the state of		
		/gi-4505696 /ug-H\$. 129226 /ieii- 1510			
	0.04.500		101 00111		
7581	0.014599	FK506 binding protein 5 (FKBP5),	NM_004117	Hs.7557	NP_004108
		mRNA /cds=(154,1527)			
. *		/gb=NM_004117 /gi=17149847			
		/ug=Hs.7557 /len=3781			
7583	0.014599		BQ939558	Hs.405871	
		cDNA clone IMAGE:6484442 5', mRNA			
		sequence /clone=IMAGE:6484442			
. `.		/clone_end=5' /gb=BQ939558			
gradien.		/gi=22355036 /ug=Hs.405871		}	1 to 1
		/len=1129		9 J 1	
7588	0.030249	prp28, U5 snRNP 100 kd protein (U5-	NM_004818	Hs.184771	NP 004809
		100K), mRNA /cds=(40,2502)	-		-
	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	/gb=NM 004818 /gi=4759277	ing production and		<b>∫</b> , this
7000	0.045005	/ug=Hs.184771 /len=3237	1114 "002"44	11 70500	NE 004 405
7603	0.015895	eukaryotic translation initiation factor	NM_001414	Hs.78592	NP_001405
1		2B, subunit 1 alpha, 26kDa (EIF2B1),			1
*	in a final	mRNA /cds=(11,928) /gb=NM_001414			
**.		/gi=4503502 /ug=Hs.78592 /len=1658			
· .					
7636	7.41F-04	ferritin, light polypeptide (FTL), mRNA	NM_000146	Hs.430150	NP 000137
	', ', ', '	/cds=(189,716) /gb=NM_000146			
		/gi=20149497 /ug=Hs.430150 /len=878			
		/gi-20149497 /ug-Hs.4501507len-676			
7050	0 000045		<b>111.1 0000.10</b>		ND GOOGG
7659	0.003213	ubiquitination factor E4B (UFD2 yeast)	NM_006048	Hs.24594	NP_006039
		(UBE4B), mRNA /cds=(86,3994)			
	4 7 4 7	/gb=NM_006048 /gi=5174482			
		/ug=Hs.24594 /len=5314		1	1
7663	0.022106	cDNA FLJ10131 fis, clone	AK000993	Hs.274128	
		HEMBA1003041. /gb=AK000993			
		/gi=7021996 /ug=Hs.274128 /len=2065			1
•	1	/gj=702   550 /dg=113:274120 /iCi1=2005	. •		
7666	0.000000	EL 144102 for close MANMA 4000040	AK004464	110 204044	<del> </del>
7666	0.032030	FLJ14102 fis, clone MAMMA1000940	AK024164	Hs.301811	
. •		/cds=UNKNOWN /gb=AK024164			
		/gi=10436477 /ug=Hs.301811			1
		/len=1878		<u> </u>	<u> </u>
7673	0.032636	hypothetical protein FLJ10970	NM_018286	Hs.173233	NP_060756
		(FLJ10970), mRNA /cds=(229,633)			1 -
	3	/gb=NM_018286 /gi=8922795			1
		/ug=Hs.173233 /len=1670			1
7000	0.040704		NIM OCCOSO	110 470404	ND FORFOR
7686	U.U18784	protein tyrosine phosphatase, receptor	NM_002838	Hs.170121	NP_563580
		type, C (PTPRC), transcript variant 1,	].		1
		mRNA /cds=(93,4007) /gb=NM_002838		{ · · · · · · · · · · · · · · · · · · ·	1
		/gi=18641346 /ug=Hs.170121			
	4	/len=5026	I	1	1

		nding To Differentially Expr ssed Gen		RA .	<u>.</u>
Spot	p-value	Description	Gen	Unigene	Protein
			Accession No.	Accession No.	Accession No.
7690	0.020388	emopamil binding protein (sterol	NM_006579	Hs.75105	NP_006570
		isomerase) (EBP), mRNA			
		/cds=(112,804) /gb=NM_006579	. 10 1		
		/gi=5729809 /ug=Hs.75105 /len=1073			
7695	0.011238	FLJ31548 fis, clone NT2RI2001017	AK056110	Hs.61712	NP 002601
, 000	0.011200	/cds=UNKNOWN /gb=AK056110	7 (1, 0,000 ) 7 (0,000)	110.01112	
		/gi=16551424 /ug=Hs.61712 /len=2054		( )	
		/gi=1033.1424./ug=113.017.12./ieii=2034			
7704	0.007807	solute carrier family 35 (CMP-sialic acid	NM 006416	Hs.82921	NP 006407
1104	0.007607		MINI_0004 10	115.02321	NF_000407
		transporter), member 1 (SLC35A1),		<b>.</b>	
		mRNA /cds=(28,1041) /gb=NM_006416			
		/gi=20149579 /ug=Hs.82921 /len=1883			
7700	0.00004		NINA 000500	11- 70570	ND 445000
7708	0.003947	histidine triad nucleotide binding protein	NM_032593	Hs.70573	NP_115982
		2 (HINT2), mRNA /cds=(31,522)	kang and a		
		/gb=NM_032593 /gi=14211922			
		/ug=Hs:70573 /len=632			
7710	0.022802	cDNA: FLJ21531 fis, clone COL06036.	AK025184	Hs.102941	*/, * * * *
		/gb=AK025184 /gi=10437647			
		/ug=Hs.102941 /len=2671			
7711	0.03788	death inducer with SAP domain DIS	AF465616	Hs.183779	NP_060707
	1	mRNA, complete cds /cds=(120,3572)		Į	
	1	/gb=AF465616 /gi=27497117			
		/ug=Hs.183779 /len=3856			
7719	5.79E-04	endothelial differentiation,	NM_057159	Hs.75794	NP_476500
		lysophosphatidic acid G-protein-			-
		coupled receptor, 2 (EDG2), transcript			2.
		variant 2, mRNA /cds=(394,1488)			
		/gb=NM 057159 /gi=16950637			
		/ug=Hs.75794 /len=2732			
7738	0.018784	te65d01.x1 Soares NFL T GBC S1	Al377292	Hs.410753	- 1
	]	cDNA clone IMAGE:2091553 3', mRNA			1
•		sequence /clone=IMAGE:2091553		1	
		/clone_end=3' /gb=Al377292	le di e		
		/gi=4187145 /ug=Hs.410753 /len=238			1
		/gi 10/ 1-0/ug-119.410/00/ici1-200	l	• .	
7739	0.040751	hypothetical protein MGC12458	NM_032328	Hs.330664	NP 115704
1100	0.040751	(MGC12458), mRNA /cds=(30,518)	11111_002020	1 13.000004	- 10704
		,			
		/gb=NM_032328 /gi=14150107	:		¥
7710	0.000500	/ug=Hs.330664 /len=1026	NINA 040040	110 000040	ND 020240
7740	0.003563	tripartite motif-containing 32 (TRIM32),	NM_012210	Hs.236218	NP_036342
	,	mRNA /cds=(134,2095)			
	1	/gb=NM_012210 /gi=15208649		1	
	i .	/ug=Hs.236218 /len=3160		1 .	1

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gen	Unigene	Prot in
			Acc ssion No.	Accession	Accession
				No.	No.
7741	0.002602	major histocompatibility complex, class	NM 022555	Hs.308026	NP 072049
		II, DR beta 3 (HLA-DRB3), mRNA			_
		/cds=(41,841) /gb=NM_022555			[ · · · ·
		/gi=18641371 /ug=Hs.308026			
		/len=1158			•
7746	0.014599	PHD finger protein 3 (PHF3), mRNA	NM 015153	Hs.78893	NP_055968
	0.011000	/cds=(28,6147) /gb=NM_015153	11111_010100	11.0.70000	-000000
2 1		/gi=7662017 /ug=Hs.78893 /len=6948			
7760	0.02801	hypothetical protein FLJ20651	NM 017919	Hs.200332	NP 060389
7700	0.02001	(FLJ20651), mRNA /cds=(86,994)	14141_017313	113.200332	141 _000303
		/gb=NM_017919 /gi=8923603		- '	
2		/ug=Hs.200332 /len=2678	9		
7764	0.033636	aprataxin (APTX), transcript variant 1,	NM 175073	Hs.14394	ND 779242
1104	J.0.032030	mRNA /cds=(153,1181)		11 15. 14084	NP_778243
		/gb=NM 175073 /gi=28329435			
٠.					· ·
7774	0.00507	/ug=Hs.14394 /len=2086	NUL 000040	11. 004040	ND 440007
7771	0.00587	hypothetical protein FLJ14855	NM_033210	Hs.224843	NP_149987
		(FLJ14855), mRNA /cds=(262,1896)			
		/gb=NM_033210 /gi=21361856			
		/ug=Hs:224843 /len=3290			
7774	0.004367	leucine-rich repeat-containing 5	NM_018103	Hs.44672	NP_060573
		(LRRC5), mRNA /cds=(917,2965)		· · · · · · · · · · · · · · · · · · ·	
	1	/gb=NM_018103 /gi=24431980			:
		/ug=Hs.44672 /len=3338			
7775		fibronectin gene ED-A region	X07718		
7790	0.03517	EST(zt89c05.r1 Soares testis NHT	AA398038		NP_004632
·		clone 729512 5')			
7802	0.020388	EST 380589 MAGE resequences,	AW968513		NP_057251
		MAGJ cDNA= (xj42h09.x1			
		Soares_NFL_T_GBC_S1)=( tt93e04.x1	}		
		NCI CGAP Pr28			
		)=(Soares_fetal_heart_NbHH19W)=(			].
		Soares melanocyte 2NbHM )			
7810	0.017755	EST(of65b08.s1 NCI_CGAP_Co8 clone	AA857635	1 2 2 2	
		IMAGE:1435191 3')			
7812	0.02801	EST(nw29b03.s1 NCI_CGAP_GCB0	AA714698	<del></del>	<del>                                     </del>
	0.,90,	clone IMAGE:1241837 contains Alu			
•	. ·	repeat)		ļ	
7826	0.004367	yh68a05.s1 Soares placenta Nb2HP	R32301	Hs.386871	
, 520	0.504001	cDNA clone IMAGE:134864 3', mRNA	1.102001	1.13.33337	
•		seguence /clone=IMAGE:134864	ļ ·		
		/clone_end=3' /gb=R32301 /gi=788144	1	1.	-
				[ .	
7000	0:014500	/ug=Hs.386871 /len=246	DV404020	Un 200400	<del> </del>
7828	0.0,14599	BX101939 Soares infant brain 1NIB	BX101939	Hs.269499	
	:	cDNA clone IMAGp998C11163, mRNA	1	<b>{</b> .	ł
		sequence			, .
		/clone=IMAGp998C11163_;_IMAGE:36		* *	
	1	364 /gb=BX101939 /gi=27831516	-		
•	i	/ug=Hs.269499 /len=493	1 .		1

		nding To Differentially Expressed G n			 
Spot	p-value	Description	Gen	Unigen	Protein
			Accession No.	Acc ssion	Accession
				No.	No.
7843	0.032636	EST(qu23h09.x1 NCI_CGAP_Br12	Al284640		
· .	لأنج ما ما ما م	clone IMAGE:1965665 contains Alu			
		repeat)	* .		
7850	0.025911	hypothetical protein FLJ10006	NM_017969	Hs.5570	NP_060439
		(FLJ10006), mRNA /cds=(261,2720)		25 . 14	
	] .	/gb=NM 017969 /gi=24308176			
		/ug=Hs.5570 /len=2950		`	
7859	0.010277	AJ318805 adipose tissue cDNA clone	AJ318805	Hs.86538	
		2040, mRNA sequence /clone=2040			
	}	/gb=AJ318805 /gi=18141682			} .
		/ug=Hs.86538 /len=5223			5.00
7868	0.015895	EST(yx98h12.s1 Soares melanocyte	N24829		
.000	0.0.000	2NbHM cDNA clone IMAGE:269831 3')		-	
• • • • • • •		(2.10) (M 6.514) ( 6.616 MA (6.2.2000) ( 6.7)			
7869	0.004367	hypothetical protein FLJ20534	NM 017867	Hs.44344	NP 060337
7000	0.004001	(FLJ20534), mRNA /cds=(21,1061)	11111_011001	1113.44044	
		/gb=NM 017867 /gi=8923502			
ta Table 1 style		/ug=Hs.44344 /len=1188			
7878	0.02799	EST(RC1-BT0721-050400-011-a06	BE090738	-	
1010	0.03766	BT0721)	DE090730		
7005	0.002562		NM 030040	Hs.192822	NP 112211
7885	0.003563	protein phosphatase 1, regulatory	NM_030949	IUS. 195055	INP_112211
	<b>].</b>	(inhibitor) subunit 14C (PPP1R14C),			
		mRNA /cds=(97,594) /gb=NM_030949			
-		/gi=19311005 /ug=Hs.192822	a ser ja a sa sa sa		
		/len=2133	1.75==555	10-0-0-1	
7888	0.003213	cDNA FLJ31107 fis, clone	AK055669	Hs.405954	
•		IMR322000152./gb=AK055669			
-	1	/gi=16550452 /ug=Hs.405954			
	<u> </u>	/len=2250			
7892	0.008566	EST(ze97h03.s1 Soares fetal heart	AA026679		
	]	NbHH19W clone 366965 3' contains			
	<u> </u>	Alu repeat)			1
7913	3.04E-04	EST (Soares breast 2NbHBst cDNA	R71816		
		clone IMAGE:155622 5')		<u>                                     </u>	
7936	0.03788	UI-H-BI4-apg-d-10-0-UI.s1	BF509764	Hs.439798	, , , , ,
		NCI_CGAP_Sub8 cDNA clone		ł	
		IMAGE 3087402 3', mRNA sequence			
	1 .	/clone=IMAGE:3087402 /clone_end=3'			
		/gb=BF509764 /gi=11593062			
•	1	/ug=Hs.439798 /len=1099			ĺ
•	1				
7941	0.00587	EST (EST370348 MAGE resequences,	AW958278	<del></del>	NP 112420
. • • •	]	MAGE cDNA)		-}	
7944	0.017288	EST67047 Fetal lung III Homo sapiens	AA358105	<del>                                     </del>	1
, , , , ,	0.011200	cDNA 3' end	7, 9, 10, 90, 100	1	]
7945	0.047024	hypothetical protein FLJ14708	NM 032827	Hs.135569	NP_116216
1 340	0.047031	1 · · · · · · · · · · · · · · · · · · ·	NIVI_032021	1115.133309	110210
		(FLJ14708), mRNA /cds=(198,1163)		1	1
	1	/gb=NM_032827 /gi=14249529			
	I	/ug=Hs.135569 /len=2405		1	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s

Gen s Corresponding To Differentially Expressed Genes in Figure 20 - RA						
Spot	p-value	Description	Gene	Unigene	Protein	
			Accession No.	Accession	Accession	
				No	No.	
7947	0.010277	EST (AV690707 GKC H sapiens cDNA	AV690707		NP_004577	
		ranger (m. 1964). Programmer (m. 1964).				
7948	0.043799	mRNA; cDNA DKFZp686J072 (from	AL832207	Hs.255938		
		clone DKFZp686J072) /gb=AL832207		l . "		
		/gi=21732752 /ug=Hs.255938				
		/len=7028		•		
7950	0.006463	cDNA sequence FLJ13553 fis, clone	AK023615		NP_006818	
, 000	0.000	PLACE1007454		Marie Barrier		
7956	0.049079	EST(zu24g05.s1 Soares_NhHMPu_S1	AA421768			
, 500	0.043073	cDNA clone IMAGE:738968 3' similar	70.12.1700			
	,	to gb:Z13009_rna1 EPITHELIAL-			1 16	
		CADHERIN PRECURSOR; contains Alu		10 m		
•						
	[	repetitive element;)				
7007	0.040077	Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Harris Ha	1100004		en kirjer en er en en en en en en en en en en en en en	
7967		unknown mRNA	U00684	· · · · · · · · · · · · · · · · · · ·		
7977	0.02801	pregnancy-induced growth inhibitor	AF334780			
		OKL38 gene, partial cds				
7978	0.004825	chromosome 6 open reading frame 11	NM_005452	Hs.17930	NP_005443	
		(C6orf11), mRNA /cds=(54,1886)				
. '		/gb=NM_005452 /gi=14550417				
<u> </u>		/ug=Hs.17930 /len=2074				
7981	0.013392	mRNA for KIAA1691 protein, partial	AB051478	Hs.94761		
		cds. /cds=(78,1754) /gb=AB051478				
	1	/gi=20521967 /ug=Hs.94761 /len=4816				
7986	0.013394	procollagen-proline, 2-oxoglutarate 4-	NM_000918	Hs.410578	NP_000909	
		dioxygenase (proline 4-hydroxylase),			T	
		beta polypeptide (protein disulfide				
	1	isomerase; thyroid hormone binding	1. 1:			
1.5		protein p55) (P4HB), mRNA				
		/cds=(45,1571) /gb=NM_000918	}.			
		/gi=20070124 /ug=Hs 410578				
		/len=2438				
7987	0.030240	cervical cancer 1 protooncogene	NM_015416	Hs.75884	NP_056231	
1301	0.000249	(DKFZP586A011), mRNA	1,414, 0,104,10	1.10.7.000#	1.41 _000201	
		/cds=(9,1091) /gb=NM 015416		1		
. •	1	/gi=21166356 /ug=Hs:75884 /len=2118	,			
		/yi=21100330 /uy=i18:/3004 /ieii=2116	<b>l</b> :			
7000	0.002000	hypothetical protein EL 142010	NM_022780	Uc 75277	ND 072617	
7988	0.002096	hypothetical protein FLJ13910	INIVI_U22/80	Hs.75277	NP_073617	
		(FLJ13910), mRNA /cds=(99,1274)	1	Î		
	]	/gb=NM_022780 /gi=19923839		1		
		/ug=Hs.75277 /len=3239	1.0000/05	ļ		
7992	0.018784	l e e e e e e e e e e e e e e e e e e e	AB060197	1 .		
		insert sequence				
7997	0.043799	Williams-Beuren syndrome	NM_022479	Hs.7981	NP_071924	
		chromosome region 17 (WBSCR17),	,		· ·	
		mRNA /cds=(1,1797) /gb=NM_022479			1	
		/gi=22538494 /ug=Hs.7981 /len=3298			1	
	1	1 <del>-</del>	1	1	1	

		nding To Differentially Expressed Gen			<del> </del>
Spot	p-value		Gene	Unigene	Protein
			Accession No.	Accession	Accession
			,	No.	No
8003	0.015895	transcription factor 4 (TCF4), mRNA	NM 003199	Hs.326198	NP_003190
	1777	/cds=(200,2203) /gb=NM_003199	_	}	T -
٠.		/gi=4507398 /ug=Hs.326198 /len=2500		***	
		191-4007000 74g		-	
0004	0.025477	topoisomerase (DNA) I (TOP1), mRNA	NM 003286	Hs.317	NP 003277
8004	0.035177		NNI_003286	HS.317	NP_003277
	1	/cds=(247,2544) /gb=NM_003286		ļ	
	]	/gi=19913404 /ug=Hs.317 /len=3734	+ 1		
<u> </u>				<u> </u>	
8017	0.012276	secreted frizzled-related protein 5	NM_003015	Hs.279565	NP_003006
	2.3	(SFRP5), mRNA /cds=(182,1135)		1	
	1	/gb=NM_003015 /gi=8400734			
	)	/ug=Hs.279565 /len=1905			
8022	0.03788	eukaryotic translation elongation factor	NM 001402	Hs.422118	NP 001393
عبد	5.55,50	1 alpha 1 (EEF1A1), mRNA		1	
4 +1,		/cds=(63,1451) /gb=NM_001402		,	1
والراجلين	1	I		1	
		/gi=25453469 /ug=Hs.422118			
		/len=1837	1-2-1-		1
8027	0.02801	homeodomain protein (OG12) mRNA,	AF022654	Ţ	NP_006875
		complete cds	<u> </u>	<u> </u>	
8039	0.012276	BX090877 NCI_CGAP_Ut3 cDNA	BX090877	Hs.359704	
		clone IMAGp998N165642;			
1		IMAGE:2278479, mRNA sequence			
		/clone=IMAGp998N165642_; IMAGE:2			
•		278479 /gb=BX090877 /gi=27824565			<b>1</b>
	1	/ug=Hs.359704 /len=471			
8040	0.044220	zinc finger protein 331; zinc finger	NM_018555	Hs.147644	NP 061025
0040	0.011238	1	[MM_0.19999	ITS. 147044	[NP_001025
		protein 463 (ZNF361), mRNA			
		/cds=(660,2051) /gb=NM_018555	1	[*	1
	{	/gi=20127571 /ug=Hs.147644		ĺ	1
	<u> </u>	/len=2196	L	<u> </u>	
8042	0.01045	thioredoxin-like 2 (TXNL2), mRNA	NM_006541	Hs.42644	NP_006532
	ĺ	/cds=(5,1012) /gb=NM_006541			[
	1	/gi=5730103 /ug=Hs.42644 /len=1942			
8046	0.011238	cDNA FLJ10423 fis, clone	AK001285	Hs.106909	
•		NT2RP1000259./gb=AK001285			
		/gi=7022444 /ug=Hs.106909 /len=1837		1	
,	1	100000 Nen-1007			
9050	0.005044	hypothetical protein El 192557	NM 024713	He 106101	ND 070000
8050	0.025911	hypothetical protein FLJ22557	INIVI_U24713	Hs.106101	NP_078989
.*		(FLJ22557), mRNA /cds=(87,1001)	<b>1</b>		
		/gb=NM_024713 /gi=13376012	1		
	<u> </u>	/ug=Hs 106101 /len=2676			1
8051	0.009388	cDNA FLJ38352 fis, clone	AK095671	Hs.376222	1
		FEBRA1000148. /gb=AK095671		1.	1
		/gi=21754980 /ug=Hs.376222	1	1	1
	1	/len=2233	1	1	1
8052	0.035177	hypothetical protein MGC14697	NM 032747	Hs.171625	NP_116136
3002	3.303177	(MGC14697), mRNA /cds=(264,440)	1.111_0021 41	1	1
*	1			1	1
	1	//gb=NM_032747 /gi=14249375	1		
	-l	/ug=Hs.171625 /len=581	1	1	1

		nding To Differentially Expressed Gen			
Spot	p-valu	Description	Gene Accession No.	Unigene Accession	Protein Accession
				No.	No.
8059	0.009388	myotubularin related protein 2	NM_016156	Hs.181326	NP_057240
	- aranian (	(MTMR2), mRNA /cds=(342,2273)			
		/gb=NM_016156 /gi=20357517			
<u> </u>		/ug=Hs.181326 /len=4681			
8060	0.022106	hypothetical protein HSPC155	NM_016406	Hs.177507	NP_057490
		(HSPC155), mRNA /cds=(241,744)	*	,	
÷.		/gb=NM_016406 /gi=7705480		}	<b>.</b>
		/ug≂Hs.177507 /len=1137			
8066	3.47E-04	clone IMAGE:4551222, mRNA	BC017324	Hs.98710	
		/gb=BC017324 /gi=23398507		<b>}</b>	
		/ug=Hs.98710 /len=2031			
8067	8.37E-04	zinc finger protein 289, ID1 regulated	NM_032389	Hs.256310	NP_115765
		(ZNF289), mRNA /cds=(9,1574)			1
		/gb=NM_032389 /gi=14150222			
		/ug=Hs.256310 /len=2753			
8068	0.001339	hypothetical protein FLJ10726	NM_018195	Hs.268561	NP_060665
		(FLJ10726), mRNA /cds=(176,622)			
		/gb=NM_018195 /gi=8922622		1	
		/ug=Hs.268561 /len=2800			
8069	5.79E-04	Similar to nuclear localization signals	BC016981	Hs.244624	
		binding protein 1, clone MGC:21810			
• •		IMAGE:4183576, mRNA, complete cds			
		/cds=(58,375) /gb=BC016981			
		/gi=16877469 /ug=Hs.244624		1	
		/len=2059			
8085	0.013394	dimerization cofactor of hepatocyte	NM_032151	Hs:150186	NP_115527
		nuclear factor 1 ( HNF1) from muscle			
2 !	1.	(DCOHM), mRNA /cds=(21,413)		1	1.
		/gb=NM_032151 /gi=14149824	.,		
**.		/ug=Hs 150186 /len=5641			
8091	0.02801	latrophilin 1 (LPHH1), mRNA	NM 012302	Hs.24212	NP 036434
		/cds=(217,4428) /gb=NM_012302		1	
		/gi=6912463 /ug=Hs.24212 /len=5479			
8119	9.43E-04	mRNA for KIAA1949 protein.	AB075829	Hs.101150	
		/cds=(1149,3137) /gb=AB075829		<b>,</b>	<b>)</b> .
		/gi=18916754 /ug=Hs.101150			
		/len=4015			
8120	0.022106	centrosome-associated protein 350	NM_014810	Hs.92200	NP_055625
		(CAP350), mRNA /cds=(168,9521)	-		1
		/gb=NM_014810 /gi=18378734			
•		/ug=Hs.92200 /len=11740			
8125	0.001339	mitochondrial ribosomal protein S17	NM_015969	Hs.44298	NP_057053
	1	(MRPS17), nuclear gene encoding		1	
·					
· .					
		mitochondrial protein, mRNA /cds=(31,423) /gb=NM_015969			

		nding To Differentially Expressed Gen			<u> </u>
Spot	p-value	Description	Gene	Unigen	Protein
			Accession No.	Accession No.	Accession No.
8130	0.004825	hypothetical protein FLJ31951	NM 144726	Hs.349306	NP 653327
		(FLJ31951), mRNA /cds=(28,2103)			
		/gb=NM_144726 /gi=21389514			
		/ug=Hs.349306 /len=3362			·
8133	2.03E-04	ADP-ribosylation factor guanine	NM_015310	Hs.6763	NP 056125
0.00		nucleotide factor 6 (EFA6R), mRNA			
		/cds=(53,1657) /gb=NM_015310			
		/gi=7662395 /ug=Hs.6763 /len=6722			
8151	0.047031	cDNA: FLJ23115 fis, clone LNG07933.	AK026768	Hs.98728	
<b></b> ,		/gb=AK026768 /gi=10439696			
		/ug=Hs.98728 /len=1917			
÷					
8152	0.025911	COP9 constitutive photomorphogenic	NM_006837	Hs.380969	NP-006828
	, , , , , , ,	subunit 5 (Arabidopsis) (COPS5),	<del>-</del>		
		mRNA /cds=(121,1125)			
± .		/gb=NM_006837 /gi=5803045			
		/ug=Hs.380969 /len=1277			
8153	0.023945	hypothetical protein DKFZp586E1923	NM 020425	Hs.70769	NP 065158
		(DKFZP586E1923), mRNA			
		/cds=(1,294) /gb=NM_020425			
*		/gi=10092684 /ug=Hs.70769 /len=294			1
8161	0.00587	cDNA: FLJ22930 fis, clone KAT07255.	AK026583	Hs.90790	
		/gb=AK026583 /gi=10439467			
7.		/ug=Hs:90790 /len=1600			
					1
8163	0.006463	NADH dehydrogenase (ubiquinone) 1	NM 002491	Hs.109760	NP 002482
	1	beta subcomplex, 3, 12kDa (NDUFB3),	_		_
	l	mRNA /cds=(253,549) /gb=NM_002491		1	
		/gi=4505360 /ug=Hs.109760 /len=693	Contract of the second		1
8167	0.001878	component of oligomeric golgi complex	NM 031431	Hs.13392	NP_113619
		3 (COG3), mRNA /cds=(102,2588)	_		T -
		/gb=NM 031431 /gi=14591930			<b>[</b> ]
•		/ug=Hs 13392 /len=4500		1	<b>,</b>
				l'	1
8168	0.003947	hypothetical protein FLJ23221	NM_024579	Hs. 18397	NP_078855
	}	(FLJ23221), mRNA /cds=(24,419)			
		/gb=NM_024579 /gi=13375757			
		/ug=Hs.18397 /len=519			<u> </u>
8178	0.013394	TAF9-like RNA polymerase II, TATA	NM_015975	Hs.171723	NP_057059
		box binding protein (TBP)-associated			
		factor, 31kDa (TAF9L), mRNA			
	1.	/cds=(91,846) /gb=NM 015975	<b>1</b>		1
		/gi=21166377 /ug=Hs.171723	(		
		/len=2734	1	1	1

Genes	Correspon	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
	p-value	Description	Gene	Unigen	Protein
•			Accession No.	Accession	Accession
				No.	No.
8182	0.030249	general transcription factor IIH,	NM 001515	Hs.191356	NP_001506
0.02	0.0002.0	polypeptide 2, 44kDa (GTF2H2), mRNA	TIM_00 10 10	1113.101000	1111 _00 1000
		/cds=(1,1188) /gb=NM_001515			
	,				
i.		/gi=6681761 /ug=Hs.191356 /len=1188			
0404	0.044500	-DNA FILIOMOS 6	44654007		1.00.00
8184	0.014599	cDNA FLJ30135 fis, clone	AK054697	Hs.34906	NP_776170
		BRACE2000061. /gb=AK054697		· .	
ja na	100	/gi=16549295 /ug=Hs.34906 /len=2024			
1 1 9					
8186	0.006463	Arkadia (ARK), mRNA /cds=(374,1486)	NM_017610	Hs.12504	NP_060080
		/gb=NM_017610 /gi=24111229			
		/ug=Hs.12504 /len=3010			
¥ 7,					
8187	0.006508	calcium channel, voltage-dependent, L	NM_000719	Hs.89925	NP 000710
		type, alpha 1C subunit (CACNA1C),	_		- No. 1
		mRNA /cds=(266,6682)			
, ,		/gb=NM_000719 /gi=27597079			
		/ug=Hs.89925 /len=8374			1
8188	0.047031	hypothetical protein FLJ20287	NM 017746	Hs.26369	NP_060216
	9.0 00 .	(FLJ20287), mRNA /cds=(132,2921)		110.2000	111 _000210
		/gb=NM_017746 /gi=8923268			
		/ug=Hs.26369 /len=3043			1
8190	0.010277		AF258591	LIA 204204	ND COOSAA
0190	0.010277	PP784 mRNA, complete	AF256591	Hs.284281	NP_689514
-	• •	cds/cds=(198,581) /gb=AF258591			
e George		/gi=10834727 /ug=Hs.284281/len=2145	a a a		
3		= XM_052614.3			
8205	0.015895	histone H2A.F/Z variant (H2AV),	NM_138635	Hs.301005	NP_619541
	• • • • • •	transcript variant 2, mRNA			
		/cds=(172,516) /gb=NM_138635	la de la companya de la companya de la companya de la companya de la companya de la companya de la companya de La companya de la companya de la companya de la companya de la companya de la companya de la companya de la co		
		/gi=20357598 /ug=Hs.301005			
		/len=3453			<u>"                                    </u>
8222	0.018784	, , , , , , , , , , , , , , , , , , , ,	NM_002624	Hs.288856	NP_665904
,		1, mRNA /cds=(36,500)			1
	".	/gb=NM_002624 /gi=22202632			
		/ug=Hs.288856 /len=661			
8224	0.008566	hypothetical protein, MGC:7199	NM 138459	Hs.289008	NP 612468
		(LOC116150), mRNA /cds=(174,1055)	[ -		· <del>-</del>
		/gb=NM_138459 /gi=20270242		j ',	}
. "		/ug=Hs 289008 /len=2645			
8226	0.004367	splicing factor 3a, subunit 1, 120kDa	NM_005877	Hs.406277	NP_005868
		(SF3A1), mRNA /cds=(132,2513)	,_,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		
	. •	/gb=NM_005877 /gi=20127483			
		/ug=Hs.406277 /len=2944			
8227	0.012276	hypothetical protein FLJ20628	NIM 017010	Ho 22256	ND 060300
0221	0.012270	1 * '	NM_017910	Hs.32356	NP_060380
	· .	(FLJ20628), mRNA /cds=(23,1456)			ļ
	'	/gb=NM_017910 /gi=13435382			
		/ug=Hs.32356 /len=1846	L	l	L

Genes	Correspo	nding To Differentially Express d Gen	es in Figure 20 ·	- RA	
	p-value	Description	Gene	Unigene	Protein
- :			Accession No.	Accession	Accession
				No.	No.
8229	0.018784	hepatitis C virus core-binding protein 6	NM_023934	Hs.283674	NP_076423
· · · · · · · · · · · · · · · · · · ·		(HCBP6), mRNA /cds=(114,683)			<u>-</u>
		/gb=NM_023934 /gi=24371247			
		/ug=Hs.283674 /len=1157			
8230	0.007807	mRNA for KIAA0592 protein, partial	AB011164	Hs.439367	
i j		cds. /cds=(1,4062) /gb=AB011164			<u>.</u>
		/gi=3043707 /ug=Hs.439367 /len=4623			
				· .	
8261	0.012276	cDNA FLJ10878 fis, clone	AK001740	Hs.15144	NP_064715
is,"		NT2RP4001893, highly similar to		1	<b>√</b>
	}	mRNA; cDNA DKFZp564O043.			1
2	]	/gb=AK001740 /gi=7023191			
		/ug=Hs.15144 /len=2599			
8274	8.37E-04	mRNA; cDNA DKFZp451L0319 (from	AL833086	Hs.43213	
		clone DKFZp451L0319) /gb=AL833086			1.
		/gi=21733677 /ug=Hs 43213 /len=4614			
			<u>[</u>		1
8277	0.009388	checkpoint with forkhead and ring	NM_018223	Hs.23794	NP_060693
• • • •		finger domains (CHFR), mRNA			
		/cds=(65,1936) /gb=NM_018223	i		1
		/gi=8922674 /ug=Hs 23794 /len=3138			
8309	0.030249	hypothetical protein FLJ14906	NM_032859	Hs.183528	NP_116248
		(FLJ14906), mRNA /cds=(131,736)			
		/gb=NM_032859 /gi≈14249591			
		/ug=Hs.183528 /len=2492		<u> </u>	
8311	0.043799	clone IMAGE:5295441, mRNA	BC043222	Hs.405253	
		/gb=BC043222 /gi=28175025			i.
\$1.5 4.5		/ug=Hs.405253 /len=2712			
8316	0.02801	clone IMAGE:4794726, mRNA	BC042028	Hs.367688	
		/gb=BC042028 /gi=27469506		1	
		/ug=Hs.367688 /len=1479			
8324	0.043799	hypothetical protein (FLJ10562 fis,	AK001424		NP_057116
		clone NT2RP2002701)			di di
8338	0.013394	cDNA FLJ14181 fis, clone	AK024243	Hs.130874	
	}	NT2RP2004300. /gb=AK024243			}
		/gi=10436570 /ug=Hs.130874		,	.]
		/len=4411			<u> </u>
8358	0.032636	EST from cd34_stem cells Human	AF150123		
		sapiens cDNA clone CBCALE06		ļ	<u> </u>
8363	0.02801	hypothetical protein FLJ14753	NM_032558	Hs.13453	NP_115947
5.55	<b>(</b>	(FLJ14753), mRNA /cds≃(247,1095)			
	1	/gb=NM_032558 /gi=14211858		1	
		/ug=Hs.13453 /len=2593	·	L	<u> </u>
8365	0.010277	hypothetical protein FLJ10702	NM_018184	Hs.104222	NP_060654
	] ,	(FLJ10702), mRNA /cds=(175,735)		1	
	}	/gb=NM_018184 /gi=8922600	<b>1</b>	1	1
	1	/ug=Hs.104222 /len=2944			

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
8369	0.011238	hypothetical protein FLJ20432	NM 017819	Hs.57898	NP 060289
		(FLJ20432), mRNA /cds=(603,1361)			<b>!</b> -
		/gb=NM_017819 /gi=8923404			1
		/ug=Hs.57898 /len=1654		}	
8374	0.001339	HT021 (HT021), mRNA /cds=(145,531)	NM 020685	Hš.47166	NP 065736
7,100	0.001333	/gb=NM 020685 /gi=10190735	141VI_020000	1113.47 100	NF_003730
		/ug=Hs.47166 /len=797			
0276	0.047000		A A O 4 4 2 F.C		ND 004707
8376	0.017288	EST(zk54c05.r1	AA044356		NP_001767
1 1		Soares_pregnant_uterus_NbHPU			
1 2 2		cDNA clone IMAGE:486632 5')	<u> </u>		
8378	0.001339	601556349T1 NIH_MGC_58 cDNA	BE739647	Hs.88156	
		clone IMAGE:3826069 3', mRNA			
		sequence /clone=IMAGE:3826069			<b>}</b>
÷ · · · · · ·		/clone_end=3' /gb=BE739647			
. 4		/gi=10153639 /ug=Hs.88156 /len=692			
8395	0.002337	EST xp73h11.x1 NCI_CGAP_Ov40	AW270457		
		cDNA clone IMAGE:2746053 3' similar			
		to contains Alu repetitive			
4.3	,	element contains element MER32		}	
		repetitive element;			
8405	0.013394	cDNA FLJ33992 fis, clone	AK091311	Un 200044	ND 770024
0405	0.015394		AKUSISTI	Hs.368944	NP_778231
.*		DFNES2007634. /gb=AK091311			
		/gi=21749651 /ug=Hs.368944	ter to the		
		/len=3116			<u> </u>
8406	0.03788	erythroblast membrane-associated	NM_018538	Hs.410294	NP_061008
		protein (ERMAP), mRNA			1
		/cds=(167,1594) /gb=NM_018538	,	, :	
		/gi=19923535 /ug=Hs.410294			1
* **.		/len=3381			
8413	0.020388	EST (or91g12.s1 NCI_CGAP_Lu5	AA988166	1	
		IMAGE:1603270 3')			
8418	0.02801	EST ty79e06.x1 NCI_CGAP_Kid11	Al629011		NP_055428
0.1.0	1	cDNA clone IMAGE:2285314 3'	1025011		_000,420
8419		mRNA; cDNA DKFZp586B1922 (from	AL049450	Hs.184779	<del></del>
קו דיָט	0.030249			1115.104//9	
:		clone DKFZp586B1922) /gb=AL049450			
		/gi=4500236 /ug=Hs.184779 /len=1433			
0.460	0.00=4==				1
8430	0.035177	chromosome 20 open reading frame 36	NM_018257	Hs.184628	NP_060727
		(C20orf36), mRNA /cds=(128,1213)	,		
,	~	/gb=NM_018257 /gi=8922738	,		1
		/ug=Hs.184628 /len=3655	:		
	ŀ '				ŀ
8438	0.008566	mRNA sequence /qb=L26969	L26969	Hs.362852	
8438	0.008566	mRNA sequence /gb=L26969 /gi=16905391 /ug=Hs.362852	L26969	Hs.362852	

		nding To Differentially Expressed Gen			· · · · · · · · · · · · · · · · · · ·
Spot	p-value	Description	Gen	Unigene	Protein
**			Acc ssion No.	Accession	Accession
	]			No.	No.
8439	0.02801	Similar to nasopharyngeal carcinoma	BC025283	Hs.401412	
		susceptibility protein, clone		e e e e e e e e e e e e e e e e e e e	
		IMAGE:5018419, mRNA			e e e e e e e e e e e e e e e e e e e
		/gb=BC025283 /gi=19263927			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
4 1		/ug=Hs.401412 /len=2812			
8447	9 43F-04	cDNA FLJ32621 fis, clone	AK057183	Hs.425445	
		STOMA2000395. /gb=AK057183	,		
a.		/gi=16552779 /ug=Hs.425445	·		
		/len=2648			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
8449	0.043799	hypothetical protein FLJ10619	NM 018156	Hs.191436	NP 060626
0443	0.0437.99	(FLJ10619), mRNA /cds=(65,1894)	NN_0 10 130	1115.131430	141 _000020
. 1	1	/gb=NM 018156 /gi=8922552			
8451	0.004905	/ug=Hs.191436 /len=3989	DE160711	S	5. 14.
0401	0.004825	EST (PM1-HT0422-170100-005-c12	BE160711		
Õ.457	0.040070	HT0422)	700404		
8457	0.0122/6	EST (T98494 ye60e05.s1 Soares fetal	T98494		
		liver spleen 1NFLS cDNA clone			
· · · · · · · · · · · · · · · · · · ·		IMAGE:122144-3')			
8458	0.007807	cDNA FLJ35666 fis, clone	AK092985	Hs.233382	
		SPLEN2017781. /gb=AK092985			
		/gi=21751702 /ug=Hs.233382			
		/len=2153		V. L	
8461	0.02801	cDNA FLJ39764 fis, clone	AK097083	Hs.181297	
		SPLEN2000143. /gb=AK097083			
		/gi=21756734 /ug=Hs.181297			
	} _	/len=2530			
8472	0.030249	cDNA FLJ14188 fis, clone	AK024250	Hs.288671	
~i .	1	NT2RP2005980. /gb=AK024250		1	
		/gi=10436579 /ug=Hs.288671			
		/len=2289			
8489	0.002096	CLK4 mRNA sequence	AF212224	Hs.406557	
್ರಾಪ್ಕ		/cds=(154,1515) /gb=AF212224			land the second
		/gi=9437514 /ug=Hs.406557 /len=1865			
~					
8501	0.032636	hypothetical protein FLJ40137	NM 173478	Hs.412708	NP 775749
	3.002000	(FLJ40137), mRNA /cds=(149,1141)	,,,,,,,	1.15 2.700	
	În.	/gb=NM_173478 /gi=27735056			
. ,	1.1 - 1.5 -	/ug=Hs.412708 /len=2241	1.		
8507	0.001501	hypothetical protein FLJ20015	NM 018996	Hs.375614	NP_061869
0007	0.001501		LIAINI O LOBBO	115.373014	145_00.1009
		(FLJ20015), mRNA /cds=(32,523)			
		/gb=NM_018996 /gi=9506648	:		
0544	0.00740=	/ug=Hs.375614 /len=1457	N24400	<u> </u>	
8511		EST(yx64g06.r1 clone 266554 5')	N31192	ļ	
8516	0.002096	EST (MR1-SN0033-100400-001-a10	AW867013		
	·	SN0033)		1	
8521	J 0.047031	cDNA, 5' end /clone=IMAGE:4182762	BF337076	Hs.213129	
i .		/clone_end=5' /gb=BF337076			
]		/gi=11283172 /ug=Hs.213129 /len=974			
				1	

		nding To Differentially Expr ssed Gen			
Spot	p-value	Description	Gen	Unig ne	Protein
			Acc ssion No.	Acc ssion	Accession
				No.	No.
8523	0.007107	EST (0x48a03.x1	Al038291		NP_612206
		Soares_total_fetus_Nb2HF8_9wlMAGE			
		:1659532 3')			
8525	0.013394	7f26a06.x1 NCI_CGAP_CLL1 cDNA	BE676253	Hs.436350	7 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -
. !		clone IMAGE:3295762 3' similar to	**   1	]	
		contains Alu repetitive element; contains			
٠.		element MER22 repetitive element ,,	* *		
	[·	mRNA sequence			
		/clone=IMAGE:3295762 /clone end=3'	<b>X</b>	,	
-1	tain Tarana	/gb=BE676253 /gi=10036794			
	· · · · · ·	/ug=Hs.436350 /len=492			
1	· · · ·				
8528	3.95E-04	EST (602152342F1 NIH MGC 81	BF671599		
		cDNA clone IMAGE:4293442.5')		The second of	
8530	0.049079	UI-E-EJ0-ahq-g-22-0-UI.s1 UI-E-EJ0	BM674631	Hs.444500	
37-7		cDNA clone UI-E-EJ0-ahq-g-22-0-UI 3',			
		mRNA sequence /clone=UI-E-EJ0-ahq-			
	(	g-22-0-UI /clone_end≈3'			
		/gb=BM674631 /gi=18984529			
		/ug=Hs.444500 /len=1272			
8531	0.043700	cDNA FLJ40915 fis, clone	AK098234	Hs.207079	
0001	0.045799	UTERU2005450. /gb=AK098234	1/4/(030/204	113.207073	
41	1	/gi=21758205 /ug=Hs.207079	and the second of the second		
	(	/len=21739			
8532	0.036556	sin3-associated polypeptide, 18kDa	NM 005870	Hs.23964	NP 005861
0002	0.030330	(SAP18), mRNA /cds=(65,526)	INIVI_003070	115.25304	147 _003601
		/gb=NM_005870 /gi=23510407			
0541	0.047024	/ug=Hs.23964 /len=2035 EST(hh01c12.x1 NCI_CGAP_Kid11	AW614572	-	NP 714916
8541	0.047031	cDNA clone IMAGE:2953846 3')	AVVO 14372		INF_/ 14910
0540	0.010704		BF748890	<del>                                     </del>	
8548	1 0.0 18784	EST (RC1-BN0413-041000-021-a09	BF / 4009U		25
0667	0.040704	BN0413)	BQ017647	Hs.124747	1
8557	0.018/84	UI-H-ED0-awy-a-01-0-UI.s1	DQU1/04/	глъ. (24/4/	
- '		NCI_CGAP_ED0 cDNA clone IMAGE:5825160 3', mRNA sequence			<b>∮</b>
		/clone=IMAGE:5825160 /clone_end=3'			
		/gb=BQ017647 /gi=19752924		1	
		/ug=Hs.124747 /len=1445			
0.555	0.005455	1	D000000	115 400757	<del>                                     </del>
8559	0.035177	clone MGC:5564, mRNA, complete cds	IRC003681	Hs.188757	
		/cds=(227,304) /gb=BC003697			
		/gi=13277575 /ug=Hs.188757			
	<u> </u>	/len=2145	<del></del>	<u> </u>	
8560	3.95E-04	ribosomal protein L28 (RPL28), mRNA	NM_000991	Hs.356371	NP_000982
		/cds=(43,456) /gb=NM_000991			
		/gi=13904865 /ug=Hs.356371 /len=500			
(				1	1 .

		nding To Differentially Expr ssed Gen			
Spot	p-value	Description	Gene	Unigen	Protein
			Accession No.	Accession	Accession
				No.	No.
8561	0.035177	UI-H-BI2-agy-f-12-0-UI⋅s1	AW292315	Hs.435074	
-		NCI_CGAP_Sub4 cDNA clone			
**		IMAGE:2726158 3', mRNA sequence		,	
2		/clone=IMAGE:2726158 /clone_end=3'			
		/gb=AW292315 /gi=6698951	1 .		
		/ug=Hs.435074 /len=1117	4.4		
8565	0.004825	EST(DKFZp313E1524_r1 313	AL599090	•	
0000	0.00 .020	(synonym: hlcc2) Homo sapiens cDNA	, 1200000	]	_
. 4		clone DKFZp313E1524 5')			
8568	0.004825	EST(clone IMAGE:4733034.5')	BG619661	<del></del>	
8570		EST hz28e05.x1 NCI CGAP GC6	BE466897		
6570	0.012270	cDNA clone IMAGE:3209312 3	DL400091		
0577	0.035177	RC5-FT0194-271100-022-B06 FT0194	DE050625	Hs.270272	
8577	0.035177		DL020032	IDS.210212	
		cDNA, mRNA sequence /gb=BF858635			
er.		/gi=12246379 /ug=Hs.270272 /len=590			
8584	0.007807	AGENCOURT_6417307 NIH_MGC_67	ВМ799896	Hs.304926	
	· ·	cDNA clone IMAGE:5492062 5', mRNA	and the second second		
		sequence /clone=IMAGE:5492062			
7.4		/clone_end=5' /gb=BM799896			
		/gi=19116719 /ug=Hs.304926 /len=913			
					·
8585	0.004825	ok48d01.s1 NCI_CGAP_Lei2 cDNA	AA903192	Hs.276518	
	*	clone IMAGE:1517185 3', mRNA			
	Ì	sequence /clone=IMAGE:1517185			
		/clone_end=3' /gb=AA903192			
1.1		/gi=3038315 /ug=Hs.276518 /len=357			
8586	0.003947	UPF3 regulator of nonsense transcripts	NM 023011	Hs.399740	NP 542418
0000		A (yeast) (UPF3A), transcript variant 1,		. 10.000	7 -7 7
		mRNA /cds=(38,1468) /gb=NM_023011			
- 1		/gi=18375523 /ug=Hs.399740		1 3 7 4 8	
		/len=2381	10.4		
				10 March 1997	
0E02	0.005225	loc26g08 v4 Potingl sigmost	CA392625	Hs 389253	-
8593	0.005325	cs26g08.y1 Retinal pigment	CA39Z0Z3	IUS 208723	
	]	epithelium/choroid cDNA (Un-		1.20	
		normalized, unamplified): cs cDNA			1
		clone cs26g08 5', mRNA sequence			1
t .	1	/clone=cs26g08 /clone_end=5'		1	
	1	/gb=CA392625 /gi=24725520			
		/ug=Hs.389253 /len=648			
8594	0.00168	EST(nh89a01.r1 NCI_CGAP_Br1.1	AA513780		
		cDNA clone IMAGE:965640 5' similar			
		to contains Alu repetitive element)			
	<u>.i </u>			11. 1.0500	110 000050
8595	1.33E-04	ribosomal protein L3 (RPL3), mRNA	NM_000967	Hs.119598	NP_000958
8595	1.33E-04	ribosomal protein L3 (RPL3); mRNA /cds=(27,1238) /gb=NM_000967	NM_000967	Hs.119598	NP_000958
8595	1.33E-04		NM_000967	Hs.119598	NP_000958

	p-value	nding To Differentially Expressed Gen Description	Gen	Unigene	Prot in
Spor	P=value	Description	Accession No.	Accession	Accession
8609	0.003947	UI-H-BI0-aah-f-11-0-UI.s1	AW014024	No. Hs.443573	No.
		NCI CGAP Sub1 cDNA clone			
	<u>.</u>	IMAGE:2709285 3', mRNA sequence			
		/clone=IMAGE:2709285 /clone_end=3'	***		
		/gb=AW014024 /gi=5862781			
		/ug=Hs.443573 /len=594			}
615	0.032636	cDNA clone IMAGE:3918063 5'	BE895919		NP_055157
,010	0.002000	601432861F1 NIH MGC 72	DE-030313		141 _000 107
622	0.010277	FLJ30623 fis, clone CTONG2001748	AK055185	Hs.351574	NP 079050
022	0.010277	/cds=UNKNOWN /gb=AK055185		1115.551574	INF_079030
	and the second	/gi=16549855 /ug=Hs.351574			
	100	/len=2870	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		+ - + ¹ .
626	0.047031	yf81h04.s1 Soares infant brain 1NIB	R40376	Hs.388213	
JZU	0.047037	cDNA clone IMAGE:29029 3', mRNA	P. 100/0	1 13.0002 13	1
		seguence /clone=IMAGE:29029			
		/clone_end=3' /qb=R40376 /qi=821119			
,				)	
eo ż	0.00004	/ug=Hs.388213 /len=439	AKOECADA	U- CC54	ND 00075
627	0.02801	FLJ31562 fis, clone NT2RI2001422	AK056124	Hs.6651	NP_003753
		/cds=UNKNOWN /gb=AK056124			
000	0.00000	/gi=16551441 /ug=Hs.6651 /len=2253	Books		 
632		cDNA clone IMAGE:4769918 5'	BG623330	11. 004000	NP_777568
635	0.023945	ESTs, cDNA, 3' end /clone_end=3'	BI789108	Hs.304928	
	'	/gb=BI789108 /gi=15816833			
007	0.000040	/ug=Hs.304928 /len=529	10040		
637	0.030249	mitochondrial translational initiation	NM_152912	Hs.406591	NP_690876
		factor 3 (MTIF3), mRNA			
		/cds=(237,1073) /gb=NM_152912			
		/gi=24432096 /ug=Hs.406591			
		/len=1693	272 - 772 - 772		<u> </u>
640	0.043799	Ül-H-Bl1-abw-g-10-0-Ul.s1	AW138102	Hs.444831	
		NCI_CGAP_Sub3 cDNA clone		, ,	
		IMAGE:2713530 3', mRNA sequence			
		/clone=IMAGE:2713530 /clone_end=3'			
		/gb=AW138102 /gi=6142420			
<u> </u>	0.00:00=	/ug=Hs.444831 /len=772	 		lub cook
643	0.004825	ESTs, cDNA, 5' end	BG532473	Hs.107265	NP_003426
	1	/clone=IMAGE:4699685 /clone_end=5'	,		
		/gb=BG532473 /gi=13524012			
		/ug=Hs.107265 /len=774			
0.10	0.005044	5112 = 122 - 122	7.72.22.22		
646	0.025911	cDNA FLJ39413 fis, clone	AK096732	Hs.194339	'5' .
	)	PLACE6015729. /gb=AK096732		,	J
		/gi=21756291 /ug=Hs.194339			
		/len=1957		ļ	ļ.,
8648	0.03788	hypothetical protein MGC40157	NM_152350	Hs.295362	NP_689563
	1	(MGC40157), mRNA /cds=(106,498)		1	]
		/gb=NM_152350 /gi=22748758			1
	I '	/ug=Hs.295362 /len=1250	1.		.1

Genes	Correspoi	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No
8649	0.020388	nah90b12.x1 NCI_CGAP_HN19 cDNA	BG272785	Hs.440690	
		clone IMAGE:4257766 similar to			
	·	P39194 ALU SUBFAMILY SQ			
	,	SEQUENCE CONTAMINATION			
		WARNING ENTRY. [1] ;contains Alu			
		repetitive element;, mRNA sequence			
		/clone=IMAGE:4257766 /gb=BG272785	A 18 18 18 18 18 18 18 18 18 18 18 18 18		ļ
		/gi=12982288 /ug=Hs.440690 /len=360			
		/gi=12902200 / <b>ug</b> =113.440000 /ici1=000			r
8654	0.04244	cDNA FLJ33942 fis, clone	AK091261	Hs.434532	
0034	0.04244	CTONG2018147. /gb=AK091261	ARUS 1201	1115.434332	
		/gi=21749590 /ug=Hs.434532			
an energy	1.	//gi=217493907ug=H\$,434332 //len=2356			
0000	0.004267	nk74h02.s1 NCI CGAP Sch1 cDNA	AA551072	11- 20004	-
8660	0.004367		MA33 10/2	Hs.368624	
		clone IMAGE:1019283 3 similar to			
		contains Alu repetitive element; contains			
		element LTR5 repetitive element ;,			
7 - 7 -		mRNA sequence			
		/clone=IMAGE:1019283 /clone_end=3'			
	1	/gb=AA551072 /gi=2321324			
**		/ug=Hs.368624 /len=477		·	<u> </u>
8666	0.018784	EST(UI-H-EU1-bab-e-09-0-UI.s1	BQ446611		NP_037506
	1	NCI_CGAP_Ct1 cDNA clone UI-H-EU1-			, ,
		bab-e-09-0-UI 3')			
8669	7.41E-04	cDNA FLJ10190 fis, clone	AK001052	Hs.274546	
		HEMBA1004753. /gb=AK001052			
<b>.</b>		/gi=7022081 /ug=Hs.274546 /len=1318	L	·	
·					
8675	0.010277	UI-H-EI0-ayo-a-20-0-UI.s1	BQ004581	Hs.412459	
		NCI_CGAP_EI0 cDNA clone			
		IMAGE:5841307 3', mRNA sequence		1	
<u> </u>		/clone=IMAGE:5841307 /clone_end=3'		*	
		/gb=BQ004581 /gi=19729481			
-		/ug=Hs.412459 /len=1095			
				]	
8685	0.043799	Similar to ubiquitin protein ligase E3A	BC040187	Hs.25320	
<u> </u>		papilloma virus E6-associated protein,			,
1		Angelman syndrome), clone			
1	j.	IMAGE:4811444, mRNA	1	· .	
ŀ		/gb=BC040187 /gi=25455694			
	1	/ug=Hs.25320 /len=4823			
8686	0.004367	mRNA, cDNA DKFZp564P016 (from	AL049337	Hs.132571	
		clone DKFZp564P016) /gb=AL049337	1		1
		/gi=4500118 /ug=Hs.132571 /len=1938	1		
			•.		,
8692	0.032636	EST383274 MAGE resequences,	AW971186	Hs.442674	
3332	3.302000	MAGL cDNA, mRNA sequence			1
	ļ	/gb=AW971186 /gi=8161031			
		/ug=Hs.442674 /len=603	<u> </u>		
		rug-118:442014 Hell=000		<u> </u>	<del></del>

8694	0.043799	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) (PRKAR1A), mRNA /cds=(88,1233) /gb=NM_002734 /gi=4506062 /ug=Hs.183037 /len=3036 clone IMAGE:3909623, mRNA, partial cds /cds=(1,178) /gb=BC015894 /gi=16198445 /ug=Hs.33264 /len=2980 UI-H-EU0-azs-p-18-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE:	Gene Accession No. NM_002734 BC015894	Unigene Accession No. Hs.183037 Hs.33264	Protein Accession No. NP_002725
8699	0.020388	regulatory, type I, alpha (tissue specific extinguisher 1) (PRKAR1A), mRNA /cds=(88,1233) /gb=NM_002734 /gi=4506062 /ug=Hs.183037 /len=3036 clone IMAGE:3909623, mRNA, partial cds /cds=(1,178) /gb=BC015894 /gi=16198445 /ug=Hs.33264 /len=2980 UI-H-EU0-azs-p-18-0-UI:s1 NCI_CGAP_Car1 cDNA clone IMAGE:	NM_002734 BC015894	No. Hs.183037 Hs.33264	No.
8699	0.020388	regulatory, type I, alpha (tissue specific extinguisher 1) (PRKAR1A), mRNA /cds=(88,1233) /gb=NM_002734 /gi=4506062 /ug=Hs.183037 /len=3036 clone IMAGE:3909623, mRNA, partial cds /cds=(1,178) /gb=BC015894 /gi=16198445 /ug=Hs.33264 /len=2980 UI-H-EU0-azs-p-18-0-UI:s1 NCI_CGAP_Car1 cDNA clone IMAGE:	BC015894	Hs.183037	
8699	0.020388	regulatory, type I, alpha (tissue specific extinguisher 1) (PRKAR1A), mRNA /cds=(88,1233) /gb=NM_002734 /gi=4506062 /ug=Hs.183037 /len=3036 clone IMAGE:3909623, mRNA, partial cds /cds=(1,178) /gb=BC015894 /gi=16198445 /ug=Hs.33264 /len=2980 UI-H-EU0-azs-p-18-0-UI:s1 NCI_CGAP_Car1 cDNA clone IMAGE:	BC015894	Hs.33264	NP_002725
8699	0.020388	regulatory, type I, alpha (tissue specific extinguisher 1) (PRKAR1A), mRNA /cds=(88,1233) /gb=NM_002734 /gi=4506062 /ug=Hs.183037 /len=3036 clone IMAGE:3909623, mRNA, partial cds /cds=(1,178) /gb=BC015894 /gi=16198445 /ug=Hs.33264 /len=2980 UI-H-EU0-azs-p-18-0-UI:s1 NCI_CGAP_Car1 cDNA clone IMAGE:	BC015894		
	0.020388	extinguisher 1) (PRKAR1A), mRNA /cds=(88,1233) /gb=NM_002734 /gi=4506062 /ug=Hs.183037 /len=3036 clone IMAGE:3909623, mRNA, partial cds /cds=(1,178) /gb=BC015894 /gi=16198445 /ug=Hs.33264 /len=2980 UI-H-EU0-azs-p-18-0-UI:s1 NCI_CGAP_Car1 cDNA clone IMAGE:			
	0.020388	/cds=(88,1233) /gb=NM_002734 /gi=4506062 /ug=Hs.183037 /len=3036 clone IMAGE:3909623, mRNA, partial cds /cds=(1,178) /gb=BC015894 /gi=16198445 /ug=Hs.33264 /len=2980 UI-H-EU0-azs-p-18-0-UI:s1 NCI_CGAP_Car1 cDNA clone IMAGE:			
	0.020388	/gi=4506062 /ug=Hs.183037 /len=3036 clone IMAGE:3909623, mRNA, partial cds /cds=(1,178) /gb=BC015894 /gi=16198445 /ug=Hs.33264 /len=2980 UI-H-EU0-azs-p-18-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE:			
		clone IMAGE:3909623, mRNA, partial cds /cds=(1,178) /gb=BC015894 /gi=16198445 /ug=Hs.33264 /len=2980 UI-H-EU0-azs-p-18-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE:			
		cds /cds=(1,178) /gb=BC015894 /gi=16198445 /ug=Hs.33264 /len=2980 UI-H-EU0-azs-p-18-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE:			
		cds /cds=(1,178) /gb=BC015894 /gi=16198445 /ug=Hs.33264 /len=2980 UI-H-EU0-azs-p-18-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE:			
8720	0.02801	/gi=16198445 /ug=Hs.33264 /len=2980 UI-H-EU0-azs-p-18-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE:	BQ183906	Hs 356538	
8720	0.02801	UI-H-EU0-azs-p-18-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE:	BQ183906	Hs 356538	
8720	0.02801	NCI_CGAP_Car1 cDNA clone IMAGE:	BQ183906	Hs 356538	
8720	0.02801	NCI_CGAP_Car1 cDNA clone IMAGE:	BQ183906	THe 356538	1
				113.00000	
		FOEDAGE OF ALBANA			[ ] - [ ] - [
		5853185 3', mRNA sequence	gran end man		
3		/clone=IMAGE:_5853185 /clone_end=3'			
24.7	+	/gb=BQ183906 /gi=20359457			1
		/ug=Hs.356538 /len=1068			
	•				
8728	0.040751	DKFZp547N166_r1 547 (synonym:	AL134698	Hs.272048	
0.20	0.0.0.	hfbr1) cDNA clone DKFZp547N166 5',			
·		mRNA sequence			
. 1		/clone=DKFZp547N166 /clone_end=5			
		/gb=AL134698 /gi=6602885			
	0.040=51	/ug=Hs.272048 /len=586	41000047	11 477004	
8738	0.040751	tb26b01.x1 NCI_CGAP_Kid12 cDNA	Al308217	Hs.177064	
		clone IMAGE:2055433 3' similar to			
		contains Alu repetitive element;, mRNA			
		sequence /clone=IMAGE:2055433	a i		
-		/clone_end=3' /gb=Al308217	· · · · · · · · · · · · · · · · · · ·		
		/gi=4002852 /ug=Hs:177064 /len=421			
8760	0.007807	EST(cDNA clone IMAGE:5258751 5')	BI457491		NP 031394
8767		UMP-CMP kinase (UMP-CMPK),	NM_016308	Hs.11463	NP 057392
	<del>.</del>	mRNA /cds=(31,717) /gb=NM 016308			
		/gi=7706496 /ug=Hs.11463 /len=2836			
	4	//gr / / 00500 /ug=119. į 1500 /ieii=2000* 			
8769	0.010277	EST(adult brain Danio rerio cDNA clone	BI420083		
0109	0.010211				
	Section 1	4966301 5' similar to SW:RLA1_CHICK	1		
		P18660 60S ACIDIC RIBOSOMAL			1
Ì		PROTEIN P1. ;contains element		1	1
. ]	•	MER22 repetitive element ; )		1 1	
الــــــــــــــــــــــــــــــــــــ					ļ
8776		EST(cDNA clone IMAGE:3249148 3')	BE673393	<u> </u>	NP_003109
8777	0.002337	UI-E-EO1-ajc-l-12-0-UI r1 UI-E-EO1	BM718946	Hs.364651	1
J		cDNA clone UI-E-EO1-ajc-l-12-0-UI 5',			
. ]		mRNA sequence /clone=UI-E-EO1-ajc-l		1	
· ·		12-0-UI /clone_end=5' /gb=BM718946			
ł		/gi=19037365 /ug=Hs.364651	1	1 1	i i
J.	\$ 4 * -	/len=1031		1	1

		nding To Differentially Expressed Gen			D. 4
Spot	p-valu	1	Gene	Unig ne	Prot in
			Accession No.	Accession	Accession
8778	0.005325	EST(Stratagene lung (#937210) Homo	AA491482	No.	No.
0110	0.000020	sapiens cDNA clone IMAGE:841389 5	701401402		1 1 11 11
		)		. *-	
3780	0.030340	MR2-CI0186-291100-010-a06 CI0186	BF814502	Hs.446594	
5700	0.000249	cDNA, mRNA sequence /gb=BF814502	014002	113.440004	
•		/gi=12147047 /ug=Hs.446594 /len=530			
		/gi=12147047 /ug=115.440554 /ieii=550			
3787	0.009388	CLK4 mRNA sequence	AF212224	Hs.406557	1
,,,,,		/cds=(154,1515) /gb=AF212224	, ,, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		
· *·.		/gi=9437514 /ug=Hs.406557 /len=1865	A CONTRACTOR	•	
:	Part of the	/gi=040/014/4g=113.40000///ici1=1000			
8794	0.005325	AGENCOURT_8475922	BQ721341	Hs.128076	
		Lupski_sympathetic_trunk cDNA clone			
		IMAGE:6195208 5', mRNA sequence			
		/clone=IMAGE:6195208 /clone end=5'			
		/gb=BQ721341 /gi=21860238			
	1 - 1 - 1	/ug=Hs.128076 /len=1186	• •		
3795	0.02801	mRNA; cDNA DKFZp451B1818 (from	AL832623	Hs.77554	
		clone DKFZp451B1818) /gb=AL832623			
		/gi=21733198 /ug=Hs.77554 /len=6240			
3796	0.006463	ESTs, cDNA, 3' end /clone=UI-E-EJ0-	BM681301	Hs.355029	
And the		aii-l-19-0-Ul /clone end=3'			
·		/gb=BM681301 /gi=18991197			
		/ug=Hs.355029 /len=591			
8797	0.010277	ESTs, cDNA, 5' end	BG697291	Hs.374415	NP 112200
	7 7	/clone=IMAGE:4803370 /clone end=5'			
		/gb=BG697291 /gi=13963346		ļ	
		/ug=Hs.374415 /len=909	-		
7 4 4 5 7, 1	\$ 1500 m				
8799	0.001501	ubiquitin specific protease 7 (herpes	NM_003470	Hs.78683	NP_003461
٠.		virus-associated) (USP7), mRNA			
		/cds=(200,3508) /gb=NM_003470		1	
		/gi=4507856 /ug=Hs.78683 /len=4022			
808	0.020388	EST(cDNA clone CS0DF021YG07 5	AL535948	*	NP_006612
	.,	prime )		: 2	
8809	0.008566	cDNA: FLJ23013 fis, clone LNG00740.	AK026666	Hs.372737	an an
		/gb=AK026666 /gi=10439567		1	
	,	/ug=Hs.372737 /len=1909			
	l		<u> </u>		
8814	0.032636	UI-1-BB1p-aun-c-05-0-UI.s1	BQ023929	Hs.283502	
		NCI_CGAP_Pl6 cDNA clone UI-1-BB1p		1	
		aun-c-05-0-UI 3', mRNA sequence		1 .	1
٠		/clone=UI-1-BB1p-aun-c-05-0-UI		1	
		/clone_end=3' /gb=BQ023929			
		/gi=19759208 /ug=Hs.283502 /len=584			
,			*		
3834	0.047024	No significant match, ORF+2(41~249)	SEQ.ID.No.9	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	3 a

		nding To Differ ntially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
	4			No.	No.
8836	0.004367	No significant match	SEQ.ID.No.33		
8837		no significant match	SEQ.ID.No.39		
8839		No significant match, ORF-1(3~472)	SEQ.ID.No.49	<u> </u>	
8851		No significant match			1
	0.00000	(ORF:+3:3~167[166]; +1:49~167[120])		·	
			SEQ.ID.No.14		
8860	0.035177	clone 23612 mRNA sequence	U90902	Hs.82141	
0,000	0.000117	/gb=U90902 /gi=1913880	000002	1113.02.141	
		/ug=Hs.82141 /len=1548			
8867	0.021262	mRNA; cDNA DKFZp686M2414 (from	AL832164	Hs.282596	
0007	Ü.U3 130 <u>2</u>		1	IDS.202090	
	e December	clone DKFZp686M2414) /gb=AL832164	**************************************		
1.		/gi=21732708 /ug=Hs 282596			
	0.001070	/len=2712			
8874	0.001878	No significant match	050 10 11 00	[	
		(ORF:+1:256~491[237])	SEQ.ID.No.26		
8887		No significant match (ORF:+3~234)	SEQ.ID.No.16		4.
8908	0.032636	hypothetical protein FLJ32861	NM_144995	Hs.344530	NP_659432
		(FLJ32861), mRNA /cds=(206,1507)			* •
. ~		/gb=NM_144995 /gi=21450696			
		/ug=Hs.344530 /len=1837			
8909	0.032636	WW domain-containing adapter with a	NM_100264	Hs.70333	NP_567823
		coiled-coil region (WAC), transcript			- "
		variant 2, mRNA /cds=(332,2140)			
		/gb=NM 100264 /gi=18379329			
		/ug=Hs.70333 /len=3088			
8912	0.008566	AGENCOURT_6542493	BM553059	Hs.380110	20.45
		NIH MGC 119 cDNA clone			
**	2	IMAGE:5742803 5', mRNA sequence		7	
		/clone=IMAGE:5742803 /clone end=5'			2
		/gb=BM553059 /gi=18791456	* • .	. •	
		/ug=Hs.380110 /len=1179		ļ.,	4 4
	t in the				
8918	0.013304	EST EST72587 Ovary II cDNA 5' end	AA362818		NP 057226
8920		hypothetical protein FLJ22347	NM 022830	Hs.106004	NP 073741
0920	0.013394	(FLJ22347), mRNA /cds=(60,2684)	INIVI_UZZQ3U	113.100004	NF_0/3/41
. , .				, -	
		/gb=NM_022830 /gi=12383073			
0005	0.047000	/ug=Hs.106004 /len=2747	DEGLIERO		
8925	0.017288	EST TCBAP1D1176 Pediatric pre-B	BE244548		
		cell acute lymphoblastic leukemia			
		Baylor-HGSC project=TCBA cDNA			
		clone TCBAP1176			<del> </del>
8928	6.56E-04	cDNA: FLJ23313 fis, clone HEP11919.	AK026966	Hs.10862	
		/gb=AK026966 /gi=10439954			
		/ug=Hs.10862 /len=2527	1		
		<u> </u>	<u>l · · </u>	<u> </u>	
8931	0.023945	chromosome 21 open reading frame 6	NM_016940	Hs.34136	NP_058636
	[.	(C21orf6), mRNA /cds=(92,1051)	_	1	1 -
		/gb=NM_016940 /gi=8393017			
	1	/ug=Hs.34136 /len=1729	· · · ·	I .	

		nding To Differentially Expressed Gen			-
Spot	p-value	Description	Gene Accession No.	Unigen Accession No.	Prot in Accession No.
8942	0.001193	mRNA for Sec24 protein (Sec24A	AJ131244	Hs.211612	
		isoform), partial /cds=(1,3237)			
		/gb=AJ131244 /gi=3947687		,	
		/ug=Hs.211612 /len=5967			
0050	0.007407		A)(004204	U- 7000	
8953	0.007107	cDNA FLJ34005 fis, clone	AK091324	Hs.7626	
		FCBBF1000272. /gb=AK091324			
'		/gi=21749666 /ug=Hs.7626 /len=4549			- <u></u>
8955	1.53E-04	cDNA FLJ39389 fis, clone	AK096708	Hs.120785	
	-:	PLACE6003621./gb=AK096708			
la de la composição de la composição de la composição de la composição de la composição de la composição de la		/gi=21756262 /ug=Hs.120785		*.	
	*	/len=1350			
8961	0.019142	EST (RC3-ST0197-120200-015-c04	AW813761		· <del>    </del>
	3.5.5,132	ST0197)			
3966	0.024722	EST (AV764100 MDS cDNA clone	AV764100	<del>                                     </del>	<del>                                     </del>
ივიი	0.024732		AV / 04 100		
	0.0050	MDSBAE09 5')	AATOOFO	7 ( 1 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	
3977	0.025911	EST(oa33c09.s1 NCI_CGAP_GCB1	AA766521		
		clone IMAGE:1306768 contains L1.t3	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s		
	i:	L1 repeat)			
8978	0.004367	Similar to procollagen, type V, alpha 2,	BC014149	Hs.162411	
		clone IMAGE:3613441, mRNA			
		/gb=BC014149 /gi=15559579			
		/ug=Hs.162411 /len=1335		* *	
8980	0.003213	EST yq55e03.r1 Soares fetal liver	R96686	<del></del>	1
0000	0.000210	spleen 1NFLS H sapiens cDNA clone	1130000		1
	7			,	
		IMAGE:199708 5' similar to contains	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	1
**		Alu repetitive element;			*
8992	0.02801	hypothetical protein MGC4677	NM_052871	Hs.432419	NP_443103
		(MGC4677), mRNA /cds=(1337,1495)		,	
		/gb=NM_052871 /gi=16418372			
•	}	/ug=Hs.432419 /len=1607			1
8998	0.030249	neuroepithelial cell transforming gene 1	NM 005863	Hs.25155	NP_005854
		(NET1), mRNA /cds=(147,1775)			
y. + 47,		/gb=NM_005863 /gi=19923326			
		/ug=Hs.25155 /len=3236			
8999	0.006463	EST(AV650904 GLC cDNA clone	AV650904	T	
ივვვ	J 0.000403		1440000A		
0000	0.00707	GLCCJF12 3')	ALCOGETOS	111 400545	<del>                                     </del>
9006	0.03788	cDNA FLJ38383 fis, clone	AK095702	Hs.433517	
		FEBRA2003726. /gb=AK095702		1	
		/gi=21755022 /ug=Hs.433517			1.
		/len=3240			
9011	0.030249	EST(yb62b08.r1 Stratagene ovary	T58561		NP 002088
		(#937217) cDNA clone IMAGE:75735			
	1 .			1	

		nding To Differentially Expressed Gen			<b>5</b> 1
Spot	p-value	Description	Gene	Unigene	Prot in
			Accession No.	Accession	Accession
	* .			No.	No.
9017	0.025911	UI-H-FH1-bfk-m-06-0-UI.s1	BU618627	Hs.192435	
		NCI_CGAP_FH1 cDNA clone UI-H-FH1			
		bfk-m-06-0-UI 3', mRNA sequence			
		/clone=UI-H-FH1-bfk-m-06-0-UI		- 6	
		/clone_end=3'/gb=BU618627			<u> </u>
			• • • • • • • • • • • • • • • • • • •	,	1
		/gi=23284842 /ug=Hs.192435	and the second		
		/len=1099			- <del>1</del> +2+ <del>15</del> 2+1++++++++++++++++++++++++++++++++++
9018	0.012526	EST382162 MAGE resequences,	AW970081	Hs.325603	
	** *	MAGK cDNA, mRNA sequence			
		/gb=AW970081 /gi=8159926			
		/ug=Hs.325603 /len=423			•
9022	0.007807	hypothetical protein MGC13183/	NM 032358	Hs.59791	NP 115734
,		(MGC13183), mRNA /cds=(94,1560)			· — .:
		/gb=NM 032358 /gi=14150164			
	1	/ug=Hs.59791 /len=2299			
0040	0.047024		DUICOCCA	11- 072020	The same of the same
9042	0.047031	UI-CF-FN0-aeu-b-13-0-UI.s1 UI-CF-	BU689604	Hs.273830	
		FN0 cDNA clone UI-CF-FN0-aeu-b-13-			
e ter Grand		0-UI 3', mRNA sequence /clone=UI-CF-			
		FN0-aeu-b-13-0-UI /clone_end=3'	**		
		/gb=BU689604 /gi=23547505			
· · · · ·		/ug=Hs.273830 /len=1066			
9046	0.022106	EST(xa08a12.x1	AW074833		
00.10	0.022.00	Soares_NFL_T_GBC_S1 cDNA clone			
		IMAGE:2567710 3')			
0050	0.004504		AIZ057004	Hs.16979	<del>                                     </del>
9050	0.001501	cDNA FLJ25252 fis, clone STM03814.	AK057981	HS. 10979	
		/gb=AK057981 /gi=16553973		.**	
		/ug=Hs.16979 /len=2005		<u> </u>	
9053	0.006463	UI-H-FL1-bgw-f-18-0-UI.s1	BU634141	Hs.32163	
		NCI_CGAP_FL1 cDNA clone UI-H-FL1-			
		bgw-f-18-0-UI 3', mRNA sequence			
		/clone=UI-H-FL1-bgw-f-18-0-UI			
		/clone_end=3' /gb=BU634141			
		/gi=23301396 /ug=Hs.32163 /len=1068	Section 1		
		/gi-2330 1390 /gg-118.32 103 /ie1i=1000			
0050	0.000400		NIM 020040	115 22022	ND 440004
9059	0.022106	tumor endothelial marker 7-related	NM_032812	Hs.33033	NP_116201
		precursor (TEM7R), mRNA			
		/cds=(10,1599) /gb=NM_032812			
		/gi=17511212 /ug=Hs.33033 /len=2160			
				1	
9060	0.008566	EST(yq85a08.s1 Soares fetal liver	H53800		NP 056067
, -, -, -	1	spleen 1NFLS clone IMAGE:202550 3')	· ·		_
-	,	Constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the cons			
0004	0.000505	ADMA EL 122060 fig. close	AK001270	Hs.126465	7
9061	0.002505	cDNA FLJ33960 fis, clone	AK091279	105.120400	
	[ .	CTONG2018843. /gb=AK091279		1	1
	Ĭ .	/gi=21749612 /ug=Hs.126465			
	<u> </u>	/len=2849			
9063	0.035177	clone 23612 mRNA sequence	U90902	Hs.82141	
		/gb=U90902 /gi=1913880			
	1	/ug=Hs.82141 /len=1548		1	1

		nding To Diff rentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
9065	0.018784	UI-H-BI0p-abb-b-05-0-UI.s1	AW015262	Hs.440665	
	g 1 - 1 - 3 - 4	NGI CGAP Sub2 cDNA clone			.:
		IMAGE:2711001 3', mRNA sequence			
		/clone=IMAGE:2711001 /clone end=3			
		/gb=AW015262 /gi=5863949			ı
		/ug=Hs.440665 /len=854			
9078	0.001062	cDNA FLJ13207 fis, clone	AK023269	Hs.14355	
9070	0.001002	NT2RP4000023. /gb=AK023269	A11023209	11 15. 14333	
2121					
		/gi=10435128 /ug=Hs.14355 /len=2633		•	
~~~~	0.005044		A14005000	11.04004	· · · · · · · · · · · · · · · · · · ·
9079	0.025911	cDNA FLJ38641 fis, clone	AK095960	Hs.24831	
		HHDPC2003983. /gb=AK095960			
		/gi=21755328 /ug=Hs.24831 /len=2685			
			1	<u></u>	
9102	0.027314	cDNA FLJ10071 fis, clone	AK000933	Hs.28661	
	J.	HEMBA1001702. /gb=AK000933			
		/gi=7021908 /ug=Hs.28661 /len=2570			
9113	0.043799	chromosome 9 open reading frame 19	NM_022343	Hs.302766	NP_071738
		(C9orf19), mRNA /cds=(35,499)			
	· .	/gb=NM_022343 /gi=22095361			
	•	/ug=Hs.302766 /len=1900		i .	
9114	0.003947	EST(cDNA clone IMAGE:2504565 3')	AW009489		1
9115		nac28g05.x1 Lupski_sciatic_nerve	BG151547	Hs.302830	1
	•.•••	cDNA clone IMAGE:3394737 3', mRNA		1.10.0020,00	
150		sequence /clone=IMAGE:3394737			
•		/clone_end=3' /gb=BG151547			
	4.5	/gi=12663577 /ug=Hs.302830 /len=514			
		/gi=12003377 /ug=H\$.302630 /ieii=314			
0440	0.005044	50.40.4	41700404		
9119	0.025911	wg58a10.x1	AI760121	Hs.295720	
	÷.	Soares_NSF_F8_9W_OT_PA_P_S1			
-		cDNA clone IMAGE:2369274 3', mRNA			,
		sequence /clone=IMAGE:2369274			1
	54 1	/clone_end=3' /gb=AI760121			
wi i	1	/gi=5175788 /ug=Hs.295720 /len=457		:	,
		• •			
9120	0.022802	EST(cDNA clone IMAGE:4371289 5')	BG112978		NP_001767
9129		EST(cDNA.	AW896077		
9130		CGI-18 protein (CGI-18), mRNA	NM_015947	Hs.121599	NP_057031
		/cds=(421,1491) /gb=NM_015947	-		
		/gi=7705601 /ug=Hs.121599 /len=2305		1	
0404	2 32F_04	ESTs, cDNA, 5' end	BF342391	Hs.30469	NP 055313
un ∢n ⊣	. L.ULL"UH	Leonal opiania eng	DI 07403 I	113.00403	1.41 _000010
9131		/clone=IMACE 4148000 /clone and=51		ı	
9131		/clone=IMAGE:4148900 /clone_end=5' /gb=BF342391 /gi=11289392			

		nding To Differ ntially Expressed G n			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
ta il				No.	No.
9133	0.003563	UI-H-BW1-anh-g-07-0-UI.s1	BF514691	Hs.437157	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
		NCI_CGAP_Sub7 cDNA clone	- 1.4.4.4.1		
		IMAGE:3082548 3', mRNA sequence			
		/clone=IMAGE:3082548 /clone_end=3'	•.		
		/gb=BF514691 /gi=11599870	,		
7 -		/ug=Hs.437157 /len=608			•
9134	0.002096	te65d01.x1 Soares NFL T GBC S1	Al377292	Hs.410753	
		cDNA clone IMAGE:2091553 3', mRNA		÷	
		sequence /clone=IMAGE:2091553			/
		/clone_end=3' /gb=Al377292			
		/gi=4187145 /ug=Hs.410753 /len=238			
9153	0.025911	AGENCOURT 8584280	BQ876563	Hs.346743	
		Lupski_sympathetic_trunk cDNA clone			
		IMAGE:6192820 5', mRNA sequence			
		/clone=IMAGE:6192820 /clone end=5'			
		/gb=BQ876563 /gi=22268571			
		/ug=Hs.346743 /len=925			
9154	0.014599	mRNA; cDNA DKFZp564B213 (from	AL049240	Hs.380268	
		clone DKFZp564B213) /gb=AL049240			***
1 12-		/gi=4499973 /ug=Hs.380268 /len=767			
9155	0.009388	cDNA FLJ36544 fis, clone	AK093863	Hs.101689	
		TRACH2006378. /gb=AK093863			
		/gi=21752807 /ug=Hs.101689			
		/len=2670			
9157	0.018784	mRNA; cDNA DKFZp451O1818 (from	AL832650	Hs.12396	and the second second
	**	clone DKFZp451O1818) /gb=AL832650	Programme and the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of		
in the terminal parties and the second second second second second second second second second second second se		/gi=21733226 /ug=Hs.12396 /len=4870		The state of the state of	
9158	0.047031	FLJ14877 fis, clone PLACE1003044	AK027783	Hs.200073	NP_060918
		/cds=(117,1328) /gb=AK027783	** *** ** *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *** * *	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	–
		/gi=14042716 /ug=Hs.200073		1.	
•		/len=2786			
9174	0.008566	UI-E-EJ0-ahs-e-16-0-UI.r1 UI-E-EJ0	BM714718	Hs.446458	
		cDNA clone UI-E-EJ0-ahs-e-16-0-UI 5'.			
		mRNA sequence /clone=UI-E-EJ0-ahs-			
-		e-16-0-UI /clone end=5'			
:		/gb=BM714718 /gi=19027976			
		/ug=Hs.446458 /len=1136			
9178	0.032636	EST(cDNA clone IMAGE:2954041 3')	AW612522	70	NP 065898
9191		xe48d03.x1 NCI_CGAP_Ut3 cDNA	AW080070	Hs 245603	
		clone IMAGE:2611109 3', mRNA			
		sequence /clone=IMAGE:2611109			
		/clone end=3 /gb=AW080070			
		1, 0, 0, 10 0 1 1 0 1 0 0 1 1 1 1 0 0 0 0	f	1 '	I

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
- ^			Accession No.	Accession	Accession
				No.	No.
9210	0.023945	cDNA: FLJ23285 fis, clone HEP09071.	AK026938	Hs.406650	
		/gb=AK026938 /gi=10439914			***
· .		/ug=Hs.406650 /len=2245			
		/ug=H5.400000 /lett=2240			
.:	0.00000	L 1044 OF 5005050 BNIA	D0007700	11 007040	
9232	0.032636	clone IMAGE:5265853, mRNA	BC037736	Hs.397840	
		/gb=BC037736 /gi=23337068			
		/ug=Hs.397840 /len=3811			
9236	0.047031	cDNA FLJ38586 fis, clone	AK095905	Hs.293821	
		HCHON2009384. /gb=AK095905	interior de la servición.		,
:		/gi=21755256 /ug=Hs:293821			
		/len=2631			
9240	0.004367	cDNA /gb=AW971782 /gi=8161628	AW971782	Hs.193559	NP 079130
U.Z-70		/ug=Hs.193559 /len=619	,	1.10.100000	-0,3130
0254		wf29f08.x1 Soares NFL T GBC S1	Al827467	Hs.245510	
9254	0.032030		MIOZ1401	15.245510	
		cDNA clone IMAGE:2357031 3', mRNA			1
		sequence /clone=IMAGE:2357031			
** **		/clone_end=3' /gb=Al827467			
		/gi=5448138 /ug=Hs.245510 /len=520		. .	
9260	0.015895	eukaryotic translation initiation factor 4	NM 001418	Hs.183684	NP_001409
	777 777	gamma, 2 (EIF4G2), mRNA			
		/cds=(307,3030) /gb=NM_001418			
	r s seed a	/gi=4503538 /ug=Hs 183684 /len=3820			to the state
0000	000045	8.11	41/00/000	055000	
9268	0.023945	cDNA FLJ10976 fis, clone	AK001838	Hs 355608	
		PLACE1001399. /gb=AK001838			
		/gi=7023355 /ug=Hs.355608 /len=2116			
•	- A				
9271	0.012276	fj53d02.x1 adult brain Danio rerio cDNA	AW281691		
		3' similar to SW:EF2 CHICK Q90705		 	
		ELONGATION FACTOR 2			
9275	0.011238	ESTs, cDNA, 5' end	BF035134	Hs.195789	
ال الميان	0.011200	/clone=IMAGE:3857750 /clone_end=5'	2. 000104	1.10.100700	, i
		1 · · · · · · · · · · · · · · · · · · ·		1, 1	
		/gb=BF035134 /gi=10742846			
		/ug=Hs.195789 /len=847		ļ:	
	<u> </u>			<u> </u>	<u> </u>
9298	0.007807	ad47h05.s1 Stratagene lung carcinoma	AA669458	Hs.445542	
		937218 cDNA clone IMAGE:884889 3'			•
	, .	similar to gb:X51956_rna1 GAMMA			
		ENOLASE Alu repetitive			
	1	element;contains element TAR1			
		repetitive element ;, mRNA sequence			
	· ·	/clone=IMAGE:884889 /clone_end=3'			· ·
	1				
		/gb=AA669458 /gi=2630957			1.
		/ug=Hs.445542 /len=926			
-					
	10.015805	No significant match	SEQ.ID.No.29	1	L
9303	T 6.0 10030				
9303 9307		No significant match,			

Gen s Corresponding To Differentially Expressed Genes in Figure 20 - RA					
Spot	p-value	Description	G ne	Unigene	Protein
			Accession No.	Accession	Accession
9312	0.032636	No significant motch OPE 1/49~350)	SEQ.ID.No.78	No.	No.
9312 9318		No significant match, ORF-1(48~350) No significant match	SEQ.ID.No.102	 	
		EST(fetal liver spleen 1NFLS cDNA	T97113		ND OFFE
9328	0.004367	clone IMAGE:120299 5')	19/113		NP_055559
9350	0.007807	No significant match, ORF+2(389~530)			7
			SEQ.ID.No.87		
9352	0.017288	Novel	SEQ.ID.No.92	The second second	
9355	7.41E-04	No significant match (ORF:-		± .4 · · · · · · · · · · · · · · · · · ·	
- 4		3:4~240[237])	SEQ.ID.No.19		
9386	0.012276	cDNA: FLJ21243 fis, clone COL01164.	AK024896	Hs.268016	
: :		/gb=AK024896 /gi=10437310			
14 d		/ug=Hs.268016 /len=1880			
					1
9390	6.56E-04	ribosomal protein L13a (RPL13A),	NM <u>′</u> 012423	Hs.389335	NP_036555
		mRNA /cds=(23,634) /gb=NM_012423	_		
11.	*.	/gi=14591905 /ug=Hs.389335			
he.		/len=1142		1	
9392	0.004367	AGENCOURT 6400386 NIH MGC 67	BM799714	Hs.356635	1. N. 1. A.
* .		cDNA clone IMAGE:5495662 5', mRNA			
i maxili	,	sequence /clone=IMAGE:5495662			
	1.0	/clone_end=5' /gb=BM799714			
		/gi=19116537 /ug=Hs.356635			
		/len=1153			
					5
9400	0.002096	SKB1 (S. pombe) (SKB1), mRNA	NM_006109	Hs.12912	NP 006100
e e		/cds=(92,2005) /gb=NM_006109			
• :	1	/gi=20070219 /ug=Hs.12912 /len=2413			
· ·				**	
9405	0.010277	ferritin, light polypeptide (FTL), mRNA	NM 000146	Hs.430150	NP_000137
,	N	/cds=(189,716) /gb=NM_000146	-		-
+ !		/gi=20149497 /ug=Hs.430150 /len=878			
14 - 12					
9423	0.032636	vesicle amine transport protein 1 (T	NM_006373	Hs.157236	NP_006364
•		californica) (VAT1), mRNA	-		
		/cds=(57,1238) /gb=NM_006373	<u> </u>		
		/gi=18379348 /ug=Hs.157236			
		/len=2738			·
9424	0.004367	MCM4 (MCM4) and DNA-PKcs	U63630	17.	
· · · · · · ·		(PRKDC) genes, partial cds			
9431	0.011238	chromosome 11 open reading frame 24	NM 022338	Hs.303025	NP_071733
		(C11orf24), mRNA /cds=(403,1752)			
		/gb=NM_022338 /gi=11641238			
1		/ug=Hs.303025 /len=2058		.,	
-:		1749 113.000020 NCH-2000	İ		
9442	0.001103	GTP binding protein overexpressed in	NM 005261	Hs.79022	NP 005252
J.74	0.001100	skeletal muscle (GEM), mRNA	1000201	13.7 5022	
		/cds=(214,1104) /gb=NM_005261			
		/gi=4885262 /ug=Hs.79022 /len=2156			:
	i .	/u -4003202 /uu-ms./ 9022 /leff=2156	1 ' '	1	1

		nding To Differentially Expressed Gen			
Spot	p-valu	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
9445	0.002096	barrier to autointegration factor	NM_003860	Hs.433759	NP_003851
,	,, -,, -,	(BCRP1), mRNA /cds=(508,777)		in the second	
		/gb=NM_003860 /gi=11038645			
		/ug=Hs.433759 /len=1192			
9450	0.02801	FK506 binding protein 3, 25kDa	NM_002013	Hs.379557	NP 002004
3		(FKBP3), mRNA /cds=(412,1086)	_	,	- .
		/gb=NM_002013 /gi=17149845			• ::
	in the in	/ug=Hs.379557 /len=1420			
9451	0.00587	phospholipase A2-activating protein	NM_004253	Hs.27182	NP 004244
		(PLAA), mRNA /cds=(29,2245)			
		/gb=NM 004253 /gi=21361288			
4.		/ug=Hs.27182 /len=3240			
9453	0.007107	mRNA for KIAA1705 protein, partial	AB051492	Hs.7076	
		cds. /cds=(1714,3210) /gb=AB051492			
		/gi=12697954 /ug=Hs.7076 /len=3949			
9455	0.040751	likely ortholog of mouse tumor	NM_020755	Hs.146668	NP_065806
		differentially expressed 1, like (TDE1L),			
		mRNA /cds=(76,1437) /gb=NM 020755			
		/gi=24308212 /ug=Hs.146668			
		/len=3149			
9458	0.043799	solute carrier family 38, member 2	NM_018976	Hs.298275	NP 061849
	0.0.0	(SLC38A2), mRNA /cds=(352,1872)			
		/gb=NM_018976 /gi=21361601			
100		/ug=Hs.298275 /len=4795			100
9466	0.007107	hypothetical protein FLJ10891	NM_018260	Hs.274169	NP_060730
		(FLJ10891), mRNA /cds=(128,1525)			
		/gb=NM 018260 /gi=8922743			
		/ug=Hs.274169 /len=2864			
9479	0.003947	ALS2CR18 mRNA (=cDNA FLJ12667	AB053320		NP_079528
		fis)			
9486	0.001193	neural precursor cell expressed,	NM 004404	Hs.155595	NP_004395
		developmentally down-regulated 5	· · · · · · · · · · · · · · · · · · ·		
		(NEDD5), mRNA /cds=(259,1344)			
ř.		/gb=NM_004404 /gi=4758157			
		/ug=Hs.155595 /len=3433			
9491	6.35F-05	clone IMAGE:2960008, mRNA	BC017253	Hs.433345	
• .	552 50	/gb=BC017253 /gi=16878090			
		/ug=Hs.433345 /len=1405		1	
9512	0.047031	mitochondrial ribosomal protein L32	NM 031903	Hs.50252	NP_114109
- -		(MRPL32), nuclear gene encoding			-
		mitochondrial protein, mRNA			
		/cds=(47,613) /gb=NM_031903			
		/gi=13994260 /ug=Hs.50252 /len=903	;		
9515	0.03788	beta-amyloid binding protein precursor	NM 032027	Hs.333541	NP_114416
,	0.00700	(BBP), mRNA /cds=(304,927)	14141_032021	11.13.0000,41	- 144 10
	,	/gb=NM_032027 /gi=17738309			
-		/ug=Hs.333541 /len=1250	1	1	}
	<u></u>	//ug=ris.3330#1 /icii=1200	<u> </u>	<u> </u>	L

		nding To Differentially Expressed Gen		RA	
Spot	p-value	Description	Gene	Unig ne	Protein
-			Accession No.	Acc ssion	Accession
				No.	No.
9530	0.015895	hypothetical protein FLJ10856	NM_018247	Hs.108530	NP_060717
		(FLJ10856), mRNA /cds=(148,1233)			
		/gb=NM 018247 /gi=8922719			
		/ug=Hs.108530 /len=3720			
9533	0.009388	hypothetical protein FLJ20303	NM_017755	Hs.17138	NP_060225
		(FLJ20303), mRNA /cds=(86,1681)	-	, , , , , , , , , , , , , , , , , , , ,	
		/gb=NM_017755 /gi=8923284			
		/ug=Hs.17138 /len=2427			· .
9536	0.043799	DKFZP586D0824 protein, clone	BC032345	Hs.128797	NP 056475
		MGC:40527 IMAGE:5208411, mRNA,			
• .		complete cds /cds=(65,1078)	1 16		
. :		/gb=BC032345 /gi=21595443			
	Note that the	/ug=Hs.128797 /len=1499			:
9543	0.002602	NADH dehydrogenase (ubiquinone) Fe-	NM 004551	Hs.429506	NP 004542
00.10	0.002002	S protein 3, 30kDa (NADH-coenzyme Q	00.100.1		90 /0 /2
	1975 - A. 1	reductase) (NDUFS3), mRNA	And the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second o		
		/cds=(13,807) /gb=NM_004551			* *.
		/gi=4758787 /ug=Hs.429506 /len=899			
		/gi=4/30/07/ug=113.423300/ici1=033	•'		
9551	0.00587	transmembrane protein vezatin	NM 017599	Hs.24135	NP_060069
3331	0.00007	(VEZATIN), mRNA /cds=(177,1886)	11111_017333	113.24100	-000000
\$		/gb=NM_017599 /gi=19923537			:
•	_	/ug=Hs.24135 /len=3949			
9555	0.025911	D15F37 pseudogene, S3 allele, mRNA	AF041080	Hs.426451	
3000	0.023311	sequence /gb=AF041080 /gi=3660662		113.420401	
5		/ug=Hs.426451 /len=6071			
, -		rug-113.4204317/len-0071			
9566	0.004825	cDNA FLJ31107 fis, clone	AK055669	Hs.405954	
3300	0.004023	IMR322000152. /gb=AK055669	AIX033003	1113.400904	
		/gi=16550452 /ug=Hs.405954			144
	10g a 4 c	/len=2250		in the second	
9586	0.023045	NRRL 4123 mitochondrial ribosomal	U29233		4
3300	0.023943	RNA, small subunit, mitochondrial	029233		
		gene, partial sequence			
9594	0.03788	serine (or cysteine) proteinase inhibitor,	NM 006216	Hs.21858	NP_006207
3334	0.03700	clade E (nexin, plasminogen activator	14141_000210	113.2 1000	_000207
,		inhibitor type 1), member 2			
		(SERPINE2), mRNA /cds=(210,1406)			4
		/gb=NM_006216 /gi=24307906			•
			,		
9598	0.019254	/ug=Hs.21858 /len=2129 mRNA; cDNA DKFZp761C169 (from	AL161991	Hs.71252	NP 075064
จกลด	0.010254			113.7 1232	NF_0/3004
		clone DKFZp761C169); partial cds			
		/cds=(997,2475) /gb=AL161991			
0000	0.000500	/gi=7328122 /ug=Hs.71252 /len=3324	NIM COCCCC	He 00004	ND 000044
9608	0.003563	sarcoglycan, alpha (50kDa dystrophin-	NM_000023	Hs.99931	NP_000014
		associated glycoprotein) (SGCA),			1
		mRNA /cds=(12,1175) /gb=NM_000023			
		/gi=4506910 /ug=Hs.99931 /len=1404			
	·				

		nding To Differentially Expressed Gen			<u></u>
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
9609		wingless-type MMTV integration site	NM_003392	Hs.152213	NP_003383
 V		family, member 5A (WNT5A), mRNA			
		/cds=(758,1855) /gb=NM_003392			
* 1 1. 1 1.1		/gi=17402917 /ug=Hs.152213			
		/len=4428			
9623	0.030249	KIAA0854 protein (KIAA0854), mRNA	NM_014943	Hs.30209	NP_055758
		/cds=(305,2818) /gb=NM_014943			
		/gi=7662341 /ug=Hs 30209 /len=4089			
642	0.036556	FK506 binding protein 11, 19 kDa	NM_016594	Hs.24048	NP_057678
		(FKBP11), mRNA /cds=(73,678)			
		/gb=NM_016594 /gi=7706130			
		/ug=Hs.24048 /len=727			
645	0.018784	SET domain and mariner transposase	NM_006515	Hs.265855	NP_006506
		fusion gene (SETMAR), mRNA			*
. :		/cds=(23,2038) /gb=NM_006515	$x = \frac{(\frac{1}{2} - \frac{2t}{2t})^{-\frac{t}{2t}}}{(\frac{1}{2} - \frac{t}{2t})^{-\frac{t}{2t}}}$		1
		/gi=5730038 /ug=Hs.265855 /len=2063			
	1				
646	0.010277	mitochondrial ribosomal protein S5	NM_031902	Hs.433117	NP_114108
		(MRPS5), nuclear gene encoding			
		mitochondrial protein, mRNA			
		/cds=(219,1511) /gb=NM_031902			
		/gi=16554614 /ug=Hs.433117			
		/len=1678			1
648	0.043799	Similar to RIKEN cDNA 1500009M05	BC032300	Hs.295953	- "
		gene, clone MGC:40370			
	. , -	IMAGE:5105935, mRNA, complete cds			1
		/cds=(45,452) /gb=BC032300			
1		/gi=21619026 /ug=Hs.295953			1
		/len=1617			
9676	0.020388	EST(hh39d05.x1 NCI_CGAP_Co14	AW612954		
JU, U	0.020000	clone IMAGE:2957481 3' contains			
		MER33 repeat)			
682	0.005325	BX091044 Soares retina N2b4HR	BX091044	Hs.435655	
,JUZ	0.000020	cDNA clone IMAGp998D18828;	12/100/1044		
		IMAGE:360161, mRNA sequence		,	
		/clone=IMAGp998D18828_;_IMAGE:36			
		0161 /gb=BX091044 /gi=27826224		1 .	
	,	/ug=Hs.435655 /len=644		1 . *	
683	0.010704	cDNA FLJ12246 fis, clone	AK022308	Hs.188853	
7003	0.010704		الانديدة	1115.100000	
* .		MAMMA1001343. /gb=AK022308			
		/gi=10433677 /ug=Hs.188853			
2000	0.004005	/len=1766	A125 4222	1	
9699	0.001339	EST(zeh1487.seq F Zebrafish	Al354098		
· • • •		Embryonic Heart cDNA Library cDNA	1		
		[5')		<u>`- </u>	1

		nding To Differentially Expressed Gen	Gene		Drotoir
spot	p-value	Description		Unigene	Protein
			Accession No.	Acc ssion	Accession
0740	0.005225	wl54c05.x1 NCI_CGAP_Brn25 cDNA	AI864553	No. Hs.371597	No.
9712	0.005325		A1004003	HS.37 1597	
		clone IMAGE:2428712-3', mRNA sequence /clone=IMAGE:2428712			
		/clone_end=3' /gb=Al864553			
9721	0.010704	/gi=5528660 /ug=Hs.371597 /len=474 EST(yj01e06.r1 clone 147490 5')	R81297	*	NP_057707
9725		EST UI-H-BI0p-aav-d-02-0-UI.s1	AW016422		NP_05/70/
9125	0.043799	NCI CGAP_Sub2 cDNA clone	AVV010422		
1.00		IMAGE:2710683 3'			
9736	0.020240	EST(wl38a07.x1 NCI_CGAP_Ut1 clone	A1050415		NP 079457
91.30	0.030249	IMAGE:2427156 3')	A1000410		INP_0/945/
9747	0.015005	EST(ya49e04.r2 clone 53081 5')	R16260	 	
9747		hypothetical protein	NP 060190	 	-
9/51	0.032030	• •	NP_060 190		
		FLJ20234=AK000241) unnamed			
0750	0.000300	protein product [Homo sapiens]	AL598463	Un 277540	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
9759	0.009388	DKFZp313I1120_r1 313 (synonym:	AL396463 	Hs.277519	
	l fara i	hlcc2) cDNA clone DKFZp313I1120 5',	rija o		
		mRNA sequence			
•		/clone=DKFZp313l1120 /clone_end=5'		·	
		/gb=AL598463 /gi=15161154			
		/ug=Hs.277519 /len=765			1 2
9774	0.043799	cDNA FLJ36605 fis, clone	AK093924	Hs.379100	
		TRACH2015316, highly similar to	**************************************		
		VIMENTIN. /cds=(631,1317)			
		/gb=AK093924 /gi=21752883		N .	
		/ug=Hs.379100 /len=2665			
9804	2.66E-04	RNA polymerase III subunit RPC2	NM_018082	Hs.197642	NP_060552
		(RPC2), mRNA /cds=(54,3455)			
-		/gb=NM_018082 /gi=24475856	radio de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya del companya de la companya del companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de l	, t	
		/ug=Hs.197642 /len=4102			
9805	0.035177	EST (qh12h02.x1	Al240516		
		Soares_NFL_T_GBC_S1			
		IMAGE:1844499.3')			
9812	0.010277	mRNA; cDNA DKFZp313C1042 (from	AL833436	Hs.376859	
		clone DKFZp313C1042) /gb=AL833436			
		/gi=21734078 /ug=Hs.376859			
		/len=2103		<u> </u>	
9818	0.025911	EST (zn89e09.s1 Stratagene lung	AA127265		
		carcinoma 937218 cDNA clone			
		IMAGE:565384 3')			
9819	0.001193	EST (yq42a05.r1 Soares fetal liver	R94397	\$	
· 		spleen	* 1.		<u> </u>
9820	0.002602	EST (nk75h03.s1 NCI_CGAP_Sch1	AA551135		
	1	cDNA clone IMAGE:1019381 3')			1

		nding To Differentially Expressed Gen			ļ
Spot	p-valu	Description	Gene	Unig ne	Protein
			Accession No.	Acc ssion	Accession
				No.	No.
9821	0.03788	602583204F1 NIH_MGC_76 cDNA	BG565597	Hs.430998	
		clone IMAGE:4710961 5', mRNA			
		sequence /clone=IMAGE:4710961			
		/clone_end=5' /gb=BG565597			
		/gi=13573250 /ug=Hs.430998 /len=827	1		
9827	0.009388	EST CB H sapiens cDNA clone	AV743921		
		CBCCHD05 5'			
9836	0.013394	clone IMAGE:3629966, mRNA	BC005082	Hs.334575	
i ee		/gb=BC005082 /gi=13937698			
		/ug=Hs.334575 /len=1734			
9837	0.018784	growth differentiation factor 8 (GDF8),	NM 005259	Hs.41565	NP 005250
est in section of a		mRNA /cds=(134,1261)			
		/gb=NM 005259 /gi=4885258			
٠.		/ug=Hs.41565 /len=2823			
9850	0.025911	cDNA FLJ11946 fis, clone	AK022008	Hs.323231	. Propher
	1 0.0200	HEMBB1000709. /gb=AK022008	/ 11022000	113.020201	
		/gi=10433321 /ug=Hs.323231			
-		//len=3241			
9857	0 000388	vesicle-associated membrane protein 5	NIM DOSSA	Hs.74669	NP 006625
9031	0.009300	(myobrevin) (VAMP5), mRNA	14141_000034	IDS. / 4009	NP_000025
	Professional Control				
		/cds=(58,408) /gb=NM_006634			
0050	0.000500	/gi=5730111 /ug=Hs.74669 /len=618	41/050705		
9858		FLJ32223 fis, clone PLACE6004312	AK056785		
9859	0.03788	FLJ11812 fis, clone HEMBA1006364	AK021874	Hs.23837	
		/cds=UNKNOWN /gb=AK021874			
7.1		/gi=10433160 /ug=Hs.23837 /len=1369	5 T		
9875	0.023945	heat shock 27kDa protein 2 (HSPB2),	NM_001541	Hs.78846	NP_001532
		mRNA /cds=(70,618) /gb=NM_001541	a de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de l		, n
		/gi=4504518 /ug=Hs.78846 /len=874	A. S. A.		\$ Q
*.					
9890	6.56E-04	FKSG64 (FKSG64) mRNA, complete	AF338199	Hs.143740	
		cds /cds=(66,440) /gb=AF338199			
		/gi=12802898 /ug=Hs.143740 /len=916			
	· Paragraphy		1 121		
9891	0.002096	isocitrate dehydrogenase 2 (NADP),	NM_002168	Hs.5337	NP 002159
		mitochondrial (IDH2), nuclear gene	_		
	ŀ	encoding mitochondrial protein, mRNA			
		/cds=(87,1445) /gb=NM 002168			
		/gi=28178831 /ug=Hs.5337 /len=1740	l.,		
		J			
9903	0.010277	hypothetical protein MGC40157	NM 152350	Hs.295362	NP_689563
		(MGC40157), mRNA /cds=(106,498)	1,4.11_1,52,500	1.0.200002	
		/gb=NM 152350 /gi=22748758			
		/ug=Hs.295362 /len=1250			
	I	rug-rig. 200002 rigiti- 1200	1	1	1

Spot	Corr spor	lue Description (Gene	Unigene	Protein
:		C	Accession No.	Accession	Accession
				No.	No.
9904	0.005325	O-linked mannose beta1,2-N-	NM_017739	Hs.183860	NP_060209
Q		acetylglucosaminyltransferase		∤ • •	
		(FLJ20277), mRNA /cds=(142,2124)			
	la per en la	/gb=NM_017739 /gi=8923252		1 .	
		/ug=Hs.183860 /len=2737			
9907	0.040751	glucuronidase, beta (GUSB), mRNA	NM 000181	Hs.183868	NP_000172
	0.0.0.0.	/cds=(27,1982) /gb=NM 000181		110.100,000	111000172
A 44	44.1	/gi=4504222 /ug=Hs.183868 /len=2191			1
41.		/gi-4504222 /ug-ris. 165666 /ieii-2191			4
0000	0.000040		50007740	10046	
9909	0.030249	clone IMAGE:5263531, mRNA	BC037740	Hs.18016	
gr d		/gb=BC037740 /gi=22902216			1 1 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
		/ug=Hs.18016 /len=5036			
9919	0.040751	B-cell receptor-associated protein	NM_018844	Hş.27135	NP_061332
		BAP29 (BAP29), mRNA /cds=(47,775)			
1		/gb=NM_018844 /gi=9994198			
# \$7 \P*		/ug=Hs.27135 /len=1085			
9940	0.023945	BRF2, subunit of RNA polymerase III	NM 018310	Hs.274136	NP_060780
		transcription initiation factor, BRF1-like	-		.
11.7		(BRF2), mRNA /cds=(111,1370)			
y		/gb=NM_018310 /gi=22035561			and the second
		/ug=Hs.274136 /len=1978			
9941	0.030349	ribonucleotide reductase M1	NM 001033	Hs.2934	NP 001024
JJ-1	0.000240	polypeptide (RRM1), mRNA	14141_00 1000	113.2354	_001024
	· 神教 。 5 1		4 7 4		
		/cds=(233,2611) /gb=NM_001033		1.	
0050	0.000500	/gi=21071083 /ug=Hs.2934 /len=3117	11/00/4400	111 00150	110 074040
9952	0.008566	FLJ00023 protein, partial cds	AK024433	Hs.23450	NP_071942
		/cds=UNKNOWN /gb=AK024433			
		/gi=10440374 /ug=Hs.23450			
9966	0.030249	chromosome 2 open reading frame 6	NM_018221	Hs.196437	NP_060691
	1	(C2orf6), mRNA /cds=(184,834)			
		/gb=NM_018221 /gi=8922670			
		/ug=Hs.196437 /len=2543			
9967	0.003563	cDNA FLJ13630 fis, clone	AK023692	Hs.432871	12.40
		PLACE1011057. /gb=AK023692			1
		/gi=10435695 /ug=Hs.432871			
٠,		/len=2234			1
9989	0.032636	protein tyrosine phosphatase, receptor-	NM_002851	Hs.78867	NP 002842
5505	0.002030	type, Z polypeptide 1 (PTPRZ1), mRNA	14.11_002001	1,13.7,0007	_002042
• •		/cds=(148,7092) /gb=NM 002851			
*					
		/gi=4506328 /ug=Hs 78867 /len=7941			
0000	0.0075	<u></u>		1	l.:
9990	0.025911	hypothetical protein FLJ23467	NM_024575	Hs.16179	NP_078851
-		(FLJ23467), mRNA /cds=(103,657)	• .		
		/gb=NM_024575 /gi=13375749		j.	
	1	/ug=Hs.16179 /len=1196			

		nding To Differentially Expressed Gen			
Spot	p-value	D scription	Gene Accession No.	Unigene Acc ssion	Protein Accession
				No.	No.
10000	0.035177	Delta sleep inducing peptide,	AB025432	Hs.75450	NP 004080
		immunoreactor, mRNA for GILZ,	المناه المستحدين المتأثر	,	
		complete cds /cds=(233,637)			7
		/gb=AB025432 /gi=11527558			
		/ug=Hs.75450 /len=2028 (=TSC-22			
•		related protein (TSC-22R) mRNA,	3.7		
		complete cds, AF153603.1)	· · · · · · · · · · · · · · · · · · ·		
10003	0.040751	of rat nadrin (RICH1), mRNA	NM 018054	Hs.14169	NP 060524
		/cds=(71,2482) /gb=NM_018054			
	4 de/a - 1 de/a - 1	/gi=21361735 /ug=Hs.14169 /len=3219			1
		/gi. 2100 17.00 /ug 110.11100 /icii 0210			
10009	0.047031	nucleolar protein GU2 (GU2), mRNA	NM 024045	Hs.7392	NP_076950
, OOO	0.047.001	/cds=(108,2321) /gb=NM_024045	14101_025050	113.7002	111 _070000
	1. 49%	/gi=13129005 /ug=Hs.7392 /len=2575			j
10026	0.030340	dishevelled associated activator of	NM 014992	Hs.197751	NP 055807
10020	0.030249		INIVI_U14992	ПS. 191151 	INP_055607
		morphogenesis 1 (DAAM1), mRNA			
¥		/cds=(126,3362) /gb=NM_014992			
		/gi=21071076 /ug=Hs.197751			
	0.000045	/len=4256	NIN 004050	11. 00040	ND 070005
10033	0.023945	hypothetical protein FLJ11753	NM_024659	Hs.62348	NP_078935
		(FLJ11753), mRNA /cds=(14,832)	Comment of	1.1	
	4	/gb=NM_024659 /gi=13375910			1
N		/ug=Hs.62348 /len=1868			
10036	1.53E-04	src 3 domain-containing protein HIP-55	NM_014063	Hs.183373	NP_054782
		(HIP-55), mRNA /cds=(31,1326)			
		/gb=NM_014063 /gi=21361669		:	
		/ug=Hs.183373 /len=2170			
10049	0.015895	FLJ12209 fis, clone MAMMA1000962	AK022271	Hs.366548	
		/cds=UNKNOWN /gb=AK022271			
-		/gi=10433630 /ug=Hs 366548			
4	·	/len=1239	eg e Y		1
10052	0.024732	casein kinase (LOC149420), mRNA	NM_152835	Hs.29911	NP_690048
All the N	7	/cds=(290,1315) /gb=NM_152835			
		/gi=22779869 /ug=Hs.29911 /len=4299			
10057	6.22E-04	nucleosome assembly protein 1-like 3	NM 004538	Hs.21365	NP_004529
·		(NAP1L3), mRNA /cds=(265,1785)			
		/gb=NM 004538 /gi=21327709			
		/ug=Hs.21365 /len=2634			3
10058	0.014599		NM 001001	Hs.419465	NP 000992
. 5555	3.917090	mRNA /cds=(95,415) /gb=NM_001001		1.75,410400	
		/gi=16306559 /ug=Hs.419465 /len=537		1	•
		/gi- 10000000 /ug-115.4 10400 /left=00/		1	1
IOOEO	G DET OF	I CN protoin (HCHE4000), mDNA	NM: 012206	Un 270220	ND 027420
10059	0.305-05	LGN protein (HSU54999), mRNA	NM_013296	Hs.278338	NP_037428
		/cds=(174,2207) /gb=NM_013296		.:	
		/gi=9558734 /ug=Hs.278338 /len=2336			1 .
	l ·			l	

Genes Corresponding To Differentially Expressed Genes in Figur 20 - RA					
		Description	Gene	Unigene	Protein
			Accession No.	Accession No.	Accession No.
10060	0.004367	roundabout, axon guidance receptor, 1	NM 133631	Hs.301198	NP_598334
		(Drosophila) (ROBO1), transcript	 -		- -
		variant 2, mRNA /cds=(964,5802)		and the second second	100
	,	/gb=NM_133631 /gi=19743805			**
		/ug=Hs.301198 /len=7475			
10062		ubiquitin-like, containing PHD and	NM 152306	Hs.348602	NP 690856
	0.0202.0	RING finger domains 2 (URF2),			
5.7		transcript variant 1, mRNA	l de la familia de la familia de la familia de la familia de la familia de la familia de la familia de la fami La familia de la familia de la familia de la familia de la familia de la familia de la familia de la familia d		. 1.
r'		/cds=(341,1852) /gb=NM_152306			
		/gi=23312361 /ug=Hs.348602	Variable Control		
		/len=3720			1
10069	0.022106	hypothetical protein FLJ20297	NM_017751	Hs.94491	NP_060421
10009	0.022100	(FLJ20297), mRNA /cds=(111,2507)	14141_017731	113.54451	141 _000421
		/gb=NM 017751 /gi=8923276			
		/ug=Hs.94491 /len=3682			
10081	0.017200	CDC5 cell division cycle 5-like (S.	NM_001253	Hs.155174	NP_001244
10001	0.017200	pombe) (CDC5L), mRNA	14141_001233	1113, 100 174	141 _00 1244
		/cds=(260,2668) /gb=NM_001253			
		/gi=16357499 /ug=Hs.155174			
we in a			+ 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		
40000	0.000000	/len=3012	AKOOOOC	Uo 56947	
10083	0.009388	cDNA FLJ12874 fis, clone	AK022936	Hs.56847	
		NT2RP2003769. /gb=AK022936			
	•	/gi=10434613 /ug=Hs.56847 /len=2867			
10001	0.00000		NINA 004 450	11. 400070	ND 440044
10084	0.009388	hypothetical protein MGC11034	NM_031453	Hs.103378	NP_113641
		(MGC11034), mRNA /cds=(246,641)		'	
		/gb=NM_031453 /gi=13899290			
<u> </u>		/ug=Hs.103378 /len=3301			
10085	2.32E-04	mRNA for KIAA0931 protein, partial	AB023148	Hs.173373	
		cds. /cds=(1,2205) /gb=AB023148		·	
		/gi=4589505 /ug=Hs.173373 /len=6167			
10087	0.010277		AK054626	Hs.188504	6
t : .		ADRGL2000323. /cds=(118,516)			
		/gb=AK054626 /gi=16549205	* .		
	<u> </u>	/ug=Hs.188504 /len=2081			
10094	0.00168	nuclear factor of kappa light polypeptide	NM_013432	Hs.323834	NP_038460
		gene enhancer in B-cells inhibitor-like		1	
		2(NFKBIL2), mRNA /cds=(473,4132)		1	
		/gb=NM_013432/gi=15718771			
		/ug=Hs.323834 /len=4501			1.
8.7					
10102	0.020388	hypothetical protein FLJ23445	NM_025075	Hs.288151	NP_079351
,		(FLJ23445), mRNA /cds=(44,658)			
		/gb=NM_025075 /gi=13376622			
	1	/ug=Hs.288151 /len=963		1	1.

Spot		nding To Differentially Expr ssed Gen	Cominguie 20 -		
	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10103	0.013394	eukaryotic translation elongation factor	NM_001404	Hs.256184	NP_001395
		1 gamma (EEF1G), mRNA			I
		/cds=(38,1351) /gb=NM_001404			
		/gi=25453475 /ug=Hs.256184			; :
40444	0.005.04	/len=1429	NIM 000040	11- 400050	NID GOODS
10111	2.66E-04	ubiquitin-conjugating enzyme E2G 2	NM_003343	Hs.192853	NP_003334
		(UBC7 yeast) (UBE2G2), mRNA /cds=(56,553) /gb=NM_003343			
		/gi=4507780 /ug=Hs.192853 /len=2900			
		/gi=430/760/ug=148.192033/te11=2900			
10112	0.043799	COP9 constitutive photomorphogenic	NM 006837	Hs.380969	NP 006828
		subunit 5 (Arabidopsis) (COPS5),			
	,	mRNA /cds=(121,1125)			4-10
		/gb=NM_006837 /gi=5803045			
		/ug=Hs:380969 /len=1277			
10130	0.021	UI-H-EU1-bad-c-14-0-UI.s1	BQ447141	Hs.445111	
		NCI_CGAP_Ct1 cDNA clone UI-H-EU1-			
		bad-c-14-0-UI 3', mRNA sequence			
		/clone=UI-H-EU1-bad-c-14-0-UI			
	T.	/clone_end=3' /gb=BQ447141			
,		/gi=21250253 /ug=Hs.445111			
40450	0.007407	/len=1032			
10152	0.007107	EST(oa36e01.s1 NCI_CGAP_GCB1	AA766399	-	
		clone IMAGE:1307064 contains Alu			
10170	0.012204	repeat) (low match) EST (ts95a10.x1 NCI_CGAP_GC6	Al635513	,	*
10170	0.013394	cDNA clone IMAGE:2239002 3')	A1035513		
10177	0.02801	EST	W44584		
1 1 1 1 1	0.02001	Soares_senescent_fibroblasts_NbHSF	••••		
1		cDNA clone IMAGE:323750 3'			
10178	0.010277	EST382135 MAGE resequences,	AW970055	Hs.324815	
		MAGK cDNA, mRNA sequence			
· +		/gb=AW970055 /gi=8159900			
		/ug=Hs.324815 /len=764			
.10180	0.02801	WW45 protein (WW45), mRNA	NM_021818	Hs.288906	NP_068590
		/cds=(339,1490) /gb=NM_021818			3 ×
		/gi=18860913 /ug=Hs.288906		**	4.
40.400		/len=3031		1	
10186	0.047031	transmembrane 4 superfamily member	NM_003270	Hs.121068	NP_003261
		6 (TM4SF6), mRNA /cds=(104,841)			
		/gb=NM_003270 /gi=21265115		3	
,		/ug=Hs.121068 /len=2069			
1.	L	DADCA	NIM OGGGG	11- 5000	ND 002960
10206	n na3799	IKARNA Member Kas oncodene tamiiv	LIMINE DILLEMAN	IHS DO 3D	HALF HALLANDII
10206	0.043799	RAB6A, member RAS oncogene family (RAB6A), mRNA /cds=(427, 1053)	NM_002869	Hs.5636	NP_002860
10206	0.043799	(RAB6A), member RAS oncogene family (RAB6A), mRNA /cds=(427,1053) /gb=NM 002869 /gi=19923230	INIVI_UUZ009	HS.5036	NP_002860

Genes	Corr spor	nding To Diff rentially Express d Gen	es in Figure 20 -	RA	
		Description	Gene	Unigene	Protein
			Acc ssion No.	Accession	Accession
į.	:			No.	No.
10212	0.017288	EST(ye51h07.s1 Soares fetal liver	T96639	110.	110.
, , ,		spleen 1NFLS clone IMAGE:121309 3			
		similar to contains Alu repetitive			
		element; contains L1 repetitive element)		, , ,	
	* -	oloment, contains Et repetitive element,			
10219	0.02801	chemokine-like factor super family 6	NM 017801	Hs.380627	NP_060271
102.0	0.02001	(CKLFSF6), mRNA /cds=(108,659)	11111_017007	113.500027	141 _000271
		/gb=NM_017801 /gi=8923369			
	12 1 1 1	/ug=Hs.380627 /len=1904			
10229	0.017755	complement C1r-like proteinase	NM 016546	11a 00574	ND 057020
10229	0.017733		NIVI_U 10040	Hs.98571	NP_057630
		precursor, (LOC51279), mRNA			
		/cds=(18,1481) /gb=NM_016546	1		
10040	0.007407	/gi=7706082 /ug=Hs.98571 /len=3345	NA 000070	11-40000	ND 4450.5
10240	0.007107	hypothetical protein DKFZp586C1924	NM_032273	Hs.108338	NP_115649
	na to parameter	(DKFZp586C1924), mRNA			
		/cds=(106,693) /gb=NM_032273	•		
		/gi=14150016 /ug=Hs.108338 /len=782			
10266	0.017288	EST yi39c07.s1 Soares placenta	R69076		
٠.		Nb2HP cDNA clone IMAGE:141612 3'			
		similar to contains Alu repetitive			
v 1	11	element;			
10267	0.047031	BX114194 Soares melanocyte 2NbHM	BX114194	Hs.176420	
	The second	cDNA clone IMAGp998J14570, mRNA			
		sequence			
		/clone=IMAGp998J14570 ; IMAGE:26	1 · • • • • • • • • • • • • • • • • • •		
		1229 /gb=BX114194 /gi=27838661			
		/ug=Hs.176420 /len=687	1 -11		
10276	0.00587	Hypothetical protein(cDNA sequence	AK002173		NP_689971
		FLJ11311 fis, clone PLACE1010102)			
		(=cDNA sequence DKFZp566J2146)			
10278	0.007807	7b50e11.x1 NCI_CGAP_Lu24 cDNA	BE550231	Hs.282013	JA
		clone IMAGE:3231692 3', mRNA		· · · · · · · · · · · · · · · · · · ·	
		sequence /clone=IMAGE:3231692			
		/clone_end=3' /gb=BE550231			
	,	/gi=9791923 /ug=Hs.282013 /len=550			
10282	0.040751	EST (7083a06.x1 NCI_CGAP_Kid11	BF197462	 	
	2.0.10101	cDNA clone IMAGE:3642898 3')	51 101704]	
10286	0.003563	Similar to cell death activator CIDE-3,	BC043599	Hs.432698	
.02.00	3.00000	clone MGC:50748 IMAGE:5204770,	DO040099	1113.432030	
		mRNA, complete cds /cds=(432,617)	٠.		
		/gb=BC043599 /gi=27694390			
10007	0.435.04	/ug=Hs.432698 /len=1832	T07044		
10287	9.43⊑-04	EST (ye08g06.r1 Stratagene lung	T87941		
		(#937210) cDNA clone IMAGE:117178	:		
40000	0.00000	5')	1,1000-10	· · · · · · · · · · · · · · · · · · ·	<u> </u>
10292	0.002337	EST (qn52a04.x1 NCI_CGAP_Kid5	AI302546		
		IMAGE:1901838 3')		L	

G nes	Correspoi	nding To Diff rentially Express d Gen	es in Figur 20	RA	
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
10205	0.040751	EST(hi61a05.x1	AW631139	No.	No.
10233	0.040731	Soares_NFL_T_GBC_S1 cDNA clone	AVVOJITOS		
		IMAGE:2976752 3')		•	
10312	0.033876	TATA box binding protein (TBP)-	NM 005681	Hs.153088	NP 647603
10012	0.000070	associated factor, RNA polymerase I,		113.10000	141 _047,003
ye et i		A, 48kDa (TAF1A), transcript variant 1,	A STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STA		
		mRNA /cds=(190,1542)	,		
		/gb=NM_005681 /gi=21536363			
		/ug=Hs.153088 /len=1893			
10313	0.001339	UI-E-CI1-agf-h-05-0-UI r1 UI-E-CI1	BM705313	Hs.406335	
	**************************************	cDNA clone UI-E-CI1-agf-h-05-0-UI 5',		,	
		mRNA sequence /clone=UI-E-CI1-agf-h			
		05-0-UI /clone_end=5' /gb=BM705313			
		/gi=19018571 /ug=Hs.406335			
	1	/len=1200	A.		
10324	5.79E-04	HNC49-1-E8:R HNC Normal Cartilage)	BG929317	Hs.244283	
		cDNA, mRNA sequence			
		/gb=BG929317 /gi=14323840			
		/ug=Hs.244283 /len=755			
10325	0.001501	EST IL2-UM0076-130500-084-A01	AW802834		
		UM0076 cDNA			
10330	0.004367	EST xa58b09.x1 NCI_CGAP_HSC2	AW073612		
		cDNA clone IMAGE:2570969 3' similar			
		to contains Alu repetitive element;			
10343	0.008566	cDNA FLJ14028 fis, clone	AK024090		
10010	0.00000	HEMBA1003838	711102-1000		
10352	2 32F-04	EST RC2-HT0977-211100-018-b02	BF837494		
	L.OLL O	HT0977 cDNA			
10353	0.039408	EST (clone MGC:8720	BC011369.1		AAH11369.1
v		IMAGE:3868798 /cds=(12,431)			
10354	3.04E-04	EST (cn12g10.x1 Normal Trabecular	AI751952		NP 037359
		Bone Cells H.sapiens cDNA clone			_
		NHTBC_cn12g10 random)			
10355	0.018784	selenoprotein H (SELH), mRNA	NM_170746 -	Hs.290874	NP 734467
		/cds=(243,611) /gb=NM_170746	-		1 - 7 - 1
		/gi=25014108 /ug=Hs.290874 /len=834			
			#		
10357	0.040751	ribosomal protein L23 (RPL23), mRNA	NM_000978	Hs.234518	NP_000969
		/cds=(27,449) /gb=NM_000978	*	1	
		/gi=14591907 /ug=Hs.234518 /len=493			
10358	0.003947	cDNA, 5' end /clone=IMAGE:4148900	BF342391	Hs.30469	NP 055313
	3.3300 //	/clone_end=5' /gb=BF342391		1.0.00	
		/gi=11289392 /ug=Hs.30469 /len=803			
10361	0.040751	Est (zf66a10.s1 Soares retina N2b4HR	AA058771	<u> </u>	1
	1	IMAGE:381882 3')	, , , , , , , , , , , , , , , , , , , ,	1	

		nding To Diff rentially Expressed G n			· · · · ·
Spot	p-value	D scription	Gene	Unigene "	Protein
			Accession No.	Accession	Accession
				No.	No.
10363	0.002337	Similar to RIKEN cDNA 2310026P19	BC043352	Hs.35096	
		gene, clone MGC:49935			
•	•	IMAGE:6175382, mRNA, complete cds			
		/cds=(288,3329) /gb=BC043352			
		/gi=27694113 /ug=Hs.35096 /len=5900	*		
		/gi-2/034 13 /ug-115.33030 /ieii=3300			
10364	0.035177	EST (QV3-NN1023-130500-178-g10	AW902437		
10304	0.033177	NN1023)	AVV302431		
10267	0.004267	hypothetical protein BC009518	NM 138363	Hs.135265	NP 612372
10367	0.004507		NIVI_ 130303	ns.133263	NP_012372
	-	(LOC90799), mRNA /cds=(59,2524)			
-		/gb=NM_138363 /gi=19923898			
		/ug=Hs.135265 /len=2705			
10390	0.001878	EST (tf13a08.x5 NCI_CGAP_Brn23	AI939444		
		cDNA clone IMAGE:2096054 3')	<u></u>		
10392	0.002096	ribosomal protein, large, P1 (RPLP1),	NM_001003	Hs.424299	NP_000994
		mRNA /cds=(130,474) /gb=NM_001003			
		/gi=16905511 /ug=Hs.424299 /len=512		1	
	4.			*. *. *. *. *. *. *. *. *. *. *. *. *. *	
10397	0.012276	maternal G10 transcript (G10), mRNA	NM_003910	Hs.380233	NP_003901
		/cds=(380,814) /gb=NM 003910			
-	:	/gi=4503836 /ug=Hs.380233 /len=1003			
10400	0.001062	EST (602616324F1 NIH_MGC_79	BG619143		
		cDNA clone IMAGE:4730333 5')			
10401	7.41F-04	EST (Clontech human aorta polyA	C14262		
		mRNA (#6572) cDNA clone GEN-	7.1.		
		041E02.5')			
10403	0.023945	wb40b11.x1 NCI_CGAP_GC6 cDNA	Al652865	Hs.374238	
10403	0.023943	clone IMAGE:2308125 3', mRNA	A1002000	113.07-1200	
		sequence /clone=IMAGE:2308125		* * * * * * * * * * * * * * * * * * * *	
19.0					
. The T		/clone_end=3' /gb=Al652865			
40400	0.000000	/gi=4736844 /ug=Hs.374238 /len=598	00004757	11- 445074	<u> </u>
10436	0.032636	Indian hedgehog (Drosophila), clone	BC034757	Hs.115274	
		MGC:34815 IMAGE:5182642, mRNA,			1. 1.
		complete cds /cds=(74,955)			1 - 1 - 1
		/gb=BC034757 /gi=21961329			
		/ug=Hs.115274 /len=1760			
10437	0.017288	UI-H-EI1-aze-c-02-0-UI.s1	BQ003590	Hs.29698	
		NCI_CGAP_EI1 cDNA clone			
*		IMAGE:5847481 3', mRNA sequence		1	
		/clone=IMAGE:5847481 /clone_end=3'			
		/gb=BQ003590 /gi=19728490			
		/ug=Hs.29698 /len=1051	1		
, .	İ.,				
10439	0.017288	clone IMAGE:4157625, mRNA	BC033767	Hs.271450	T
		/gb=BC033767 /gi=22832873			
		/ug=Hs.271450 /len=1515		1	1
	 	EST(hh87d09.x1 NCI CGAP GU1	AW627547	 	
10459	L0 003563	IESTON8/009XTNGLGGAP GO	IAVV02/04/		

		nding To Differentially Expressed Gen			<u> </u>
Spot	p-value	Description	Gene	Unig ne	Prot in
			Accession No.	Accession	Accession
			<u> </u>	No.	No.
10466	0.001878	cDNA, 5' end /clone=IMAGE:4592424	BG400792	Hs.83286	NP_714916
	A	/clone_end=5' /gb=BG400792	and the second of the second of	The second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon	
· ·		/gi=13294240 /ug=Hs 83286 /len=973		<u></u>	<u> </u>
10467	4.50E-04	cDNA, 3' end /clone=IMAGE:826617	AA521497	Hs.272095	NP_690601
•		/clone_end=3' /gb=AA521497		\	
		/gi=2262040 /ug=Hs.272095 /len=657			1.
10491	0.017288	UI-H-DH0-aul-j-10-0-UI.s1	BM994461	Hs.434057	
		NCI_CGAP_DH0 cDNA clone			
		IMAGE:5871081 3', mRNA sequence			
		/clone=IMAGE:5871081 /clone_end=3'			
		/gb=BM994461 /gi=19719362			
		/ug=Hs.434057 /len=2059			
	30 80				
10496	0.011238	zh69e06.s1	W89192	Hs.194238	
. 5-55	0.011230	Soares_fetal_liver_spleen_1NFLS_S1	V V U J I J Z	1113.134230	
arti Turka		cDNA clone IMAGE:417346 3', mRNA			
	j	sequence /clone=IMAGE:417346			
			Lagrania de la compansión de la compansión de la compansión de la compansión de la compansión de la compansión		
- 1.21	r: 51.7 " 1	/clone_end=3' /gb=W89192			
10407	0.005000	/gi=1404504 /ug=Hs.194238 /len=471	0.4.00000	11 00000	
10497	0.005898	UI-H-DF0-bek-n-06-0-UI.s1	CA426336	Hs.20300	
		NCI_CGAP_DF0 cDNA clone UI-H-DF0			
		bek-n-06-0-UI 3', mRNA sequence			· · · · · ·
		/clone=UI-H-DF0-bek-n-06-0-UI			
		/clone_end=3' /gb=CA426336	i		
		/gi=24789062 /ug=Hs.20300 /len=1060		į .	
10504	0.025911	AGENCOURT_8152128	BU145410	Hs.304440	
		Lupski_dorsal_root_ganglion cDNA			
		clone IMAGE:6184005 5', mRNA			
		sequence /clone=IMAGE:6184005			
		/clone_end=5' /gb=BU145410			
		/gi=22658942 /ug=Hs.304440 /len=889			
10506	0.018784	K-EST0187941 L14ChoiCK0 cDNA	CB135678	Hs.435110	
		clone L14ChoiCK0-30-C05 5', mRNA		(· '
•		sequence /clone=L14ChoiCK0-30-C05			
		/clone_end=5' /gb=CB135678	• • • • • • • • • • • • • • • • • • •		
		/gi=28102621 /ug=Hs.435110 /len=419			Į.
**					
10509	0.009388	UI-H-DF0-bek-k-02-0-UI.s1	CA426088	Hs.285174	
		NCI_CGAP_DF0 cDNA clone UI-H-DF0			
	ļ. '	bek-k-02-0-UI'3', mRNA sequence	i	į.	1
		/clone=UI-H-DF0-bek-k-02-0-UI			: 1
		/clone_end=3' /gb=CA426088			1
3		/cione_end=3 /gb=CA426066 /gi=24788814 /ug=Hs.285174			1
		/len=1052			
	<u> </u>	men-100Z	L	L	<u> </u>

Genes	Correspo	nding To Differentially Expressed Gen	s in Figure 20 -	RA	
Spot	p-value	Description	Gene Accession No.	Unigene Acc ssion	Protein Accession
7 1			2.0	No.	No.
10511	0.011238	cDNA FLJ34603 fis, clone KIDNE2013388. /gb=AK091922 /gi=21750400 /ug=Hs.304130	AK091922	Hs.304130	
		/len=1992			
10512	0.043799		· · · · · · · · · · · · · · · · · · ·	 	
		UI-H-EI1-ayz-p-10-0-UI.s1	BQ006715	Hs.29088	
10010	0.010033	NCI_CGAP_EI1 cDNA clone	DQ000713	113.23000	
		IMAGE:5845881 3', mRNA sequence /clone=IMAGE:5845881 /clone_end=3'			1
		/gb=BQ006715 /gi=19731615			1
	*	/ug=Hs.29088 /len=1062			, , , , ,
		7ug=113.29000 //en=1002			
10520	0.005325	ribosomal protein L35a (RPL35A),	NM_000996	Hs.288544	NP_000987
		mRNA /cds=(74,406) /gb=NM_000996			
		/gi=16117790 /ug=Hs.288544 /len=511			
10535	0.01/1500	heterogeneous nuclear	NM 031844	Hs.103804	NP 114032
10000	0.014333	ribonucleoprotein U (scaffold	14141_031044	1115.103004	114032
A		attachment factor A) (HNRPU),			
	A 4 4	transcript variant 1, mRNA			
		/cds=(218,2692) /gb=NM_031844			
		/gi=14141162 /ug=Hs.103804			
		/len=3500			
10536	0.011238	nascent-polypeptide-associated	NM_005594	Hs.32916	NP_005585
		complex alpha polypeptide (NACA),			
		mRNA /cds=(26,673) /gb=NM_005594		ļ.	
		/gi=5031930 /ug=Hs.32916 /len=797			
10539	2.32E-04	ribosomal protein, large, P1 (RPLP1),	NM_001003	Hs.424299	NP_000994
		mRNA /cds=(130,474) /gb=NM_001003		*	
l		/gi=16905511 /ug=Hs.424299 /len=512			
· ·					
10544	0.003183	hypothetical protein LOC153339	NM_174909	Hs.374538	NP_777569
İ		(LOC153339), mRNA /cds=(21,239)	**		
١.		/gb=NM_174909 /gi=28372532	5 ·		
10547	0.030340	/ug=Hs.374538 /len=726 mRNA; cDNA DKFZp564B032 (from	AL049975	Hs.274510	ļ
10347	0.050249	clone DKFZp564B032) /gb=AL049975	AL049975	FIS.274510	
		/gi=4884225 /ug=Hs.274510 /len=1943			
	,	1940			
10551	0.007107	EST(cDNA clone IMAGE:814978 3'	AA465709		
I		similar to TR:E91737 E91737			
1		REVERSE TRANSCRIPTASE			
		HOMOLOG {L1 REPETITIVE		1	
		ELEMENT); contains L1.t1 L1 repetitive			
		element ;)			
10555	0.015895	clone IMAGE:5001859, mRNA	BC040072	Hs.194051	
!		/gb=BC040072 /gi=25303948			
,	<u> </u>	/ug=Hs.194051 /len=3016		<u> </u>	

		nding To Differentially Express d Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
			<u> </u>	No.	No.
10558	0.017288	ESTs, cDNA /clone=IMAGE:1372579	AA833868	Hs.156300	
		/gb=AA833868 /gi=2908636	and the second of the second		
		/ug=Hs.156300 /len=495			
10568	0.032636	UI-E-EO1-ajd-j-06-0-UI.s1 UI-E-EO1	BM683224	Hs.445152	
	-	cDNA clone UI-E-EO1-ajd-j-06-0-UI 3',			·
		mRNA sequence /clone=UI-E-EO1-aid-i			
		06-0-UI /clone_end=3' /gb=BM683224			,
		/gi=18993120 /ug=Hs.445152			
		/len=1041			
10574	0.022802	cDNA FLJ38300 fis, clone	AK095619	Hs.34969	1 1
.00.	0.022002	FCBBF3017288. /gb=AK095619	, , ,	1	
		/gi=21754917 /ug=Hs.34969 /len=3695			
				Programme of	
10583	0.02801	AV700930 GKC cDNA clone	AV700930	Hs.285894	
، دېږي	0.02001	GKCBRB12 3', mRNA sequence	,	1.13.200034	
		/clone=GKCBRB12 /clone_end=3'			
1 44	5 500 9	/gb=AV700930 /gi=10302901	9.4		
		/ug=Hs.285894 /len=746			
10593	0.002002	twisted gastrulation 1 (Drosophila)	NM 020648	Un 247202	ND OCECOO
10593	0.002093		NNI_U2U048	Hs.247302	NP_065699
		(TWSG1), mRNA /cds=(106,777)			
		/gb=NM_020648 /gi=21314788			
40504	0.040070	/ug=Hs.247302 /len=3693	5.555500		
10594	0.012276	UI-H-EZ1-bbh-j-15-0-UI.s1	BQ575990	Hs.445509	
		NCI_CGAP_Ch2 cDNA clone UI-H-EZ1		100	
	* * *	bbh-j-15-0-UI 3', mRNA sequence			
	1	/clone=UI-H-EZ1-bbh-j-15-0-UI			
- 1		/clone_end=3' /gb=BQ575990			
		/gi=21479307 /ug=Hs 445509			
		/len=1032			
	0.035177	EST(cDNA clone IMAGE:5402358 5')	BI868276		NP_003109
10600	0.017288	EST(cDNA clone IMAGE:429436 3'	AA007616		
		similar to contains L1.t1 L1 repetitive			
- **		element;)			
10603	0.009388	eukaryotic translation elongation factor	NM_001402	Hs.422118	NP_001393
	İ	1 alpha 1 (EEF1A1), mRNA		1 .	
•		/cds=(63,1451) /gb=NM_001402			
		/gi=25453469 /ug=Hs 422118			
		/len=1837			
10610	0.002337	cDNA, 3' end /clone=IMAGE:3476408	BF058813	Hs.319312	NP_001454
		/clone_end=3' /gb=BF058813	:		ļ . [—] :
		/gi=10812709 /ug=Hs.319312 /len=382	. ,		
				1	
10612	0.023945	cDNA FLJ39382 fis, clone	AK096701	Hs.293799	
,		PERIC2000473. /gb=AK096701			1 -
	·	/gi=21756253 /ug=Hs.293799		•	1
		/len=2425	l .	٠.	
10621	0.000388	EST (383946 MAGE resequences	AW971857		
10021	3.555500	(MAGL)	1,110,100,		
	L	EST(cDNA clone IMAGE:4775876-5')	BG740183		NP-078806

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
-]			Accession No.	Accession	Accession
	, e			No.	No.
0628	0.018784	ESTs, cDNA, 3' end	AI732470	Hs.191157	
		/clone=IMAGE:565677 /clone end=3	and see the second	للمحاي بالم	الماقد والالمجادية
i		/gb=Al732470 /gi=5053583	e dita	A CONTRACT	
		/ug=Hs.191157 /len=596			
0633		UI-E-CL1-afa-n-02-0-UI.r1 UI-E-CL1	BM696235	Hs.446332	
		cDNA clone UI-E-CL1-afa-n-02-0-UI 5',			
	٠,	mRNA sequence /clone=UI-E-CL1-afa-			
		n-02-0-UI /clone_end=5'			
		/gb=BM696235 /gi=19009493			
		/ug=Hs.446332 /len=1366		1	
0634		7b59h11.x1 NCI_CGAP_Lu24 cDNA	BE550855	Hs.282143	
	0.020000	clone IMAGE:3232581 3', mRNA	12200000		
		sequence /clone=IMAGE:3232581			
2		/clone_end=3' /gb=BE550855			
		/gi=9792547 /ug=Hs.282143 /len=537			l T
0636	0.005325	cDNA FLJ13571 fis, clone	AK023633	Hs.116278	1.50 Tay 10
0030	0.003323	PLACE1008405. /gb=AK023633	/NO23033	1113.110270	
A . 1		/gi=10435617 /ug=Hs.116278			3
		/len=2484			
0640	2.475.04	HSC3IC021 normalized infant brain	F13068		
0642	3.47E-04		[F13068		
00.45	0.044500	cDNA cDNA clone c-3ic02	A1040400	11- 400500	
0645	0.014599	qp48e07.x1 NCI_CGAP_Co8 cDNA	AI346102	Hs.193566	
		clone IMAGE 1926276 3' similar to			1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1
		gb:X56411_rna1 ALCOHOL			, ,
4 %		DEHYDROGENASE CLASS II PI			
		CHAIN mRNA sequence			
		/clone=IMAGE:1926276 /clone_end=3'	<i>*</i> :.		
		/gb=Al346102 /gi=4083308			
<u> </u>		/ug=Hs.193566 /len=718			
0648	0.002337	EST, cDNA, 3' end	BQ002644	Hs.364307	
		/clone=IMAGE:5843665 /clone_end=3'			
		/gb=BQ002644 /gi=19727544			l territori
		/ug=Hs.364307 /len=762			
0668	0.022106	UI-H-FH1-bfh-g-05-0-UI.s1	BU618251	Hs.396671	
		NCI_CGAP_FH1 cDNA clone UI-H-FH1			
		bfh-g-05-0-UI 3', mRNA sequence			
		/clone=UI-H-FH1-bfh-g-05-0-UI			100
		/clone_end=3' /gb=BU618251			
	, J	/gi=23284466 /ug=Hs.396671			
		/len=1126			
0679	0.003563	EST(cDNA clone IMAGE:3698005 3')	BF593414		NP_598411
0683	0.018784	EST388886 MAGE resequences,	AW976777	Hs.223578	
		MAGO cDNA, mRNA sequence		la de la companya de la companya de la companya de la companya de la companya de la companya de la companya de	
		/gb=AW976777 /gi=8168011			1
		/ug=Hs.223578 /len=519			
0684	0.007807	EST(cDNA clone IMAGE:4090855 3')	BF447403	3.3	NP_002806
		No significant match	SEQ.ID.No.46		
		Novel, ORF-3(250~456),-2(332~499)	SEQ.ID.No.98	T	

	p-value	nding To Differentially Expressed Gen Description	Gene	Unigene	Protein
Spot	p-value	Description	Accession No.	Accession No.	Accession No.
10723	0.002602	No significant match (ORF:+2:332~437[107])	SEQ.ID.No.15		
10729	0.001878	myc-induced nuclear antigen, 53 kDa	NM_032778	Hs.23294	NP 116167
		(MINA53), transcript variant 2, mRNA			
		/cds=(214,1608) /gb=NM 032778			
		/gi=23346417 /ug=Hs.23294 /len=2221	. '		
1				<u>.</u>	
10746	0.008566	No significant match			
		(ORF:+3:69~302[234])	SEQ.ID.No.27		
10779	0.018784	EST (ADB cDNA clone ADBAKA02 5')	AV704531		
.0,.0	0.010.01		/		
10787	0.006463	cDNA FLJ37147 fis, clone	AK094466	Hs.420088	
.0.0.	0.000-00	BRACE2025316, weakly similar to	711,000 1-100	113.42000	
		tRNA-splicing endonuclease subunit.		*	
		/cds=(26,559) /gb=AK094466			
		/gi=21753534 /ug=Hs.420088			
		/len=1738			
10797	0.040751	EST (366564 MAGE resequences	AW954494	100000	
10191	0.040731	MAGC)	AVV354434 		
10700	0.012204	EST (ta16g05.x1 NCI_CGAP_Lym5	Al471814	Age of the same	
10790	0.013394	IMAGE:2044280 3')	M47 10 14		
10799	0.040076	cDNA FLJ11934 fis, clone	AK021996	Hs.261699	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
10799	0.012276		AKU2 1990	IUS.50 1099	
		HEMBB1000510. /gb=AK021996			
		/gi=10433305 /ug=Hs.261699			
10000	0.000045	/len=2599	AK097311	Un 400000	
10802	0.023945	cDNA FLJ39992 fis, clone	AK09/311	Hs.126083	
		STOMA2001025, moderately similar to			
		RNA-binding protein (RBMS3) mRNA.			
		/gb=AK097311 /gi=21757015			
40004	0.00000	/ug=Hs.126083 /len=1490	1105700	<u> </u>	-
10804	0.009388	EST (yr74c11 s1 Soares fetal liver	H65780		
40005	0.00000	spleen 1NFLS IMAGE:211028 3')	1 1 2 1 5 0 0 0		<u> </u>
10805	0.002893	EST(ak84d11.s1 Barstead spleen	AA845289		
		HPLRB2 cDNA clone IMAGE:1414581			1 .
		3' similar to contains MER10.t3 MER10	:		
40007	2 22 22 42	repetitive element)	104 040050		
10807	0.030249	methyltransferase like 3 (METTL3),	NM_019852	Hs.268149	NP_062826
	Ï	mRNA /cds=(87,1829) /gb=NM_019852		<i>*</i>	
	} `	/gi=21361826 /ug=Hs.268149	1	1	1
		/len=1959		ļ	
10810	2.32E-04	EST np88f03.s1 NCI_CGAP_Thy1	AA632906		
	<u> </u>	cDNA clone IMAGE:1133405	<u> </u>	<u> </u>	
10811	0.010277	EST from clone 208499, full insert	AL355688	Hs.6655	1
		/gb=AL355688 /gi=7799136		1	· ·
		/ug=Hs.6655 /len=1831			
10815	0.003213	hypothetical protein FLJ13213	NM_024755	Hs.331328	NP_079031
	,	(FLJ13213), mRNA /cds=(234,1670)			1
		/gb=NM_024755 /gi=13376087			ļ
	` . ′	/ug=Hs.331328 /len=2617		ļ	1

		nding To Differentially Expressed Gen			
Spot	p-value	Description	G ne	Unigene	Protein
			Accession No.	Accession No.	Accession No.
10816	0.017755	hypothetical protein FLJ10769	NM-018210	Hs.8083	NP 060680
		(FLJ10769), mRNA /cds=(15,1187)			-
		/gb=NM_018210 /gi=8922653			
		/ug=Hs.8083 /len=2659			
10819	0.002337	EST (integral membrane protein 2A,	BC010511		NP_004858
		clone IMAGE:4149910, mRNA)			
10820	0.00587	hypothetical protein MGC39497	NM_152436	Hs.406728	NP_689649
		(MGC39497), mRNA /cds=(9,770)			
		/gb=NM_152436 /gi=22748922			
		/ug=Hs.406728 /len=1745			
10825	0.014599	ribosomal protein L13 (RPL13),	NM_033251	Hs.431392	NP_150254
		transcript variant 2, mRNA			
		/cds=(238,873) /gb=NM_033251			
		/gi=15431294 /ug=Hs.431392			
A		/len=1296			
10835	0.018784	UI-1-BC1p-ati-g-12-0-UI.s1	BQ011970	Hs 28625	366
	17	NCI_CGAP_PI3 cDNA clone UI-1-BC1p			
		ati-g-12-0-UI 3', mRNA sequence			
	1 44	/clone=UI-1-BC1p-ati-g-12-0-UI			
		/clone_end=3' /gb=BQ011970	```	1	
		/gi=19736871 /ug=Hs.28625 /len=1149	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	.	
			<u></u>		
10836		EST (nj28d04.s1 NCI_CGAP_AA1	AA600996		
		cDNA clone IMAGE:993799 3')			
10837	0.014599	cDNA FLJ10878 fis, clone	AK001740	Hs.15144	NP_064715
	1. The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of th	NT2RP4001893, highly similar to			
		mRNA, cDNA DKFZp564O043.	<u>.</u>		
		/gb=AK001740 /gi=7023191			1
		/ug=Hs.15144 /len=2599			
10839	0.003563	calcium binding protein Cab45	NM_016547	Hs.42806	NP_057631
		precursor (Cab45), mRNA			
		/cds=(294,1340) /gb=NM_016547			
100.40	0.047000	/gi=7706572 /ug=Hs.42806 /len=2092	 		
10840	0.017288	hypothetical protein FLJ11292	NM_018382	Hs.272246	NP_060852
		(FLJ11292), mRNA /cds=(151,615)	• I		
		/gb=NM_018382 /gi=8922980	·		
10044		/ug=Hs.272246 /len=1948			
10841	7.41L-04	zinc finger protein 306 (ZNF306),	NM_024493	Hs.66774	NP_077819
		mRNA /cds=(149,1765)			
		/gb=NM_024493 /gi=24308296			
10054	0.047024	/ug=Hs:66774 /len=2242	AVAIDO 000 1		<u> </u>
10851	0.04/031	EST xr58h08.x1 NCI_CGAP_Ov26	AW303034		
10070	0.000000	cDNA clone IMAGE:2764383 3'	DE03000	10.222.7	} -
10873	0.002893	601156470F1 NIH_MGC_21 cDNA	BE279006	Hs.444551	
		clone IMAGE:3140104 5', mRNA]	
	. ,	sequence /clone=IMAGE:3140104			ļ
		/clone_end=5' /gb=BE279006	•		
		/gi=9153993 /ug=Hs.444551 /len=549	·		

		nding To Differentially Express d Gen			<u> </u>
Spot	p-value	Description	Gen	Unigene	Protein
	(Accession No.	Accession	Accession
				No.	No.
10875	0.047031	cDNA FLJ39179 fis, clone	AK096498	Hs.104935	Tarangan N
		OCBBF2004147./gb=AK096498	A A A A A A A A A A A A A A A A A A A) · · · · · · · · · · · · · · · · · · ·	
		/gi=21756010 /ug=Hs.104935		1	
		/len=2760			
10877	0.02801	AGENCOURT_6531719	BM547886	Hs.355559	
		NIH_MGC_124 cDNA clone		Į.,	
		IMAGE:5732630 5', mRNA sequence			
		/clone=IMAGE:5732630 /clone_end=5'	8		
		/gb=BM547886./gi=18782032			at 1
		/ug=Hs.355559 /len=1182			
10878	0.010277	mRNA; cDNA DKFZp762N1910 (from	AL834470	Hs.406377	to the second
		clone DKFZp762N1910) /cds=(1,1892)		-	
		/gb=AL834470 /gi=21740235			
		/ug=Hs.406377 /len=2617			6
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1					
10882	0.02801	protein phosphatase 1, regulatory	NM 005398	Hs.303090	NP 005389
		(inhibitor) subunit 3C (PPP1R3C),			
		mRNA /cds=(58,1011) /gb=NM 005398			
		/gi=21314622 /ug=Hs.303090		∤	f
		/len=2524		4 4	1
10887	0.018784	EST(CIT-HSP-2366I22.TF CIT-HSP	AQ078010	T	
• 🚟 🖟		genomic clone 2366/22)			
10889	0.032636	hypothetical protein MGC10854	NM_032300	Hs.22222	NP 115676
11		(MGC10854), mRNA /cds=(135,1631)	-		_
		/gb=NM_032300 /gi=14150055		<u>'</u>	}
		/ug=Hs.22222 /len=2099		1 -	A Comment
10891	0.040751	EST(yh69b07.r1 Soares placenta	R31623		
		Nb2HP cDNA clone IMAGE: 134965 5'		**	
	ļ	similar to contains Alu repetitive		, ;	
		element)			
10900	0.047031	UI-1-BC1p-asx-h-02-0-UI.s1	BQ012708	Hs.191900	Triberie
		NCI CGAP PI3 cDNA clone UI-1-BC1p			
£ .		asx-h-02-0-UI 3', mRNA sequence			
•] .	/clone=UI-1-BC1p-asx-h-02-0-UI			}
		/clone_end=3' /gb=BQ012708			
+ 7	, ;	/gi=19737609 /ug=Hs.191900 /len=590			1.
)			
10901	0.047031	CCR4-NOT transcription complex,	NM_013354	Hs.380963	NP 473367
1,0001	0.0-77001	subunit 7 (CNOT7), transcript variant 1,	111111_010004	110.000000	14, 24, 000,
	[mRNA /cds=(340,1128)			1
	1.	/gb=NM 013354 /gi=17978498			1
		/ug=Hs.380963 /len=2653			1
10000	2.475.04	EST (MR1-SN0062-100500-002-q03	A1A/969490	 	
10909	J 3.47 E-04	` `	AW868480	1	, .
10046	E 70E 04	SN0062 cDNA)	AVA/E04004	_	ND 000470
10916	5./9E-04	EST(UI-HF-BN0-aln-e-12-0-UI.r1	AW504804		NP_060179
		NIH_MGC_50 cDNA clone			
		IMAGE:3080182 5')	<u>L., </u>	<u> </u>	L

		nding To Differentially Expressed G n				
Spot	p-valu	Description	Gene Accession No.	Unigen Accession No.	Protein Accession No.	
10917	0.012276	activated RNA polymerase II	NM 006713	Hs.349506	NP_006704	
	0.012210	transcription cofactor 4 (PC4), mRNA				
· · · · · · · · · · · · · · · · · · ·		/cds=(57,440) /gb=NM_006713 /gi=19923783 /ug=Hs.349506				
10005		/len=1336 clone IMAGE:4401491, mRNA	BC015388	11- 200240		
10925	0.50⊏-04	/gb=BC015388 /gi=21955390 /ug=Hs 380349 /len=1881	IBC015366	Hs.380349		
10935	0.042700	ribosomal protein S20 (RPS20), mRNA	NM 001022	Hs.8102	NP_001014	
10935	0.043799	/cds=(128,487) /gb=NM_001023	NWI_001023	IS.0102	NP_001014	
1		/gi=14591915 /ug=Hs.8102 /len=539				
10943	9.43E-04	mRNA; cDNA DKFZp547K0918 (from clone DKFZp547K0918) /gb=AL832566	AL832566	Hs.271324		
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	/gi=21733141 /ug=Hs.271324 //len=1883				
10949	7 41F-04	yo73e02.s1 Soares breast 3NbHBst	H44042	Hs.391565		
10010	7.712 07	cDNA clone IMAGE:183578 3', mRNA	,,,,			
*		sequence /clone=IMAGE:183578				
•		/clone_end=3' /gb=H44042 /gi=920094 /ug=Hs 391565 /len=417				
10959	0.035177	7p65g03.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:3650861 3', mRNA	BF436898	Hs.213352		
		sequence /clone=IMAGE:3650861				
		/clone_end=3' /gb=BF436898				
		/gi=11449213 /ug=Hs.213352 /len=426				
10976	0.013394	in56e04.x1 HR85 islet cDNA clone	BU784825	Hs.442971		
		IMAGE:6126055 3', mRNA sequence /clone=IMAGE:6126055 /clone_end=3'				
		/gb=BU784825 /gi=23830229				
		/ug=Hs.442971 /len=548				
10980	0.02801	ESTs, cDNA, 3' end	AA845360	Hs.42366		
	11.	/clone=IMAGE:1404727 /clone_end=3' /gb=AA845360 /gi=2933119				
		/ug=Hs.42366 /len=566				
10984	0.025911	ESTs, cDNA, 3' end	AI796655	Hs.132315	1	
		/clone=IMAGE:2385007 /clone_end=3' /gb=AI796655 /gi=5362118		•		
•		/ug=Hs:132315 /len=516		ľ		
10985	0.043799	E1B-55kDa-associated protein 5 (E1B-	NM_007040	Hs.155218	NP_653335	
		AP5), transcript variant 1, mRNA				
		/cds=(174,2744) /gb=NM_007040 /gi=21536325 /ug=Hs.155218				

		nding To Differentially Expr ssed Gen			<u> </u>
Spot	p-valu	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10987	0.02801	IMAGE:20075 Soares infant brain 1NIB	W18186	Hs.117688	
		cDNA clone IMAGE:20075, mRNA]
		sequence /clone=IMAGE:20075		10	
	()	/gb=W18186 /gi=1293860			
-		/ug=Hs.117688 /len=1232			e*
	. 3		-		
10994	0.010277	clone IMAGE 3888869, mRNA, partial	BC016839	Hs.182885	NP 004547
		cds /cds=UNKNOWN /gb=BC016839			
er e	titler Nijer	/gi=16877135 /ug=Hs.182885			
		/len=1186			
11009	0.045661	EST(adult retina cDNA Danio rerio	BI880587		
	0.9.000	cDNA clone 4201579 3' similar to	2.00000		
		TR:Q9YH14 Q9YH14			
	V 1	PROGESTERONE RECEPTOR			
		BINDING PROTEIN.)			
11019	0.040751	clone 23758 mRNA sequence	AF052140	Hs.141055	
	0.040701	/gb=AF052140 /gi=3360449	711 002 140	113.141000	
		/ug=Hs 141055 /len=1498			
11021	0.013304	FLJ23302 fis, clone HEP11143	AK026955	Hs.367841	NP 115652
1021	0.015594	/cds=UNKNOWN /gb=AK026955	AN020900	115.307041 	INP_115052
		•		"	
		/gi=10439937 /ug=Hs.287737			
44044	0.00000	/len=2509	1100440		
11044	0.020388	EST(fetal liver spleen 1NFLS Homo	H90418		
		sapiens cDNA clone IMAGE:241467 3'	la de la companya de la companya de la companya de la companya de la companya de la companya de la companya de		
	0.000.0)			
11055	9.43E-04	UI-E-CL1-aez-f-02-0-UI.r1 UI-E-CL1	BM695854	Hs.21509	
	1 - 5 -	cDNA clone UI-E-CL1-aez-f-02-0-UI 5',	and the great		
5.		mRNA sequence /clone=UI-E-CL1-aez-	in a la		
		f-02-0-UI /clone_end=5' /gb=BM695854			
	·	/gi=19009112 /ug=Hs.21509 /len=1260		1	1
11059	0.025911	la contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contractio	BU728934	Hs.436272	
<i>.</i>		cDNA clone UI-E-CQ1-aew-e-07-0-UI	2 15 S 2.15		
	' '	3', mRNA sequence /clone≃UI-E-CQ1-			
,	ŀ	aew-e-07-0-UI /clone_end=3']	1
*		/gb=BU728934 /gi=23651308	100	Ì	
		/ug=Hs.436272 /len=1132	. "		
11065	0.014599	clone IMAGE:4043849, mRNA	BC013940	Hs.348325	
	•	/gb=BC013940 /gi=15530292	No.	1	
		/ug=Hs.348325 /len=1355			
11068	0.03788	mRNA; cDNA DKFZp586G1520 (from	AL050148	Hs.31834	*
		clone DKFZp586G1520) /gb=AL050148			L
	* * * * * * * * * * * * * * * * * * * *	/gi=4884359 /ug=Hs.31834 /len=3030			
11070	0.040751	cDNA FLJ34585 fis, clone	AK091904	Hs.104627	
		KIDNE2008758. /gb=AK091904			'
	}	/gi=21750379 /ug=Hs.104627		*	}

Genes	Correspoi	nding To Differentially Expressed Gen	s in Figure 20 -		
Spot	p-value	D scription	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
11091	0.02801	BX091936 Soares placenta Nb2HP	BX091936	Hs.24598	
]	cDNA clone IMAGp998N02193;	a		
,		IMAGE:135745, mRNA sequence			
		/clone=IMAGp998N02193_;_IMAGE:13			ĺ
		5745 /gb=BX091936 /gi=27822661			
		/ug=Hs.24598 /len=688		1	
11092	0.003213	ESTs, cDNA, 5' end	BG741948	Hs.355530	NP 068747
		/clone=IMAGE:4779957 /clone_end=5'			
		/gb=BG741948 /gi=14052601		1	
		/ug=Hs.355530 /len=948			
f'		749 - 13.000000 /icii			
11003	0.003047	UI-E-EJ1-aje-j-02-0-UI.r1 UI-E-EJ1	BM929582	Hs.159153	
11033	0.0005 74 7	cDNA clone UI-E-EJ1-aje-j-02-0-UI 5',	Dialacador	113.103100	
		mRNA sequence /clone=UI-E-EJ1-aje-j-	en en en en		
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1				ř
		02-0-UI /clone_end=5' /gb=BM929582			
		/gi=19388755 /ug=Hs.159153			l sees the sees
44004	0.000.10	/len=1002	DIGGGGGG	11. 004700	
11094	0.030249	602969052F1 NIH_MGC_12 cDNA	BI260728	Hs.201769	
1-4		clone IMAGE:5108412 5', mRNA			
		sequence /clone=IMAGE:5108412			√
		/clone_end=5' /gb=Bl260728			
gen e Saar		/gi=14819291 /ug=Hs.201769 /len=667			
11098	0.002602	hypothetical protein MGC27466	NM_152373	Hs.145521	NP_689586
		(MGC27466), mRNA /cds=(125,733)			
1.6		/gb=NM_152373 /gi=22748802			
		/ug=Hs.145521 /len=1465			
11099	0.013394	UI-H-DT1-avz-g-14-0-UI.s1	BQ015869	Hs.353471	
·		NCI_CGAP_DT1 cDNA clone			
		IMAGE:5886373 3', mRNA sequence			
	1	/clone=IMAGE:5886373 /clone_end=3'	ľ		1
		/gb=BQ015869 /gi=19751146			
		/ug=Hs.353471 /len=1192			
].		
11105	0.03788	hypothetical protein FLJ21839	NM 021831	Hs.433334	NP_068603
		(FLJ21839), mRNA /cds=(445,2619)			
•	•	/gb=NM_021831 /gi=19923577	·	·	
		/ug=Hs.433334 /len=3252			
11109	0.022106	al60e07.s1 Soares_NFL_T_GBC_S1	AA884390	Hs.374217	
11109	0.022 100	cDNA clone IMAGE:1461732 3', mRNA		113.014211	
			}		1
		sequence /clone=IMAGE:1461732			
		/clone_end=3' /gb=AA884390			
		/gi=2993920 /ug=Hs 374217 /len=352		}	
22.455	10000	FOTO BUANTA DE CALCULA COM	10000745	 	
		EST(cDNA clone IMAGE:2815110 3')	AW268719	10.00	
11131	0.025911	clone IMAGE:4182947, mRNA	BC016962	Hs.16193	
		/gb=BC016962 /gi=16877432			7 Y 1
,	1	/ug=Hs.16193 /len=1866			L

		nding To Differentially Expr ssed Gen			
Spot	p-value	I DE TE	Gene	Unigene	Protein
			Accession No.	Accession	Accession
	- !			No.	No.
1136	0.023945	clone IMAGE:3138608, mRNA	BC007266	Hs.334566	
		/cds=UNKNOWN /gb=BC007266			
		/gi=13938277 /ug=Hs.334566	e e e e e e e e e e e e e e e e e e e	e e comerci.	
		/len=1635			
1166	5.48E-04	ym53e05.s1 Soares infant brain 1NIB	H24464	Hs.417814	And the second
		cDNA clone IMAGE:51803 3', mRNA		}	
		sequence /clone=IMAGE:51803		ļ	
		/clone_end=3' /gb=H24464 /gi=893159		1	
•		/ug=Hs.417814 /len=487			
1178	8 37F-04	No significant match (ORF:none)	SEQ.ID.No.23		No.
1180			0_4		
, 100	0.010094	ORF+2(98~316),+3(9~116,201~316)	SEQ:ID.No.55		
1198	7.06E.04	cDNA FLJ23679 fis, clone HEP09084.	AK074259	Hs.351597	
1190	1.00E-04	/gb=AK074259 /gi=18676812	MINUTHEUS	1113.001031	
		1.4			
4004	0.047000	/ug=Hs.351597 /len=2006	DC045704	Un 20404	
1201	U.U1/288 	clone IMAGE:4798349, mRNA	BC045794	Hs.29464	e Arm Committee
		/gb=BC045794 /gi=28277189			
		/ug=Hs.29464 /len=2717			
1205	0.03788	ESTs, cDNA, 5' end	BG402127	Hs.347570	
		/clone=IMAGE:4593784 /clone_end=5'	7		l tege
		/gb=BG402127 /gi=13295575			
· .		/ug=Hs.347570 /len=863			
	K. (
1215		Novel, ORF+3(39~203)	SEQ.ID.No.53		
1222	0.007806	No significant match, ORF+1(1~294)	SEQ.ID.No.88		
1257	0.009388	mRNA for FLJ00086 protein, partial	AK024487	Hs.343828	NP_835461
		cds:/cds=(1951,3150)/gb=AK024487		1	
* **		/gi=10440487 /ug=Hs.343828		· ·	
		/len=4456		1	1
1258	8.37E-04	ADP-ribosylation factor GTPase	NM_018209	Hs.25584	NP 783202
	[activating protein 1 (ARFGAP1), mRNA			
		/cds=(113,1333) /gb=NM_018209			
	1	/gi=8922651 /ug=Hs.25584 /len=3248			
		rg QUEEQUI ragris.E000# //QIII OETO		1	1
1259	3 DAE DA	actin binding LIM protein 1 (ABLIM1),	NM_002313	Hs.158203	NP_006711
1239	J.U-1L-U4	transcript variant ABLIM-I, mRNA	1411 _002010	11 13. 100200	-000711
	1.	/cds=(100,2436) /gb=NM_002313			[* ` · · · · · · · · · · · · · · · · · ·
				·	1
	i.	/gi=21284382 /ug=Hs.158203			
400.	0.04000:	/len=7581	NN 444000	115 07040	ND 050405
1261	7 0.013394	hypothetical protein MGC14480	NM_144998	Hs 37616	NP_659435
		(MGC14480), mRNA /cds=(18,209)	1 1		
		/gb=NM_144998 /gi=21450710			j
		/ug=Hs.37616 /len=844		<u> </u>	
1263	0.004367	KIAA1804 protein, partial cds	AB058707	Hs.50883	NP_115811
	}	/cds=UNKNOWN /gb=AB058707	1	1	
	ľ	/gi=14017824 /ug=Hs.50883	1	1	1

Genes	Correspo	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
	p-value	Description	Gene	Unigene	Protein
•			Accession No.	Accession	Accession
				No.	No.
11264	0.008566	Similar to RIKEN cDNA 1810014L12	BC045655	Hs.199695	
-4		gene, clone MGC:43599			
		IMAGE:5269880, mRNA, complete cds	** ** **		Programme and the
		/cds=(476,685) /gb=BC045655			
		/gi=28277116 /ug=Hs.199695			
*		/len=2133			
11266	0.013394	B-cell translocation gene 1, anti-	NM 001731	Hs.77054	NP 001722
		proliferative (BTG1), mRNA	_		
		/cds=(309,824) /gb=NM_001731			
		/gi=4502472 /ug=Hs.77054 /len=1783			
11277	0.048465	ligase I, DNA, ATP-dependent (LIG1),	NM 000234	Hs.1770	NP 000225
		mRNA /cds=(121,2880)			
		/gb=NM_000234 /gi=4557718			
		/ug=Hs.1770 /len=3083			
11287	0.03788	fucosyltransferase 4 (alpha (1,3)	NM 002033	Hs.2173	NP 002024
-: '==:		fucosyltransferase, myeloid-specific)	1 11 11 11 11 11 11 11 11 11 11 11 11 1		
		(FUT4), mRNA /cds=(174,1766)			
i est		/gb=NM_002033 /gi=4503810			
	j	/ug=Hs.2173 /len=2861			} . j
11293	0.022106	hypothetical protein (FLJ20485), mRNA	NM 019042	Hs.98806	NP 061915
11200	0.022.00	/cds=(112,729) /gb=NM_ 019042	111111_013042	113.50000	
		/gi=9506680 /ug=Hs.98806 /len=2021			
11294	0.012276	cDNA FLJ11335 fis, clone	AK002197	Hs.284270	
11201	0.012270	PLACE1010630. /gb=AK002197	/ (((002 10)	113.20-1210	
	1.7	/gi=7023924 /ug=Hs.284270 /len=1984		1 .	
11296	0.035177	mRNA for KIAA0740 protein, partial	AB018283	Hs.15099	NP_055651
1.1200	0.000111	cds./cds=(260,2350) /gb=AB018283	1,10010200	113.10095	
		/gi=6705974 /ug=Hs.15099 /len=4390			
11297	0.00587	farnesyl diphosphate synthase (farnesyl	NM 002004	Hs.335918	NP 001995
]	pyrophosphate synthetase,	1.1111_002001	1.0.000010	
	}	dimethylallyltranstransferase,			
U.		geranyltranstransferase) (FDPS),			10 miles
		mRNA /cds=(115,1374)	\		
	1	/gb=NM_002004 /gi=4503684	{		
		/ug=Hs.335918 /len=1430	{		
11299	0.004367	ATX1 antioxidant protein 1 (yeast)	NM 004045	Hs.279910	NP_004036
1.200	5.55.55/	(ATOX1), mRNA /cds=(114,320)	55,4545	1.10.2.70010	55-555
* 4. *		/gb=NM 004045 /gi=4757803			1.
1.0		/ug=Hs.279910 /len=502			1
11303	0.018784	S100 calcium binding protein A1	NM 006271	Hs.433503	NP 006262
1.000	3.5.0.04	(S100A1), mRNA /cds=(114,398)	000211	1.10.400000	000202
		/gb=NM_006271 /gi=5454031		. 1 .	
	1	/ug=Hs.433503 /len=607	1		1
11304	0.003212	hypothetical gene supported by	XM_001298	 	
11304	0.000213	D17652; X59357; NM_000983	77,101,001290		
		(LOC65281), mRNA	1	1	
	<u> </u>	KEOCOJZO I), IHIXIVA	L	ــــــــــــــــــــــــــــــــــــــ	<u> L</u>

		nding To Differ ntially Expressed Gen			5
Spot	p-value		Gene	Unigene	Protein
			Accession No.	Accession	Accession
14000	0.00000	<u></u>	P04007	No.	No.
11322	0.032636	Hypothetical protein (L1H 3' region) -	B34087		
· · · · · ·	l Harrier en la later	human (AA=69%)			1
11332	0.001062	polyadenylate binding protein-	NM_006451	Hs.109643	NP_006442
!		interacting protein 1 (PAIP1), mRNA			
		/cds=(188,1627) /gb=NM_006451		,	
		/gi=17511254 /ug=Hs.109643	ing the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second s		
		/len=2764			
11333	0.004825	hypothetical protein FLJ13615	NM_025114	Hs.288715	NP_079390
		(FLJ13615), mRNA /cds=(345,2069)			
		/gb=NM_025114 /gi=13376688		And the second	
**		/ug=Hs.288715 /len=2719			
11336	0.011238	proteasome (prosome, macropain)	NM_006814	Hs.405813	NP_848694
		inhibitor subunit 1 (PI31) (PSMF1),			
		mRNA /cds=(127,942) /gb=NM_006814			
	9 , 5	/gi=5803122 /ug=Hs.405813 /len=3188			
11338	0.043799	Similar to SRY-box containing gene 5,	BC014929	Hs.383009	
t Ma		clone IMAGE:3919439, mRNA			
		/gb=BC014929 /gi=15928923			
		/ug=Hs.383009 /len=652			
11342	0.007171	FLJ11416 fis, clone HEMBA1000943	AK021478	Hs.333150	1
		/cds=UNKNOWN /gb=AK021478			
		/gi=10432671 /ug=Hs.333150			
-		/len=1593	Large State 1.1	1	
11343	0.035177	chromosome 1 open reading frame 33	NM 016183	Hs.274201	NP 057267
110-10	0.000177	(C1orf33), mRNA /cds=(32,751)	1.111,_010100	113.27 1201	
		/gb=NM_016183 /gi=18490986			
		/ug=Hs.274201 /len=1185			
11357	0.007107	splicing factor 3a, subunit 1, 120kDa	NM_005877	Hs.406277	NP 005868
11337	0.007107	(SF3A1), mRNA /cds=(132,2513)	14141_0036 <i> </i>	113.400277	THE_000000
		/gb=NM_005877 /gi=20127483			42.5
		/ug=Hs.406277 /len=2944			
1126F	0.007407	Rho-specific quanine-nucleotide	NM 014786	Hs.45180	NP 055601
11303	0.007107	exchange factor 164 kDa	14/00 14/00	115.40100	USSOUT
• •	1 1	(P164RHOGEF), mRNA			
		1,			
		/cds=(16,6207) /gb=NM_014786			
		/gi=21361457 /ug=Hs.45180 /len=7540			1
44000	0.000045		NIA 00 1000	111-00000	ND 004050
11368	0.023945	cofactor required for Sp1 transcriptional	NM_004268	Hs.22630	NP_004259
		activation, subunit 6, 77kDa (CRSP6),			1 4
	1	mRNA /cds=(196,2151)			
		/gb=NM_004268 /gi=10835074			
	ŀ	/ug=Hs.22630 /len=2546		1	1
	1				1

G nes	Correspon	nding To Differ ntially Expressed Gen	es in Figure 20 -	RA	
		Description	Gene Accession No.	Unigen Acc ssion	Protein Accession No.
11373	0.007807	yl96f11.s1 Soares infant brain 1NIB cDNA clone IMAGE:45943 3' similar to	H09059	No. Hs 438854	NO.
		contains Alu repetitive element;, mRNA sequence /clone=IMAGE:45943 /clone_end=3' /gb=H09059 /gi=873881 /ug=Hs.438854 /len=494			
11387	0.040751	df22c07.w1 Morton Fetal Cochlea	BI492292	Hs.379172	
	***************************************	cDNA clone IMAGE:2484085 3', mRNA sequence /clone=IMAGE:2484085 /clone_end=3' /gb=Bl492292 /gi=15331636 /ug=Hs.379172 /len=359			
11401	5.11E-04	hypothetical protein PRO1843 (PRO1843), mRNA /cds=(965,1255) /gb=NM_018507 /gi=8924082 /ug=Hs.283330 /len=1268	NM_018507	Hs.283330	NP_060977
11402	0.040751	cytochrome c, somatic (CYCS), mRNA /cds=(61,378) /gb=NM_018947	NM_018947	Hs.169248	NP_061820
11404	6 56F-04	/gi=21361707 /ug=Hs.169248 /len=3990 hypothetical protein MGC3067	NM 024295	Hs.323114	NP 077271
,	0.002.04	(MGC3067), mRNA /cds=(140,895) /gb=NM_024295 /gi=13236515 /ug=Hs.323114 /len=1203			
11407	3.47E-04	Similar to proline synthetase co- transcribed (bacterial homolog), clone	BC012334	Hs.301959	NP_009129
		MGC:2667 IMAGE:3546307, mRNA, complete cds /cds=(67,894) /gb=BC012334 /gi=15147390 /ug=Hs.301959 /len=2580			
11408	0.002337	hypothetical protein FLJ30525 (FLJ30525), mRNA /cds=(422,1603) /gb=NM_144584 /gi=21389358 /ug=Hs.7962 /len=1867	NM_144584	Hs 7962	NP_653185
11410	0.004367	ring finger protein 38 (RNF38), mRNA /cds=(563,1861) /gb=NM_022781 /gi=21918874 /ug=Hs.77823 /len=4694	NM_022781	Hs.77823	NP_073618
11419	0.030249	syntaxin binding protein 3 (STXBP3), mRNA /cds=(52,1830) /gb=NM_007269 /gi=6005885 /ug=Hs.8813 /len=2508	NM_007269	Hs.8813	NP_009200
11426	0.043799	hypothetical protein BC000282 (LOC89894), mRNA /cds=(657,1394) /gb=NM_138341 /gi=24308397 /ug=Hs.8116 /len=1716	NM_138341	Hs.8116	NP_612350

Genes	Correspon	nding To Differentially Expressed Gen		RA	
Spot	p-value	Description	Gene	Unigene	Protein
	<u> </u>		Accession No.	Accession No.	Accession No.
11429	0.02801	cDNA FLJ32781 fis, clone	AK057343	Hs.78743	
		TESTI2002149, highly similar to ZINC			
		FINGER PROTEIN 131. /gb=AK057343	· · · · · · · · · · · · · · · · · · ·		**** ***
		/gi=16553000 /ug=Hs.78743 /len=2401	`.		
11433	0.032636	annexin A7 (ANXA7), transcript variant	NM_004034	Hs.386741	NP_004025
		2, mRNA /cds=(61,1527)			
	<u> </u>	/gb=NM_004034 /gi=4809278			
-		/ug=Hs.386741 /len=2176			
11437	0.004367	chitobiase, di-N-acetyl- (CTBS), mRNA	NM_004388	Hs.135578	NP_004379
		/cds=(1,1158) /gb=NM_004388		i '	
		/gi=4758091 /ug=Hs.135578 /len=1618			:
11443	0.001878	nucleoporin 54kDa (NUP54), mRNA	NM_017426	Hs.9082	NP_059122
		/cds=(129,1652) /gb=NM_017426			
		/gi=26051236 /ug=Hs.9082 /len=2358		 	<u> </u>
11444	0.002096	coproporphyrinogen oxidase	NM_000097	Hs.89866	NP_000088
2.	}	(coproporphyria, harderoporphyria)			
		(CPO), mRNA /cds=(68,1432)			* *
- 1,		/gb=NM_000097 /gi=20127405			
		/ug=Hs:89866 /len=2691			
11445	0.002096	hbc647 mRNA sequence. /gb=U68494	U68494	Hs.24385	
		/gi=1546096 /ug=Hs 24385 /len=1843			
11447	0.040751	hypothetical gene supported by	XM_072343		
	<u> </u>	AK000174 (LOC133761), mRNA			
11448	0.043799	zinc finger protein 23 (KOX 16)	NM_145911	Hs.376810	NP_666016
7.1		(ZNF23), mRNA /cds=(815,2746)			
•		/gb=NM_145911 /gi=23308736			
		/ug=Hs.376810 /len=3271	-		
11453	0.035177	DNA-damage-inducible transcript 3	NM_004083	Hs.400353	NP_004074
		(DDIT3), mRNA /cds=(191,700)			1
	1	/gb=NM_004083 /gi=21361117	Marine State	1.0	.
71.10=		/ug=Hs.400353 /len=965		05440	
11467	0.025911	SMT3 suppressor of mif two 3 1 (yeast)	NM_006936	Hs.85119	NP_008867
		(SMT3H1), mRNA /cds=(95,406)		•	
		/gb=NM_006936 /gi=5902095			
4 4 4 - 7 4	0.041000	/ug=Hs.85119 /len=1733			115 222
11471	0.011238	prostaglandin E receptor 2 (subtype	NM_000956	Hs.2090	NP_000947
· -		EP2), 53kDa (PTGER2), mRNA	-	1	,
,	1	/cds=(157,1233) /gb=NM_000956		1	
442-2	0.005===	/gi=4506254 /ug=Hs.2090 /len=2372	100 100 100	11- 40025	NE STATE
11473	0.009388	hypothetical protein BC013035	NM_138436	Hs.10018	NP_612445
		(LOC114926), mRNA /cds=(128,430)		1	
		/gb=NM_138436 /gi=19923964	1 4	ŀ	ĺ.
	1	/ug=Hs.10018 /len=836	<u> </u>	<u> </u>	<u> </u>

Gen s Corresponding To Differentially Expressed Genes in Figure 20 - RA					
		Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
11474	0.017288	solute carrier family 38, member 2	NM_018976	Hs.298275	NP 061849
		(SLC38A2), mRNA /cds=(352,1872)			1
		/gb=NM_018976 /gi=21361601	en en en en en en en en en en		
		/ug=Hs.298275 /len=4795			
11477	0.032636	mRNA for KIAA0626 protein, complete	AB014526	Hs.178121	NP 067679
	- TIT GT T NO.	cds /cds=(178,1407) /gb=AB014526			-
		/gi=3327065 /ug=Hs.178121 /len=6184			
- 4		/g/ 002/000/0g /10/// 0.2/// 0.2//	14		
11479	0.007807	B lymphocyte activation-related protein	AAL26788		
11773	0.007.007	BC-2048	, 0 (229.00		The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
11480	7.41E-04	hypothetical protein FLJ23751	NM 152282	Hs.37443	NP 689495
11700	7.541,05-04	(FLJ23751), mRNA /cds=(121,1563)	102202	113.07-10	111 _000 100
		/gb=NM_152282 /gi=22748648		la de la filipia	
	¦i na se	/ug=Hs.37443 /len=2994			
11481	0.020240	eps8 binding protein e3B1 mRNA,	AF006516		NP_005461
11401	0.030249		AFOOOSIO		111-003401
44400	0.047000	complete cds	NM 020117	Hs.6762	NP 064502
11496	0.017288	leucyl-tRNA synthetase (LARS), mRNA	NIVI_U2U117	IS.0702	INP_004502
4.5		/cds=(73,3603) /gb=NM_020117			
		/gi=24496788 /ug=Hs.6762 /len=4248			
			1114 047040	11. 004000	110 000440
11497	0.002893	FK506 binding protein 14, 22 kDa	NM_017946	Hs.264636	NP_060416
	~	(FKBP14), mRNA /cds=(146,781)		1	
1.1		/gb=NM_017946 /gi=8923658			
		/ug=Hs.264636 /len=2248		ļ.,	
11502	0.003563	mRNA for KIAA1229 protein, partial cds	AB033055	Hs 71109	
		/cds=UNKNOWN /gb=AB033055	The Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Co		
	-	/gi=6330699 /ug=Hs.71109/len=5654		l	
11503	0.008566	hypothetical protein DKFZp564K0822	NM_030796	Hs.4750	NP_110423
		(DKFZP564K0822), mRNA			
		/cds=(10,528) /gb=NM_030796	1		
		/gi=13540577 /ug=Hs.4750 /len=2789	100		
11509	0.013394	coagulation factor VIII, procoagulant	NM_000132	Hs.79345	NP_063916
		component (hemophilia A) (F8),			
		transcript variant 1, mRNA	F		
-		/cds=(172,7227) /gb=NM_000132			
A		/gi=10518504 /ug=Hs.79345 /len=9030			
			·	· · ·	·
11514	0.011238	chromosome 21 open reading frame 33	NM_004649	Hs 182423	NP_004640
		(C21orf33), mRNA /cds=(85,891)	1	1	
		/gb=NM 004649 /gi=5031690		*	
		/ug=Hs.182423 /len=1652			
11516	2.03E-04	602943821F1 NIH_MGC_19 cDNA	BI194863	Hs.444288	
		clone IMAGE:5091917 5', mRNA			
		sequence /clone=IMAGE:5091917			}
		/clone_end=5' /gb=BI194863	1		
	ł	/gi=14649883 /ug=Hs.444288 /len=863			
		1/ai=14649883 /iia=H\$ 444788 /ien=863	1		

Genes	Correspon	nding To Differentially Expressed Gen	s in Figure 20 -	RA	
		Description	Gene	Unigene	Protein
	٠.		Accession No.	Accession	Accession
	-			No.	No.
11520	0.043799	MYLE protein (MYLE), mRNA	NM_014015	Hs.11902	NP 054734
		/cds=(12,299) /gb=NM_014015			. 7 _00
5		/gi=13384596 /ug=Hs.11902 /len=1120	Maria di Karamatan		:
	_ :	/gi : 1000 1000 /ug			
11536	5 11F-04	EST(yh89e10.r1 cDNA clone 136938	R38461		NP 001002
11000	0.112-04	5') 8e-06 match	1130-101		141 _001002
11539	0.047031	mRNA for KIAA1327 protein, partial	AB037748	Hs.106204	
11333	0.047031	cds. /cds=(1,5417) /gb=AB037748	AD031140	-15.100204 	
ja se				1	İ
* .		/gi=20521883 /ug=Hs.106204			
44570	0.007007	/len=6687	D0040040	104440	
:11570	0.007807	clone IMAGE:5295896, mRNA	BC043240	Hs.104413	
		/gb=BC043240 /gi=27695834			
i Services		/ug=Hs.104413 /len=2136			
11588	0.03788	EST(oz13e06.x1	AI078464		1
ÿ :		Soares_fetal_liver_spleen_1NFLS_S1			
		clone IMAGE:1675234 3')			
11603	0.032636	EST(NIB208 Normalized infant brain,	T16965		NP_277035
		Bento Soares cDNA 3'end similar to			
		hexokinase I (MK-16)) (low match:nt 2e-			· .
	No.	10)			1
11608	0.001339	EST(MR0-HT0407-140300-013-h01	BE159552		NP 003751
		HT0407)		1	-
11612	0.022106	Tho2 mRNA, complete cds	AF441770	Hs.16411	1
		/cds=(1,4437) /gb=AF441770			
er i i		/gi=20799317 /ug=Hs.16411 /len=4452			
		/g/ 20/0001/ /dg 110.10 /11/101/ 4 /02			
11613	0.035177	cell division cycle associated 1	NM 145697	Hs.234545	NP 663735
11010	0.000177	(CDCA1), transcript variant 1, mRNA	140001	1113.204040	111 _000/00
		/cds=(299,1693) /gb=NM_145697		∮	
		/gi=22027506 /ug=Hs.234545			
		/len=2003			1
11610	0.022045	EST 0x12c12.x1	A1024094	 	
11618	0.023945		AI034084	1 .	
		Soares_fetal_liver_spleen_1NFLS_S1			
44000	0.00000	IMAGE:1656118 3'	4440040	 	ND 004770
11632	0.026797	EST(DKFZp564B1278_r1 564	AL110316		NP_001779
	((synonym:hfbr2) cDNA clone		1 75	1
	<u></u>	DKFZp564B1278 5')	<u> </u>	<u> </u>	
11633	0.014599	EST hg75g08.x1 NCI_CGAP_Kid11	AW614117		1
	<u> </u>	cDNA clone IMAGE:2951486 3'	<u> </u>		-
11652	0.003947	EST(nf43h10.s1 NCI_CGAP_Pr2 cDNA	AA573636	1	
]	clone IMAGE:916579 similar to	1		1
		contains element MER22 repetitive	· · · · ·		
	1	element)			
11680	0.02801	EST ys96h09 r1 Soares retina N2b5HR	H84275	T	
		cDNA clone IMAGE:222689 5'			
7	[·	1	:	1	1
11683	0.024732	EST (clone IMAGE: 1218466 3' similar	AA662478	 	
	0.027102	to contains	1,002,770	[
	_ننـــــــــــــــــــــــــــــــــــ	Ito contains	<u> </u>	1	

		nding To Differentially Expressed Gen Description	Gen	Unigene	Protein
opot	p-value	Description	* '		1
			Acc ssion No.	Accession	Accession
14005	0.000045	FCT (0)/4 NN0020 040500 406 c07	AW895898	No.	No.
1 1000	0.023945	EST (QV4-NN0039-040500-196-e07	Avvoanoao	A.	:
14000	0.00000	NN0039	BAB14576		
		unnamed protein product			NP 149107
11691	0.023945	cDNA sequence cDNA sequence	AL117502		INP_149107
1.50		DKFZp434D0935 (from clone cDNA			1
1000	0.000500	sequence DKFZp434D0935)	NIM 04COEO	11- 450505	ND OFOCAS
1693	บ.บบชองช	cell adhesion molecule-related/down-	NM_016952	Hs.159565	NP_058648
		regulated by oncogenes (CDON),			
		mRNA /cds=(1,3723) /gb=NM_016952			
		/gi=8393083 /ug=Hs.159565 /len=3986	La dina		
11698	0.017288	EST379919 MAGE resequences,	AW967844	Hs.190465	
		MAGJ cDNA, mRNA sequence			
		/gb=AW967844 /gi=8157683	4		
		/ug=Hs.190465 /len=581			
11699	0.03788	hypothetical protein MGC5306	NM_024116	Hs.301732	NP_077021
		(MGC5306), mRNA /cds=(207,1043)		\	
		/gb=NM_024116 /gi=13129135			
* '-		/ug=Hs.301732 /len=2336			<u> </u>
11703	0.004367	hypothetical protein MGC3295	NM_025246	Hs.101257	NP_079522
	Ť	(MGC3295), mRNA /cds=(510,1748)			
		/gb=NM_025246 /gi=13376859		1	1
á., .,		/ug=Hs.101257 /len=1958			
11705	0.017288	of yeast MAF1 (MAF1), mRNA	NM_032272	Hs.19673	NP_115648
		/cds=(393,1163) /gb=NM_032272			
		/gi=14150012 /ug=Hs.19673 /len=1674			
			*		
11710	0.009388	translocase of outer mitochondrial	NM 014765	Hs.75187	NP 055580
		membrane 20 (yeast) (KIAA0016),	[-		1 7
		mRNA /cds=(102,539) /gb=NM_014765			
÷.	ļ.,	/gi=7657256 /ug=Hs.75187 /len=3259		1.	
11725	8.37E-04	hypothetical protein FLJ13657	NM 024828	Hs.178357	NP 079104
		(FLJ13657), mRNA /cds=(88,1173)	_		
	-	/gb=NM 024828 /gi=13376229			
		/ug=Hs.178357 /len=2252			
11732	0.032636	hypothetical protein FLJ20699	NM 017931	Hs.15125	NP_060401
0_	0.002000	(FLJ20699), mRNA /cds=(33,1043)			
	<u>}</u>	/gb=NM 017931 /gi=8923627			
		/ug=Hs.15125 /len=2594			
11745	0.043700	FLJ23172 fis, clone LNG10005	AK026825	Hs.306885	-
11140	0.0-0733	/cds=UNKNOWN /gb=AK026825	1, 11,020020	1.10.00000	
;	1	/gi=10439771 /ug=Hs.306885			
÷ .	,	//len=1882		1	1
11747	0.005335	lysyl oxidase-like 1 (LOXL1), mRNA	NM 005576	Hs.65436	NP_005567
F1747	1 0.005325	/cds=(306,2030) /gb=NM_005576	LININI_005576	175.00430	JMF_005567
	1				

		nding To Differ ntially Express d Gen			
Spot	p-value	Description	Gene	Unigene	Prot in
			Accession No.	Accession	Acc ssion
				No.	No.
11765	4.50E-04	ribosomal protein L12 (RPL12), mRNA	NM 000976	Hs.405042	NP 000967
		/cds=(89,586) /gb=NM_000976	,		7
		/gi=15431291 /ug=Hs.405042 /len=632		4	lita Kanananan
	4.	/gi=15451291/ug=115.405042/left=052			
4 4 7 7 7	0.000000	Latin Control	NINA 004007	11- 404005	NP 001198
11777		basic transcription factor 3 (BTF3),	NM_001207	Hs.101025	NP_001196
_	g v	mRNA /cds=(240,728) /gb=NM_001207	enge over		
2 (\$1) (q. 1)		/gi=20070129 /ug=Hs.101025 /len=952	the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s		- j- 1
11788	0.025911	Bardet-Biedl syndrome 2 (BBS2),	NM_031885	Hs.332633	NP_114091
٠.		mRNA /cds=(422,2587)			
		/gb=NM_031885 /gi=22208996			
		/ug=Hs.332633 /len=2978			
11789	0.022106	high mobility group nucleosomal	NM 006353	Hs.236774	NP_006344
	3,322	binding domain 4 (HMGN4), mRNA	,		
•••		/cds=(239,511) /gb=NM_006353		· '	
, * ···	Bry 1. Di d	/gi=23238232 /ug=Hs.236774			
1.1700	0.01000	/len=1980	1111 000055	10.4004	115 202240
11796	0.047031	mannose-6-phosphate receptor (cation	NM_002355	Hs.134084	NP_002346
	l y n	dependent) (M6PR), mRNA			
		/cds=(171,1004) /gb=NM_002355			1
		/gi=10947032 /ug=Hs.134084			
		/len=2454			
11805	0.020388	tryptophanyl-tRNA synthetase (WARS),	NM 004184	Hs.82030	NP 004175
-, -	7	mRNA /cds=(188,1603)			
	, ,	/gb=NM 004184 /gi=7710155			
		/ug=Hs.82030 /len=2693			
11010	0.012276	clone 23698 mRNA sequence	AF052094	Hs.8136	
11010	0.012276		AF032094	113.0130	
		/gb=AF052094 /gi=3360400			
		/ug=Hs.8136 /len=1264	*****	11 400400	115 000507
11825	0.002602	insulin-like growth factor binding protein	NM_000596	Hs.102122	NP_000587
		1 (IGFBP1), mRNA /cds=(166,945)			
		/gb=NM_000596 /gi=4504614			
1.5		/ug=Hs.102122 /len=1514			
11839	0.043799	proteasome (prosome, macropain) 26S	NM 002803	Hs.61153	NP 002794
		subunit, ATPase, 2 (PSMC2), mRNA	,	· .	_
		/cds=(71,1372) /gb=NM_002803			
		/gi=24430152 /ug=Hs.61153 /len=1545	1	1	
÷		191-244-00 152 /dg=115.01 155 /left=1545			
44000	0.025044	DC4 and CEDC1 into-ating matein 4	NIM OCALAA	Hs.351305	ND 066067
11866	0.025911	PC4 and SFRS1 interacting protein 1	NM_021144	IUS:301302	NP_066967
		(PSIP1), mRNA /cds=(78,1079)			
•		/gb=NM_021144 /gi=16945969			1
· .	<u> </u>	/ug=Hs.351305 /len=1677		ļ	
11898	0.012526	intersectin 2 (ITSN2), transcript variant	NM_006277	Hs.166184	NP_671494
	1	1, mRNA /cds=(242,5332)		1	
	1 .				
,		/gb=NM_006277 /gi=22325384			,

		nding To Differ ntially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Prot in
			Accession No.	Accession	Acc ssion
				No.	No.
11912	0.018784	hypothetical protein MGC40157	NM_152350	Hs.295362	NP 689563
		(MGC40157), mRNA /cds=(106,498)		ľ	
		/gb=NM_152350 /gi=22748758			
		/ug=Hs.295362 /len=1250			
11929	0.007807	zv64c04.s1	AA393802	Hs.443312	
1 1020		Soares_total_fetus_Nb2HF8_9w cDNA	1,0,000002	113.440012	
-	•	clone IMAGE:758406 3', mRNA).		
		sequence /clone=IMAGE:758406		j	1
		l .			
•		/clone_end=3' /gb=AA393802		٦	
14000	0.075.04	/gi=2046769 /ug=Hs.443312 /len=421	VIII 444000		
11930	8.37E-04	hypothetical protein FLJ30574	NM_144629	Hs.350388	NP_653230
		(FLJ30574), mRNA /cds=(403,1908)	The second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon		
		/gb=NM_144629 /gi=21389456]
		/ug=Hs 350388 /len=3113			
11932	0.043799		AK025540	Hs.91393	NP_060832
		clone HEP03135, highly similar to			1
		AF090900 Homo sapiens clone		[
٠. ا		HQ0189 PRO0189 mRNA			
	1	/cds=UNKNOWN /gb=AK025540			
		/gi=10438087 /ug=Hs.91393 /len=2440	le de la companya de la companya de la companya de la companya de la companya de la companya de la companya de		
		, , , , , , , , , , , , , , , , , , ,			
11939	0.047031	tyrosine 3-monooxygenase/tryptophan	NM 012479	Hs.25001	NP 036611
		5-monooxygenase activation protein,		110.20001	
		gamma polypeptide (YWHAG), mRNA			. ,
	1	/cds=(192,935) /gb=NM_012479			
					1
		/gi=21464100 /ug=Hs.25001 /len=3747			1
rg i					
44040	0.047000	44 (01) (44)	NNA 452040	11- 075404	ND 700500
11940	0.017288	sorting nexin 14 (SNX14), transcript	NM_153816	Hs.375181	NP_722523
		variant 1, mRNA /cds=(182,3022)		1	
	∮. ·	/gb=NM_153816 /gi=24797144			
		/ug=Hs.375181 /len=3490		ļ <u> </u>	1
11946	0.031362	hypothetical protein FLJ20432	NM_017819	Hs.57898	NP_060289
		(FLJ20432), mRNA /cds=(603,1361)			
		/gb=NM_017819 /gi=8923404			1
· .		/ug=Hs 57898 /len=1654		<u> </u>	L
		traube (Trb), mRNA	NM_019816		NP_062790
11956	0.035177	cDNA FLJ11439 fis, clone	AK021501	Hs.287416	
	,	HEMBA1001299. /gb=AK021501		1	ŀ
* *		/gi=10432697 /ug=Hs.287416			,
	[/len=1500			1
11957	0.003539	DKFZp564I112 (from clone	AL110136	Hs.47679	,
		DKFZp564I112) mRNA; cDNA	1		
		/cds=UNKNOWN /gb=AL110136	}		
* .					
11050	0.012270	/gi=5817031 /ug=Hs.47679 /len=1885	VM 040504	 	
11959	J U.U 122/6	similar to cortistatin (H. sapiens)	XM_010524		
	L	(LOC126684), mRNA			<u> </u>

		nding To Differentially Expressed Gen			D-sts!
Spot	p-value	Description	Gen Accession No.	Unigene Accession No.	Protein Accession No.
11967	5.11F-04	TNF receptor-associated factor 5	NM_004619	Hs.29736	NP 665702
11307	3,11,2-04	(TRAF5), transcript variant 1, mRNA	14141_00-10 15	113.237.90	141 _0007 02
· ·		/cds=(194,1867) /gb=NM_004619			
		/gi=22027625 /ug=Hs 29736 /len=4132			
44000	0.005005	Block and the of many Matter (C	NIM OOG446	11-000000	ND -070400
11968	0.005325	likely ortholog of mouse Mak3p (S.	NM_025146	Hs.288932	NP_079422
		cerevisiae) (MAK3P), mRNA		[
		/cds=(301,810) /gb=NM_025146			
		/gi=13376734 /ug=Hs.288932			· ·
·		/len=3576			
11978	0.032636	mitochondrial ribosomal protein L27	NM_148571	Hs.7736	NP_683412
		(MRPL27), nuclear gene encoding			1
		mitochondrial protein, transcript variant			
		2, mRNA /cds=(32,316)	7		
		/gb=NM_148571 /gi=22547130			
		/ug=Hs.7736 /len=2472			
12002	0.040751	601820680F1 NIH_MGC_58 cDNA	BF131709	Hs.145741	
		clone IMAGE:4052611 5', mRNA			
		sequence /clone=IMAGE:4052611		5	,
		/clone_end=5' /gb=BF131709			
		/gi=10970749 /ug=Hs.145741 /len=538	*. *		
		9. 100, 0.10 (19)			
12003	0.005325	EST(zi39c11.s1 Soares fetal liver	AA680133	 	NP 660208
12000	0.000020	spleen 1NFLS S1 cDNA clone 433172	1,0,000,100		
		131)			
12022	0.005339	kinesin family protein 3B (KIF3B)	NM 004798		NP 004789
12037		EST(EST58819 Infant brain 3' contains	AA351153	 	141 _00-7705
12037	0.002337	Alu repeat)	12201100		
12020	0.03700	EST(zw86f08.r1 Soares total fetus	AA447168	 	NP 115787
12039	0.03788		AA447 100	· .	110P_115767
1		Nb2HF8 9w cDNA clone 783879 5')			
40050	0.00000	41/43bp match	1114 470000	11-004007	ND 775405
12052	0.009388	helicase-like protein (KIAA2023),	NM_173082	Hs.231907	NP_775105
		mRNA /cds=(399,5378)		,	
		/gb=NM_173082 /gi=27436872	1 1		}
	<u> </u>	/ug=Hs.231907 /len=7011	<u> </u>		
12055	0.01932	mRNA for KIAA1694 protein, partial	AB051481	Hs.19597	NP_085132
		cds. /cds=(1,2275) /gb=AB051481	1	1	+6
		/gi=12697932 /ug=Hs 19597 /len=4235	ļ.	1.	1
			<u> </u>		
12056	0.025911	EST(ak48e09.s1 Soares testis NHT	AA860225		
٠,		clone IMAGE:1409224 3')	1	L	
12066	0.025911	chromosome 1 open reading frame 19	NM 052965	Hs.32058	NP_443197
		(C1orf19), mRNA /cds=(51,566)	1		
		/gb=NM 052965 /gi=24308389	1		
	I	/ug=Hs.32058 /len=1943	1	4	1

Spot	p-value	nding To Differentially Expressed Gen Description	Gen	Unigene	Prot in
Υ Ρ 			Acc ssion No.	Accession	Acc ssion
				No.	No.
2074	0.03788	EST(as88c04.x1 Barstead colon	AI735066		110.
		HPLRB7 clone IMAGE:2335782 3'			
		TR:Q13538 Q13538 ORF2:] ; r	for the star of
	,	FUNCTION UNKNOWN; contains Alu			
		repeat)			
2076	0.015895	small nuclear ribonucleoprotein D2	NM_004597	Hs.424327	NP 808210
	0.01000	polypeptide 16.5kDa (SNRPD2), mRNA	50 1007	1.13.32.102.	111 _000210
		/cds=(31,387) /gb=NM_004597			
		/gi=7242206 /ug=Hs.424327 /len=479			
		7918 7 242200 749 113.424027 71611.5470		1	
12078	0.02801	acetyl-Coenzyme A acyltransferase 2	NM_006111	Hs.356176	NP 006102
010	0.02001	(mitochondrial 3-oxoacyl-Coenzyme A	1.4.M_000	113.000 170	
		thiolase) (ACAA2), nuclear gene			1
		encoding mitochondrial protein, mRNA			
		/cds=(49,1242) /gb=NM_006111			
	* - -	/gi=5174428 /ug=Hs.356176 /len=1584			
4 4		/gi=5174420 /ug=115.550 (70 /iei1=1504	وروز والمعتب المراز		
12081	0.040751	hypothetical protein FLJ13855	NM_023079	Hs.168232	NP_075567
12001	0.040731	(FLJ13855), mRNA /cds=(328,1068)		115.100232	NP_075567
	[/gb=NM_023079 /gi=20149671		√ 4 4	
12099	6 56E 04	/ug=Hs 168232 /len=3053 nuclear cap binding protein subunit 2,	NM 007362	110 240770	NP 031388
12099	0.56E-04			Hs.240770	NP_031300
		20kDa (NCBP2), mRNA /cds=(27,497)			
		/gb=NM_007362 /gi=19923386		J	1
-		/ug=Hs.240770 /len=2120			
12400	0.004005	 	DO400000	11- 05 4700	
12108	0.004825	ij34a12.y1 Melton Normalized Islet 4 N4	BQ129288	Hs.254789	
ng ta	ly and	HIS 1 cDNA clone IMAGE:6136606 5',	era je pover v gr		
`,		mRNA sequence	an San San San San San San San San San S		
		/clone=IMAGE:6136606 /clone_end=5'			
	in a second	/gb=BQ129288 /gi=20203199			
		/ug=Hs.254789 /len=485		ł	
10440	0.000045	TOT/TOP OA A NOU COAD COC	ALOCEODO.		
12110	0.023945	EST(qx95c04.x1 NCI_CGAP_GC6	Al365336		1
10110	0.040004	cDNA clone IMAGE:2010246 3')	100644440	ļ	115 070570
12112	0.013394	EST(xu58f03.x1 NCI_CGAP_Ut1 clone	AW511419		NP_073572
		IMAGE:2805917 3' TR:035371			
		O35371 PERIPHERIAL			
		BENZODIAZEPINE RECEPTOR			
	0.00:0==	ASSOCIATED PROTEIN)		ļ	
12140	0.001878	EST nk17g03.s1 NCI_CGAP_Co11	AA582722		
1		cDNA clone IMAGE:1013812 3'		1	
12155	0.017288	EST AV734861 cdA H.sapiens cDNA	AV734861		
		clone cdAAPC07 5'	*.	1	1 '

		orresponding To Differentially Expr ssed Gene			Drot :-	
Spot	p-value	Description	Gene Accession No.	Unigene Accession	Prot in Acc ssion	
			, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	No.	No.	
2182	0.017288	Williams-Beuren Syndrome critical	NM 145645	Hs.406306	NP 663620	
		region protein 20 copy B (WBSCR20B),	-			
		mRNA /cds=(984,1448)				
		/gb=NM_145645 /gi=21717802		,		
		/ug=Hs.406306 /len=1634				
		/ug=113,400000/1011=1004 			ļ	
2184	0.015805	cDNA FLJ11086 fis, clone	AK001948	Hs.272240		
2 104	0.013093	PLACE1005266. /gb=AK001948	1940	1113.212240		
		/gi=7023529 /ug=Hs.272240 /len=1899				
		/gi=7025529 /ug=Hs.272240 /leli=1699				
0400	0.002047	FOT AV75049C NDC II agricus aDNA	A) /75040C			
2189	0.003947	EST AV750486 NPC H.sapiens cDNA	AV750486	A 1.5		
0405	0.040004	clone NPCDCF06 5'	A1740700			
2195	0.013394	EST (as58h11.x1 Barstead colon	AI718786			
		HPLRB7 cDNA clone IMAGE:2332965				
		3' similar to contains Alu repetitive				
. 1		element)		<u> </u>		
2197	0.03788	DKFZp586E2017_r1 586 (synonym:	AL046885	Hs.413463		
4. 5.		hute1) cDNA clone DKFZp586E2017 5',				
		mRNA sequence				
	\$ 7.5 %	/clone=DKFZp586E2017 /clone_end=5'				
	1	/gb=AL046885 /gi=5936275		1		
$\langle \hat{\beta}_{ij} \rangle$	[*	/ug=Hs.413463 /len=640				
12198	0.002337	clone IMAGE:4606942, mRNA, partial	BC022881	Hs.369550		
4, .		cds /cds=(1,188) /gb=BC022881				
		/gi=18605588 /ug=Hs.369550				
		/len=1749				
12201	0.001062	EST (Soares placenta Nb2HP	R76686			
		IMAGE:143740 3')		1	1	
2202	0.030249	F-box and leucine-rich repeat protein	NM 012158	Hs.7540	NP 036290	
	0.000	3A (FBXL3A), mRNA /cds=(298,1584)	()	TO THE SEC		
		/gb=NM 012158 /gi=16306583	***			
		/ug=Hs.7540 /len=3489		***	1	
12209	0.001062	EST(zf69b06.r1	AA063201	 		
	0.001002	Soares_pineal_gland_N3HPG	1.000201	1.00		
	1	H.sapiens cDNA clone IMAGE:382163				
•		(5')				
12210	0.02801	cDNA FLJ38039 fis, clone	AK095358	Hs.46506	1-1	
یکد ال	0.02001	CTONG2013934. /gb=AK095358	LUCASSO	13.40000		
		1 · · · · · · · · · · · · · · · · · · ·		1	1	
		/gi=21754600 /ug=Hs.46506 /len=2956				
12242	0.047024	repetitive aggreence (ALLI CLIDE ANNLY	D20100	 	 	
12213	0.04/031	repetitive sequence (ALU SUBFAMILY	P39188		4	
1001=	0.00=55	[J)	1111 605151	070054	LIB GROVE	
12217	0.03788	chromosome 1 open reading frame 22	NM_025191	Hs.279951	NP_079467	
		(C1orf22), mRNA /cds=(54,2723)			1	
		/gb=NM_025191 /gi=19923618	1		1	
	1	/ug=Hs.279951 /len=6298		1	1	

		nding To Differ ntially Expr ssed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
		•	Accession No.	Accession	Acc ssion
	e de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de l			No	No.
12220	0.00168	wb40b11.x1 NCI_CGAP_GC6 cDNA	AI652865	Hs.374238	
	*	clone IMAGE:2308125 3', mRNA	7,00	1.0.07	
		sequence /clone=IMAGE:2308125			
·		/clone_end=3' /gb=Al652865			<u> </u>
		/gi=4736844 /ug=Hs.374238 /len=598		[
12221	0.00507		A DOE0750	115 445050	W. C. Carlotte
12221	0.00567	hAWMS1 mRNA, complete cds.	AB052759	Hs.445652	· · · · · · · · · · · · · · · · · · ·
		/cds=(232,444) /gb=AB052759		· .	
. 1		/gi=27529922 /ug=Hs.445652		j.	
		/len=1470			
12224	9.95E-05	gp25L2 protein (HSGP25L2G), mRNA	NM_017510	Hs.279929	NP_059980
		/cds=(76,720) /gb=NM_017510			
		/gi=24475637 /ug=Hs.279929			
		/len=1420			
12226	0.003213	EST (xb68c06.x1	AW087708		NP_002962
		Soares_NFL_T_GBC_S1 cDNA clone		l e	_
		IMAGE:2581450 3')			
12227	0.032636	cDNA, 3' end /clone=IMAGE:3038322	BE042649	Hs.275673	(4) Sec. 18 (19)
		/clone_end=3' /gb=BE042649			
-		/gi=8359628 /ug=Hs.275673 /len=435			
12228	0.002337	TSLC1-like 2 (TSLL2), mRNA	NM 145296	Hs.164773	NP 660339
IZZZO	0.002001	/cds=(50,1216) /gb=NM_145296	140230	113.104773	
		/gi=21686976 /ug=Hs.164773			
		/len≈2176			
40004	0.001402		A)A/440000		NID: 004474
12231	0.001193	EST (UI-H-BI3-akf-b-05-0-UI s1	AW449060		NP_061174
		NCI_CGAP_Sub5 clone			
		IMAGE:2734017 3')	'	<u> </u>	
12237	0.006463	EST (602496405F1 NIH_MGC_75	BG433151		
		clone IMAGE:4610376 5')			
12238	0.020388	hypothetical protein LOC115286	NM_173471	Hs.379386	NP_775742
		(LOC115286), mRNA /cds=(189,740)			
		/gb=NM_173471 /gi=27735034			
		/ug=Hs.379386 /len=1873		,	
12240	0.035177	xq09e02.x1 NCI_CGAP_Ut1 cDNA	AW517395	Hs.445194	1.0
		clone IMAGE:2750138 3' similar to			
		contains Alu repetitive element,, mRNA			
1		sequence /clone=IMAGE:2750138			
		/clone_end=3' /gb=AW517395			
		/gi=7155477 /ug=Hs.445194 /len=519			1
•]			* 4 %	1
12243	0.032636	mPNA: aDNA DVEZp212D0424 (f-am	Å1 022702	He 125010	
12243	1 0.032030	mRNA; cDNA DKFZp313P0434 (from	AL832702	Hs.125019	
1	}	clone DKFZp313P0434) /gb=AL832702			
	}	/gi=21733281 /ug=Hs.125019	}		
	l	/len=2995		ļ	
12248	0.049079	EST(yd28g06.r1 Soares fetal liver	T82238		1 .
	l .	spleen 1NFLS IMAGE:109594 5')		1	

Genes	Correspo	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
		Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
	,			No.	No.
12250	0.049079	spastic paraplegia 3A (autosomal	NM 015915	Hs.241503	NP 056999
		dominant) (SPG3A), mRNA	_	}	
. 15/		/cds=(173,1849) /gb=NM_015915	e san Selah San .	1	
		/gi=19923444 /ug=Hs 241503			
		/len=2573			
12255	0.001339	solute carrier family 38, member 2	NM 018976	Hs.298275	NP 061849
12200	0.001000	(SLC38A2), mRNA /cds=(352,1872)	11111_010010	113.230210	111 _00 10 10
		/gb=NM_ 018976 /gi=21361601].		
		/ug=Hs.298275 /len=4795			
12257	0.007807	EST390958 MAGE resequences,	AW978849	Hs.124977	Grand Signal
12201	0.007007	MAGP cDNA, mRNA sequence	7VV370043	115.124977	
		/gb=AW978849 /gi=8170126			
*		_		1	
12262	7 445 04	/ug=Hs.124977 /len=678 EST (IL3-ET0114-281000-318-C11	BF870398	[ND 027264
12262	7.41E-04		 BF870398		NP_037364
4000	0.00700	ET0114)	D0045740	11- 0070	
12264	0.03788	clone IMAGE:3909104, mRNA	BC015719	Hs.8852	
	1	/gb=BC015719 /gi=16041698			
		/ug=Hs.8852 /len=3169			
12267	0.002337	EST (op46b10.s1	AA978266		
		Soares_NFL_T_GBC_S1			
		IMAGE:1579867 3')			
12274	0.04407	AV719140 GLC cDNA clone	AV719140	Hs.444680	
		GLCDHA04 5', mRNA sequence			
		/clone=GLCDHA04 /clone_end=5'		* .	
	1	/gb=AV719140 /gi=10816292			
	<u>.</u> ,	/ug=Hs.444680 /len=454			<u> </u>
12276	0.009388	UI-1-BC1p-ald-f-02-0-UI.s1	BQ013925	Hs.312222	
		NCI_CGAP_PI3 cDNA clone UI-1-BC1p		·	
		ald-f-02-0-UI 3', mRNA sequence			
	}	/clone=ÚI-1-BC1p-ald-f-02-0-UI			
		/clone_end=3' /gb=BQ013925		ł	
		/gi=19738826 /ug=Hs.312222	()		1.
mar r		/ien=1296		F	
12277	0.023945	EST (cn13c11.y1 Normal Human	Al752038		NP_003893
		Trabecular Bone Cells clone		· · · .	
		NHTBC cn13c11 random)			
12281	0.009388	EST(EST381388 MAGE resequences,	AW969311	 	NP_116277
		MAGK)			
12292	0.023945	EST(FB3F2 Fetal brain, Stratagene	T03208	 	
		cDNA clone FB3F2 3'end)			
12294	0.023945	EST(7e58a12.x1	BE644843	1	NP_006845
,		Soares_NSF_F8_9W_OT_PA_P_S1			
	1	cDNA clone IMAGE:3286654 3')	1.0		
12300	0.023045	hypothetical protein MGC32104	NM_144684	Hs.147025	NP_653285
12300	0.023943	1 • • • • • • • • • • • • • • • • • • •	144004	11 13. 177 020	141 _0002200
:		(MGC32104), mRNA /cds=(101,1651)	· · · · · ·	, .	
		/gb=NM_144684 /gi=21389584			
	L	/ug=Hs.147025 /len=4732	<u> </u>	<u> </u>	L

		nding To Differentially Expressed Gen		<u> </u>	_
Spot	p-value	D scription	Gen	Unigene	Protein
			Accession No.	Accession	Accession
	i			No.	No.
12301	0.003947	UI-H-EZ1-bbc-h-11-0-UI.s1	BQ574842	Hs.235026	
		NCI_CGAP_Ch2 cDNA clone UI-H-EZ1			
		bbc-h-11-0-UI 3', mRNA sequence			
		/clone=UI-H-EZ1-bbc-h-11-0-UI			
		/clone_end=3' /gb=BQ574842			
		/gi=21478159 /ug=Hs.235026			
		/len=1065		(ĺ
12302	0.025911	EST(zh85g03.s1	AA002088		NP 002773
12.002	0.020011	Soares_fetal_liver_spleen_1NFLS_S1	, 4 (002,900		1111 _002770
	No1	cDNA clone IMAGE:428116 3'		er er	
12303	0.003947	imageqc 1 2001/smg463bdff41.x1	BI850999	Hs.348651	
12303	0.003347	Soares NFL_T_GBC_S1 cDNA clone	D1000999	113.040001	
		IMAGE:4571343 3', mRNA sequence			1 1
· v-s		/clone=IMAGE:4571343 /clone_end=3'			4 - 1 -
· ·		/gb=BI850999 /gi=16004486	lation de la de la filipia de la filipia. Live a la companya de la filipia de la filipia de la filipia de la filipia de la filipia de la filipia de la f		
	g see		de contide de la competencia		1
		/ug=Hs.348651 /len=632			1 1
10000	0.00400	FOT/- DNA - 1 IMA OF 007047 51 \	A A 05 0000		77.7
		EST(cDNA clone IMAGE:667817 5')	AA258698	11- 070000	ND OFCOOL
12311	7.41E-04	DKFZP566I1024 protein	NM_015411	Hs.279696	NP_056226
		(DKFZP566I1024), mRNA			[.
		/cds=(48,953) /gb=NM_015411		1	
		/gi=24308052 /ug=Hs.279696			
	ļ	/len=2005			
12333	0.00587	EST (HS_5378_B2_A05_T7A RPCI-11	AQ683118		
	(·	Human Male BAC Library genomic			
		clone Plate=954 Col=10 Row=B)			
12344		EST(cDNA clone IMAGE:5303467 5')	BI597128		
12355	0.043799	cDNA FLJ36238 fis, clone	AK093557	Hs.345588	
		THYMU2001422. /gb=AK093557			
		/gi=21752458 /ug=Hs.345588			
		/len=2269			
12369	0.017288	QV3-BN0047-150400-152-h07 BN0047	AW997115	Hs.274352	
		cDNA, mRNA sequence			
	1	/gb=AW997115 /gi=8257349			
		/ug=Hs.274352 /len=686			
12370	0.001878	mRNA; cDNA DKFZp586N2424 (from	AL157503	Hs.27552	
]	clone DKFZp586N2424) /gb=AL157503			j
		/gi=7018553 /ug=Hs.27552 /len=2220			
	1	J	·		Ī
12376	0.001637	ESTs, cDNA, 5' end	BF032850	Hs.5367	
		/clone=IMAGE:3859365 /clone_end=5'			
		/gb=BF032850 /gi=10740562			
,		/ug=Hs.5367 (=ESTs, Weakly similar to			
		T02670 probable thromboxane A2			•
	l	receptor isoform beta)		ŀ	
	1	Leochioi isolouu nera)	L	1	I

		nding To Differentially Expressed Gen			B-4-7
Spot	p-value	Description	Gen	Unigene	Protein
	 I		Accession No.	Accession	Accession
10077	0.000043	ADDO-40 -4 NOL COAD COS aDNA	A104070C	No. Hs.212310	No.
2377	0.003213	ts88e10.x1 NCI_CGAP_GC6 cDNA	Al918786	HS.212310	
		clone IMAGE:2238378 3' similar to	and the second second		
		contains L1.t3 L1 repetitive element;			
		mRNA sequence			
		/clone=IMAGE:2238378 /clone_end=3'		· /	
		/gb=Al918786 /gi=5638641			
(0000	0.047000	/ug=Hs.212310 /len=459	NC 001144	<u> </u>	
12383	0.017288	Saccharomyces cerevisiae	NC_001144 		
		chromosome XII, complete			
10004	0.040754	chromosome sequence	AK055601	Hs.311977	
12384	0.040751	FLJ31039 fis, clone HSYRA2000221	UOCCUAN	HS.311977	
		/cds=UNKNOWN /gb=AK055601			
/ ·		/gi=16550371 /ug=Hs.311977			
12399	0.025911	/len=2770 UI-E-CK1-afh-b-14-0-UI.r1 UI-E-CK1	BM702699	Hs.446508	
12,399	0.025911	I for the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second	DIVI7 02099	ITS.440000	
		cDNA clone UI-E-CK1-afh-b-14-0-UI 5',		1	
		mRNA sequence /clone=UI-E-CK1-afh-			10000
· 14		b-14-0-UI /clone_end=5'		E. and a	
		/gb=BM702699 /gi=19015957			
10440	0.205.04	/ug=Hs.446508 /len=1088	BI041924		<u> </u>
12412	2.32E-04	cDNA / IL3-NT0294-060401-533-D04 NT0294	BI04 1924		
12413	0.045005	cDNA FLJ14244 fis, clone	AK024306	Hs.397378	
12413	0.013693	fig.	JANU24300	TS.391316	
	<u> </u>	OVARC1000802. /gb=AK024306			
		/gi=10436654 /ug=Hs.397378			1
10404	0.000300	/len=1889 mRNA; cDNA DKFZp564B076 (from	AL049313	Hs.21103	
12424	0.009366		AL049313	IUS.21103	
		clone DKFZp564B076) /gb=AL049313			1
12426	0.044500	/gi=4500086 /ug=Hs 21103 /len=2208 602590145F1 NIH MGC 76 cDNA	BG564169	Hs.444093	
12420	0.014599 		100004109	1115.444093	
		clone IMAGE:4724074 5', mRNA			
		sequence /clone=IMAGE:4724074		* .	
	1.	/clone_end=5' /gb=BG564169 /gi=13571821 /ug=Hs.444093 /len=792			
		/gi=155716217ug=H\$.4440957lefi=792			
12431	0.02904	ESTs, cDNA /gb=AW993259	AW993259	Hs.113105	
1243 [0.02001	■	WAAA99759A	113.113103	1
12433	0.047024	/gi=8253410 /ug=Hs.113105 /len=678 cDNA FLJ14388 fis, clone	AK027294	Hs.9812	1
12433	0.047031	HEMBA1002716. /gb=AK027294	MNU21284	13.3014	
		/gi=14041878 /ug=Hs.9812 /len=1673			
12436	0.047024	UI-H-BW0-ajn-d-08-0-UI.s1	AW297946	Hs.444392	
14430	0.047031	NCI_CGAP_Sub6 cDNA clone	AVV231340	110.744002	
		IMAGE:2732223 3', mRNA sequence	1 .	1]
		/clone=IMAGE:2732223 /clone_end=3'			
		/gb=AW297946 /gi=6704582	1		
	I	pgp-Avvzs1s40/gi-0/Q430Z	1	-1	1

		nding To Differentially Expressed Gen	a by a second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control		
Spot	p-value	Description	Gen	Unigene	Protein
			Acc ssion No.	Accession	Accession
				No.	No.
12438	0.033876	AV686223 GKC cDNA clone	AV686223	Hs.221642	
		GKCGXH11 5', mRNA sequence			-
1	1	/clone=GKCGXH11 /clone_end=5'		,	
,		/gb=AV686223 /gi=10288086			
		/ug=Hs.221642 /len=916			
12474	0.024732	clone RP11-350H1 from 7p14-15,	AC006195	, , , , , , , , , , , , , , , , , , , ,	
		complete sequence			
2488	0.022106	ESTs, cDNA, 3' end	Al356348	Hs.369317	
		/clone=IMAGE:2028021 /clone_end=3'			
		/gb=Al356348 /gi=4107969			
		/ug=Hs.369317 /len=512			
12492	0.035213	ESTs, cDNA, 3' end	Al582192	Hs.356049	NP_660327
! .		/clone=IMAGE:2213516 /clone_end=3'	and the second second		
		/gb=Al582192 /gi=4568089		The state of	
		/ug=Hs.356049 /len=566			
2502	0.016299	QV0-HT0398-210100-096-c03 HT0398	AW606588	Hs.430335	
		cDNA, mRNA sequence	4		
11.	1 14.	/gb=AW606588 /gi=7311329			
		/ug=Hs.430335 /len=621			
12507	0.001501	UI-E-CQ1-acq-b-08-0-UI.r1 UI-E-CQ1	BM688644	Hs.253634	
		cDNA clone UI-E-CQ1-acq-b-08-0-UI			
		5', mRNA sequence /clone=UI-E-CQ1-			
	and the second	acq-b-08-0-UI /clone_end=5'			
		/gb=BM688644 /gi=19001902		1	
		/ug=Hs.253634 /len=1017			2.5
2511	1.53E-04		BC041467	Hs.151570	
		/gb=BC041467 /gi=27371097			
		/ug=Hs.151570 /len=2043			
12513	0.020388	AGENCOURT_8841454	BQ924341	Hs.442591	
		Lupski_sciatic_nerve cDNA clone			
√.		IMAGE:6199422 5', mRNA sequence	1.		
		/clone=IMAGE:6199422 /clone_end=5'			
		/gb=BQ924341 /gi=22339372]	
		/ug=Hs.442591 /len=930			E
•					
2514	0.020388	DCBCQH10 DCB cDNA, mRNA	BU198777	Hs.50273	
		sequence /gb=BU198777 /gi=22717083			
		/ug=Hs.50273 /len=867			
12515	0.015895	stress 70 protein chaperone,	NM 006948	Hs.352341	NP_008879
		microsome-associated, 60kDa (STCH),			
		mRNA /cds=(37,1452) /gb=NM_006948			}
		/gi=24431965 /ug=Hs.352341		1	1
		/len=3998	, .		1
12520	0.002893	EST(Embryonic Heart cDNA Library	Al617050	T	****
		Danio rerio cDNA 5')	1	1	L. A.
12521	0.00168	EST(Stratagene colon (#937204) Homo	AA115711		NP_002731
		sapiens cDNA clone IMAGE:511532 3'			··
		- - - - - - - - - -	1 '	1	1

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Spot	p-value	D scription	Gene	Unig ne	Protein
	, i		Accession No.	Accession	Accession
		<u> </u>		No.	No.
12528	0.029005	full length insert cDNA clone ZD75H11	AF086402		NP 055518
12539	0.017288	UI-E-CK1-afh-a-18-0-UI r1 UI-E-CK1	BM702618	Hs.103381	Hara a Maria and a
		cDNA clone UI-E-CK1-afh-a-18-0-UI 5',			,
		mRNA sequence /clone=UI-E-CK1-afh-	•		· .
		a-18-0-UI /clone_end=5'	v → ***********************************		- ·
• .		/gb=BM702618 /gi=19015876			
		/ug=Hs.103381 /len=1069	e transference de la companya de la companya de la companya de la companya de la companya de la companya de la La companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de		[
12549	0.01932	cDNA FLJ11335 fis, clone	AK002197	Hs.284270	
		PLACE1010630. /gb=AK002197	1	11.0.20 1210	
		/gi=7023924 /ug=Hs.284270 /len=1984		1	
. 4.					
12560	0.022106	cDNA FLJ12136 fis, clone	AK022198	Hs.168830	
,2300	5.522.100	MAMMA1000312./gb=AK022198	1.1.022.100	11.13.100000	
		/gi=10433542 /ug=Hs.168830			
		/len≈1905	Mark Grand and Salage		
12572	0.022106	EST, clone IMAGE:4151959, mRNA	BC011194	Hs.367863	-
12312	0.022100	/cds=UNKNOWN /gb=BC011194	BC011194	П5.307603	
		/gi=15277441 /ug=Hs.367863			
		■ □ □ □ □ □ □ □ □ □ □ □ □ □ □ □ □ □ □ □	والمراجعة الماسية	1	
10E70	0.006463	/len=1842	BE047402		ND 000700
12573		EST(cDNA clone IMAGE:3125123 3')			NP_002700
12582		No significant match	SEQ.ID.No.47		
12594	0.025911	No significant match, ORF-1(3~499),-	050 10 11 60		
40044	0.000500	2(2~499)	SEQ.ID.No.99		
12644	0.003563	EST (RC0-HT0297-301099-011-a06	BE151529		Si y
100.17	0.000040	HT0297)	[В.	
12647	0.030249	EST(tm39b03.x1 NCI_CGAP_Kid11	Al478484		
		clone IMAGE:2160461 3' contains	a a manera in compa		
		L1.b3 L1 repeat)	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	<u> </u>	
12669	0.003947	hypothetical protein FLJ31438	NM_152385	Hs.24423	NP_689598
		(FLJ31438), mRNA /cds=(347,2107)	1	1	
		/gb=NM_152385 /gi=22748824			
	· · · · · · · · · · · · · · · · · · ·	/ug=Hs.24423 /len=2266			
12677	0.007171	hypothetical protein MGC12981	NM_032357	Hs.104203	NP_115733
		(MGC12981), mRNA /cds=(225,767)			
		/gb=NM_032357 /gi=21362049			
		/ug=Hs.104203 /len=1644			
12679	0.008566	BX092629 Soares fetal liver spleen	BX092629	Hs.303022	
		1NFLS cDNA clone IMAGp998P06398	1	t t	1 / /
		; IMAGE:205685, mRNA sequence			
		/clone=IMAGp998P06398_;_IMAGE:20	1.		· · ·
		5685 /gb=BX092629 /gi=27822922			1
		/ug=Hs.303022 /len=735].	
• •				}	
12680	0.02801	EST (CM3-HT0528-010200-086-f04	BE169870		
		HT0528)	1	í	1

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Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
١				No.	No.
12681	0.013394	chromosome 1 open reading frame 9	NM 016227	Hs.108636	NP_057311
.200.	((C1orf9), mRNA /cds=(125,4342)			
***	ti i jira	/gb=NM_016227 /gi=7705321			er ar de estad
		/ug=Hs:108636 /len=5919			
12688	0.033876	myxoid liposarcoma associated protein	NM_018192	Hs.42824	NP 060662
12000	0.033670	4 (MLAT4), mRNA /cds=(199,2325)	[NINI_010192	115.42024	141 _000002
		/gb=NM_018192 /gi=27764881	and the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second s		
	. 1.5 2.1 20 2.1	/ug=Hs.42824 /len=3396			
Nazza					
12689	0.012276	hypothetical protein MGC3077	NM_024051	Hs.433404	NP_076956
		(MGC3077), mRNA /cds=(137,703)			
		/gb=NM_024051 /gi=13129017		1	
- (****) 		/ug=Hs.433404 /len=1195			
12701	0.021	EST UI-H-Bl2-ahq-e-01-0-UI.s1	AW293540		NP_006816
		NCI_CGAP_Sub4_cDNA clone			
_		IMAGE:2727648 3'			
12711	0.003563	EST(ne80b06.s1 NCI_CGAP_Ew1	AA491607		
		cDNA clone IMAGE:910547)			
12712	0.011238	EST(xg51d02.x1 NCI_CGAP_Ut4	AW150422		
		cDNA clone IMAGE:2631843 3' similar			
* *		to contains Alu repetitive element)			
20 F					
12713	0.023945	EST (QV1-CT0364-120200-065-e11	AW862302		
		CT0364 cDNA)			
12716	0.007807	EST (601506025F1 NIH_MGC_71	BE884080		NP 005117
127,10	0.00.00.	IMAGE:3907495 5')			
12717	0.011238	EST(xx99e02.x1 NCI_CGAP_Lym12	AW515834		NP_387449
	0.011200	cDNA clone IMAGE:2851802 3' similar	7.000		" _00, 110
		to contains Alu repetitive element)	:		
		to contains Aid repetitive element)		1.0	
12720	0.033636	mRNA; cDNA DKFZp667O1616 (from	AL713722	Hs.365655	
12120	0.052050	clone DKFZp667O1616) /gb=AL713722		113,500000	
	1	1. ————————————————————————————————————		1	
, .		/gi=19584452 /ug=Hs.365655		1.11	
40700	0.007407	/len=1773	NM 020213	Up 9604	ND 064500
12722	0.007107	hypothetical protein from EUROIMAGE	NIVI_UZUZ 13	Hs.8694	NP_064599
		1977056 (LOC56965), mRNA	<u>.</u>		
	,	/cds=(609,1358) /gb=NM_020213			
		/gi=9910373 /ug=Hs 8694 /len=2359			
·		g.	L.==		<u> </u>
12723	0.00587	qw21c02.x1 NCI_CGAP_Ut4 cDNA	Al290157	Hs.387096	J.,
		clone IMAGE:1991714 3' similar to		1.	
	I	contains Alu repetitive element; contains		.]	
	-{		1.	1	1
		element L1 repetitive element ;, mRNA		,	
		element L1 repetitive element;, mRNA sequence /clone=IMAGE:1991714			
		sequence /clone=IMAGE:1991714			

Genes	Correspoi	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
Spot	p-value	Description	Gene	Unigene	Prot in
			Accession No.	Accession	Accession
				No.	No.
12724	0.03788	chromatin accessibility complex 1	NM_017444	Hs.279704	NP_059140
,		(CHRAC1), mRNA /cds=(196,591)			_
	T. 1	/gb=NM 017444 /gi=24432041		•	-
		/ug=Hs.279704 /len=2496			
12725	0.014599	EST(CM3-BN0151-130400-146-f01_1	BE008220		
		BN0151)			
12732	0.032636	mitochondrion, complete genome	NC 001807		
12753		EST(ty50b10.x1 NCI_CGAP_Ut2 cDNA	Al619566		
12,00	0.00007	clone IMAGE:2282491 3')	7 (10 10000		
12754	0.007107	ribosomal protein S24 (RPS24),	NM 033022	Hs.180450	NP_148982
12.01	0.557	transcript variant 1, mRNA	000022	1.10. 100 100	
	}	/cds=(38,430) /gb=NM_033022			
	T	/gi=14916500 /ug=Hs.180450 /len=537			
i grana a r				÷	
12763	0.013304	UI-H-FG0-bct-g-21-0-UI.s1	BU627064	Hs.85999	
12703	0.013394	NCI_CGAP_EN1~2 cDNA clone UI-H-	B0027004	115.00555	
- 44 - 1 - 12	e Samer M	FG0-bct-q-21-0-UI 3', mRNA sequence			
		/clone=UI-H-FG0-bct-g-21-0-UI			
		I. • • • • • • • • • • • • • • • • • • •			\$ 150 p
		/clone_end=3' /gb=BU627064			
		/gi=23293278 /ug=Hs.85999 /len=1075		[
1222	0.000.00				Harry Land
12767	0.030249	EST (602326911F1 NIH_MGC_91	BG036175		
40700	0.044500	IMAGE:4428291 5')	DE445400	11. 040444	
12786	0.014599	hr74d11.x1 NCI_CGAP_Kid11 cDNA	BF115106	Hs.318114	÷ -
		clone IMAGE:3134229 3' similar to			
#57	5 4 5 6	contains Alu repetitive element; contains			
		element MER15 repetitive element ,,			
		mRNA sequence			
		/clone=IMAGE:3134229 /clone_end=3'			
*****	اري. ام څهکي پخري	/gb=BF115106 /gi=10984582			
	1.	/ug=Hs.318114 /len=462			
12789	0.012276	EST(UI-H-BI3-alt-d-10-0-UI.s1	AW451910		NP_640339
		NCI_CGAP_Sub5 cDNA clone	1		
		IMAGE:3068587 3')			
12791	0.03788	EST(qh31d07.x1	Al239446		
		Soares_NFL_T_GBC_S1 cDNA clone			}
		IMAGE:1846285 3')			
12802	0.032636	UI-H-FH1-bfu-h-22-0-UI.s1	BU622323	Hs.406049	
		NCI_CGAP_FH1 cDNA clone UI-H-FH1	}	<u> </u>	
		bfu-h-22-0-UI 3', mRNA sequence			
	r	/clone=UI-H-FH1-bfu-h-22-0-UI	l	1	
		/clone_end=3' /gb=BU622323			
		/gi=23288538 /ug=Hs.406049		1	
		/len=1156			
12805	0.002526	clone IMAGE:3633225, mRNA	BC012758	Hs.356377	•
		/gb=BC012758 /gi=15706478			
		/ug=Hs.356377 /len=1914	4.		1.
		rug-ris.cocorriton-1014	<u></u>		

Genes		nding To Differentially Expressed Gen			
		Description	Gene	Unigen	Protein
•	Ĭ		Accession No.	Accession	Accession
				No.	No.
12808	0.020388	AU159529 THYRO1 cDNA clone	AU159529	Hs.331418	110
		THYRO1001913 3', mRNA sequence	,		
		/clone=THYRO1001913 /clone_end=3'			
		/gb=AU159529 /gi=11021050	, *** 		1
		/ug=Hs.331418 /len=582		٠.	
12817	0.020388	cDNA FLJ39478 fis, clone	AK096797	Hs.372680	
12017	0.020300	PROST2013605. /gb=AK096797	AKUSUISI	FIS.372000	
		/gi=21756367 /ug=Hs.372680			
40004	0.007007	/len=2507	DV440777	115 12014	
12821	0.007807	BX118777 Soares fetal liver spleen	BX118777	Hs.13911	
_!		1NFLS cDNA clone IMAGp998I20122,			
		mRNA sequence			
		/clone=IMAGp998I20122_;_IMAGE:124		1	
		891 /gb=BX118777 /gi=27841377	* * * * * * * * * * * * * * * * * * * *		
<u> </u>		/ug=Hs.13911 /len=857			
12824	0.002602	ubiquitin-conjugating enzyme E2G 1	NM_003342	Hs.78563	NP_003333
	[(UBC7 C. elegans) (UBE2G1), mRNA			
		/cds=(167,679) /gb=NM_003342			
		/gi=21314607 /ug=Hs.78563 /len=2430			
				1	_
12833	0.013394	cDNA FLJ30547 fis, clone	AK055109	Hs.351021	
		BRAWH2001439. /gb=AK055109			
		/gi=16549767 /ug=Hs.351021			
155 . ·	34	/len=1830			
12835	0.032636	AGENCOURT 8856629	BQ947179	Hs.356605	
		Lupski_sciatic_nerve cDNA clone			
		IMAGE:6200636 5', mRNA sequence	· •		
		/clone=IMAGE:6200636 /clone end=5'			
		/gb=BQ947179 /gi=22362657			
	ĺ	/ug=Hs.356605 /len=1277	ĺ		
		1211		1	
12854	0.043799	EST(cDNA clone IMAGE:2281749 3'	AI862212	 	
12007	0.040755	similar to contains L1 b1 L1 repetitive	7.110022.12		
		element)	,	,	1
12855	0.017288	UI-E-EJ0-aik-i-20-0-UI r1 UI-E-EJ0	BM727413	Hs.112619	
12000	0.017200	cDNA clone UI-E-EJ0-aik-i-20-0-UI 5',	DIVI727413	113.112013	
		mRNA sequence /clone=UI-E-EJ0-aik-i-			
		1			-
		20-0-UI /clone_end=5' /gb=BM727413] -		
	,	/gi=19048746 /ug=Hs.112619	[ĺ	
400==	1.50= 5	/len=1667	20004650	<u> </u>	<u> </u>
12857		EST(cDNA clone IMAGE:4413411 5')	BG034856	10====	<u> </u>
12892	0.013394 م	ESTs, cDNA, 5' end	Al792925	Hs.137097	
]	/clone=IMAGE:1554245 /clone_end=5'		J ·	
		/gb=Al792925 /gi=5340641			
		/ug=Hs.137097 /len=585			<u> </u>
12894	0.003213	cDNA FLJ38536 fis, clone	AK095855	Hs.30089	
٠.	1	HCHON2001200 /gb=AK095855	ì		
	1	/gi=21755199 /ug=Hs.30089 /len=2950	1	1	I
		//gi 21/00/00/09 110/00000 //oi/ 2000	J.	J	1

Spot	p-value	nding To Differentially Expressed Gen D scription	Gene	Unig ne	Protein
Spot	p raido		Accession No.	Accession	Accession
				No.	No.
2902	0.011238	ESTs, FLJ25251 fis, clone STM03603	AK057980	Hş.256801	
2		/cds=UNKNOWN /gb=AK057980			
. !		/gi=16553972 /ug=Hs.256801			
		/len=1727]
2926	0.023945	clone IMAGE:4391558, mRNA	BC017743	Hs.41407	
		/gb=BC017743 /gi=17389405			.
		/ug=Hs.41407 /len=2299]
12936	0.035177	clone IMAGE:5263531, mRNA	BC037740	Hs.18016	
	"""	/gb=BC037740 /gi=22902216			'.
W 25		/ug=Hs.18016 /len=5036			1
12937	0.012276	hypothetical protein MGC45586	NM 152603	Hs.145473	NP 689816
12901	0.012270	(MGC45586), mRNA /cds=(214,2055)	1,1,1,1,1,0,2,0,0	1, 13, 13,047,0	
		/gb=NM 152603 /gi=22749238	ь	-	1
		/gg=Hs.145473 /len=2724			
10040	0.000045		AK056188	Hs.375198	
12940	0.023945	cDNA FLJ31626 fis, clone	AK020100	IUS.212180	1
		NT2RI2003317./gb=AK056188			
		/gi=16551523 /ug≆Hs.375198			
		/len=2041			<u> </u>
12965	0.032636	UI-H-ED1-axy-n-13-0-UI.s1	BQ009853	Hs.438790	
		NCI_CGAP_ED1 cDNA clone			
,		IMAGE:5835468 3', mRNA sequence			
		/clone=IMAGE:5835468 /clone_end=3')		
		/gb=BQ009853 /gi=19734754			*
		/ug=Hs.438790 /len=1069			
			 		
12973	0.023945	ESTs, cDNA, 3' end	AW009340	Hs.372482	
		/clone=IMAGE:2504343 /clone_end=3'	14		1
		/gb=AW009340 /gi=5858118			
	1	/ug=Hs.372482 /len=490			
12975	0.023945	cDNA FLJ38271 fis, clone	AK095590	Hs.231895	1
		FCBBF3002782, moderately similar to	1		
		Leptin receptor. /gb=AK095590			
		/gi=21754877 /ug=Hs.231895			
		/gi=217346777dg=118.231093 /len=2435			
12978	0.030300	mRNA; cDNA DKFZp667G172 (from	AL832859	Hs.71969	
12310	0.020300	clone DKFZp667G172) /gb=AL832859	TUCOS CODS	1, 13.7 1303	1
]	/gi=21733443 /ug=Hs.71969 /len=3463		}	
4000	0.000707	AOCHOURT COCCOCA	D\$400.4070	11-04004	
12987	0.026797	AGENCOURT_6653891	BM924870	Hs.94881	
		NIH_MGC_116 cDNA clone			1
		IMAGE:5761337 5', mRNA sequence		1	1
i		/clone=IMAGE:5761337 /clone_end=5'			
		/gb=BM924870 /gi=19375249			
	, ,	/ug=Hs.94881 /len=1142		1	
*	1 .		;		1

Genes	Correspoi	nding To Diff rentially Expressed Gen	es in Figure 20 -	RA	
		D scription	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
12997	0.040751	UI ₇ H-BI2-ahp-c-07-0-UI.s1	AW293767	Hs.437871	***
	4 4	NCI_CGAP_Sub4 cDNA clone			
.,		IMAGE:2727541 3', mRNA sequence	la de la companya de la companya de la companya de la companya de la companya de la companya de la companya de Na companya de la companya de la companya de la companya de la companya de la companya de la companya de la co		
		/clone=IMAGE:2727541 /clone_end=3			
	er grand and	/gb=AW293767 /gi=6700403			
		/ug=Hs.437871 /len=660			
12998	0.002337	UI-H-EU0-azv-i-13-0-UI.s1	BQ181732	Hs.442187	1 1 1 1 1 1
		NCI_CGAP_Car1 cDNA clone IMAGE:			
	. ere	5854164 3', mRNA sequence	•		
		/clone=IMAGE:_5854164 /clone_end=3'			
		/gb=BQ181732 /gi=20357224			
·	` .	/ug=Hs.442187 /len=1042			
		74g=113.442107 //CII=1042			
12999	0.036556	hypothetical protein FLJ32440	NM 173685	Hs.344478	NP 775956
12000	0.000000	(FLJ32440), mRNA /cds=(228,971)	11.11_17.000	1,1010,1,11,0	=
		/gb=NM_173685 /gi=27734760		,	
		/ug=Hs.344478 /len=1258			
13004	0.002006	ESTs, cDNA, 5' end	BM806490	Hs.124839	NP 647603
13004	0.002090	/clone=IMAGE:5555887 /clone_end=5'	DIVIOUOTOU	1113.12.4000	141 _047000
		/gb=BM806490 /gi=19123313			
		/ug=Hs.124839 /len=1087			
		/ug=ris.1240397ien=1007			
13005	0.012276	zx55g04.r1	AA203502	Hs.192991	landar ty
13003	0.012270	Soares_fetal_liver_spleen_1NFLS_S1	/V-1203302	113.132331	
ŀ		cDNA clone IMAGE:446454 5', mRNA			
in the		sequence /clone=IMAGE:446454			
,		/clone_end=5' /gb=AA203502			
12000	0.007107	/gi=1799213 /ug=Hs.192991 /len=952	AI800041	Hs.369733	1.00
13008	0.007107	wc41h02.x1 NCI_CGAP_Pr28 cDNA	A1600041	IU8.308/33	
		clone IMAGE:2321235 3', mRNA			
	4	sequence /clone≈IMAGE:2321235			
		/clone_end=3' /gb=Al800041			
40040	0.000040	/gi=5365513 /ug=Hs.369733 /len=504	A1A10E774.4		
13013	0.030249	EST(cDNA clone IMAGE:2542504 3'	AW057714	*	
		similar to contains Alu repetitive		12	
4001=	0.00700=	element;)	DV440007	112 400040	<u> </u>
13017	0.007807	BX116697 NCI_CGAP_Co3 cDNA	BX116697	Hs.433643	
		clone IMAGp998C232238, mRNA			
] .		sequence			1.5
1.		/clone=IMAGp998C232238_;_IMAGE:9			
l		01582 /gb=BX116697 /gi=27840179	1	1	
	L	/ug=Hs.433643 /len=682		1	<u> </u>
13035	0.049079	clone MGC:16614 IMAGE:4111344,	BC009313	Hs.398884	
		mRNA, complete cds /cds=(258,998)			
	1	/gb=BC009313 /gi=14424569		1	
1	1	/ug=Hs.373515 /len=2052	L	1	

Genes	Correspon	nding To Differentially Expressed Gen	es in Figure 20 -		
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Acc ssion	Accession
				No.	No.
13036	0.013394	UI-H-FG1-bgh-I-12-0-UI.s1	BU624037	Hs.416904	
		NCI_CGAP_FG1 cDNA clone UI-H-	2		
		FG1-bgh-I-12-0-UI 3', mRNA sequence			
		/clone=UI-H-FG1-bgh-I-12-0-UI			· · · · · · · · · · · · · · · · · · ·
1		/clone_end=3' /gb=BU624037			
		/gi=23290252 /ug=Hs.416904			
		/len=1160			
13040	0.010277	Ul-E-EJ1-aji-d-10-0-Ul s1 Ul-E-EJ1	BM684333	Hs.17910	
13040	0.010277	cDNA clone UI-E-EJ1-aji-d-10-0-UI 3',	DIVIO04500	115.17910	
		mRNA sequence /clone=UI-E-EJ1-aji-d-			
		10-0-UI /clone_end=3' /gb=BM684333			
	, T	/gi=18994229 /ug=Hs.17910 /len=1036			
	<u> </u>		050 15 11 40		
13046			SEQ.ID.No.12		3, 4, 5, 1
		no significant match	SEQ.ID.No.37		
<u>13049</u>		No significant match	SEQ.ID.No.42		
13069	0.032636	EST(PM1-HT0422-160300-009-a12	BE160886		
		HT0422 Homo sapiens cDNA, MRNA			
		sequence)			
13070	0.012276	mRNA from chromosome 5q31-33	AF010236	Hs.10323	
		region /gb=AF010236 /gi=2707623			
		/ug=Hs.10323 /len=1379			
13071	0.018784	cDNA FLJ31079 fis, clone	AK055641	Hs.350401	
		HSYRA2001595./gb=AK055641			
		/gi=16550421 /ug=Hs.350401			
	*	/len=2188		1.	
13076	0.035177	UI-H-BI1-abw-h-07-0-UI.s1	AW138111	Hs.436560	
		NCI_CGAP_Sub3 cDNA clone			
		IMAGE:2713572 3', mRNA sequence			
		/clone=IMAGE:2713572 /clone end=3'			
		/gb=AW138111 /gi=6142429			
		/ug=Hs.436560 /len=800	i.		
13083	6 56E 04	No significant match	SEQ.ID.No.31	 	
		No significant match	SEQ.ID.No.44	7	
		No significant match, ORF-1(155~328)	3EQ.ID.NO.44		
13092	0.02801	Ino significant match, ORF-1(155~526)	CEO ID No 94		
40400	0.004207	FL 122400 F TDAGU200072	SEQ.ID.No.81	11- 404705	
13133	0.004367	FLJ33100 fis, clone TRACH2000873	AK057662	Hs.181785	
	Į	/cds=UNKNOWN /gb=AK057662			
	J.	/gi=16553426 /ug=Hs.346406		**	,
		/len=2308		L	
13134	6.56E-04	sine oculis homeobox 2 (Drosophila)	NM_016932	Hs.101937	NP_058628
		(SIX2), mRNA /cds=(283,1158)	1] .	1
		/gb=NM_016932 /gi=21314676	1	1 '	1
		/ug=Hs.101937 /len=2141	<u></u>	1	L
13162	0.012276	opioid growth factor receptor (OGFR),	NM_007346	Hs.67896	NP_031372
		mRNA /cds=(206,2062)			
		/gb=NM_007346 /gi=6671492			
	1	/ug=Hs.67896 /len=2423	1	1	

		nding To Differentially Expressed Gen			In-	
Spot	p-value		Gene	Unigene	Prot in	
			Accession No.	Accession	Accession	
				No.	No	
13165	0.007171	lymphoid enhancer-binding factor 1	NM_016269	Hs.44865	NP 057353	
		(LEF1), mRNA /cds=(655,1854)	_		-	
		/gb=NM_016269 /gi=19923451				
		/ug=Hs.44865 /len=3084		\ .		
13167	0.030340	mannose phosphate isomerase (MPI),	NM 002435	Hs.75694	NP 002426	
1310/	0.030249		14141_002433	IIIS. 13094	INP_002420	
		mRNA /cds=(6,1277) /gb=NM_002435				
- :		/gi=4505234 /ug=Hs.75694 /len=1771	gradin regressive to the car			
*				<u> </u>		
13168	0.004367	clone IMAGE:4177569, mRNA	BC016402	Hs.46736		
•		/gb=BC016402 /gi=19116212				
		/ug=Hs.46736 /len=2243				
13169	0.040751	ATPase, Ca transporting, plasma	NM 001682	Hs.78546	NP 001673	
		membrane 1 (ATP2B1), mRNA			-	
		/cds=(182,3844) /gb=NM 001682				
gran iki n		/gi=4502286 /ug=Hs.78546 /len=4398				
13170	0.003803	nucleolar protein family 6 (RNA-	NM 022917	Hs.183253	NP 631981	
10110	0.002033	associated) (NOL6), transcript variant		1, 13. 100200	1.11 _00 1901	
ta de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition de la composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della composition della com						
		alpha, mRNA /cds=(61,3501)				
		/gb=NM_022917 /gi=22212928	person secretaria di salah	kan ing sa		
		/ug=Hs.183253 /len=4854				
13173	0.040751	DEAD/H (Asp-Glu-Ala-Asp/His) box	NM_004396	Hs.76053	NP_004387	
		polypeptide 5 (RNA helicase, 68kDa)				
garrana. Nasa		(DDX5), mRNA /cds=(171,2015)			1	
		/gb=NM_004396 /gi=13514826	·			
	V 1	/ug=Hs.76053 /len=2325			1	
13180	0.032636	F-box only protein 7 (FBXO7), mRNA	NM 012179	Hs.5912	NP 036311	
.5.100	0.002000	/cds=(281,1849) /gb=NM 012179	1,411,012.173	113.0012	1000011	
	. "					
40405	0.000000	/gi=15812192 /ug=Hs.5912 /len=2165	AL 000004	116-250445		
13185	0.020388	mRNA; cDNA DKFZp667H216 (from	AL833204	Hs.356145		
		clone DKFZp667H216) /gb=AL833204		• • •	}	
		/gi=21733834 /ug=Hs.356145				
V-		/len=3782			<u> </u>	
13186	0.002096	hypothetical protein DC42 (DC42),	NM_030921	Hs.72805	NP_112183	
		mRNA /cds=(463,771) /gb=NM_030921			1	
		/gi=24475707 /ug=Hs.72805 /len=1632				
+ . +						
13193	0.005339	protein phosphatase 2 (formerly 2A),	NM 002715	Hs.91773	NP 002706	
10100	0.00000	catalytic subunit, alpha isoform	14141_0027 10	11,5.51775	-002/00	
		(PPP2CA), mRNA /cds=(210,1139)				
				1 1	1	
		/gb=NM_002715 /gi=4506016	e ye karin ger		1 1	
1 1 1		/ug=Hs.91773 /len=2181	ļ.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1	1.2.2	
13197	2.45E-04	similar to rat nuclear ubiquitous casein	NM_022731	Hs.118064	NP_073568	
		kinase 2 (NUCKS), mRNA	j		1	
		/cds=(67,558) /gb=NM_022731	ļ		·	
		/gi=12232386 /ug=Hs.118064]	:	1.	
		/len=1811			1 1	
40400	0.014599	HSKM-B protein (HSKM-B), mRNA	NM 020197	Hs.66170	NP_064582	
1,3199	1 0.017000		1	1.10.00770	1 50 7002	
13199		/cds=(23,1324) /gb=NM_020197		1	l.	

		nding To Differentially Expressed Gen			to the second
Spot	p-value		Gene	Unigene	Protein
	* '		Accession No.	Accession	Accession
				No.	No.
13201	0.043799	chromosome 21 open reading frame 7	NM_020152	Hs.41267	NP_064537
	ja aja ti	(C21orf7), mRNA /cds=(130,858)			
		/gb=NM_020152 /gi=9910145		**************************************	
		/ug=Hs.41267 /len=1853			
13203	0.040751	BCL2/adenovirus E1B 19kDa	NM 004331	Hs.132955	NP 004322
		interacting protein 3-like (BNIP3L),	-		
		mRNA /cds=(83,742) /gb=NM_004331			
		/gi=4757859 /ug=Hs.132955 /len=1337			
r		/g=4/0/029/dg=115.102900/ieii=100/			la Maria
12200	0.01033	zd62d11.s1	W72877	Hs.380971	
13209	0.01932		VV12011	115.300971	
i Granda (1967) i e	House state of the	Soares_fetal_heart_NbHH19W cDNA			
		clone IMAGE 345237 3', mRNA			
	,	sequence /clone=IMAGE:345237	1,		1
		/clone_end=3' /gb=W72877			
		/gi=1383090 /ug=Hs.380971 /len=588			
13212	0.012526	hypothetical protein FLJ20060	NM_017645	Hs.54617	NP_060115
		(FLJ20060), mRNA /cds=(72,2078)			
		/gb=NM_017645 /gi=24431978			
•		/ug=Hs.54617 /len=2884			
13230	0.040751	ATP-binding cassette, sub-family E	NM_002940	Hs.12013	NP_002931
		(OABP), member 1 (ABCE1), mRNA			
		/cds=(118,1917) /gb=NM_002940			
		/gi=4506558 /ug=Hs 12013 /len=3568			
13231	0.047031	hypothetical protein PRO2369	NM 018525	· · · · · · · · · · · · · · · · · · ·	
.020.		(PRO2369), mRNA			
13236	0.005325	glutamate receptor, metabotropic 6	NM 000843	Hs.248131	NP_000834
13200	0.000020	(GRM6), mRNA /cds=(179,2812)	11111_000040	17.0.2.10101	
		/gb=NM_000843			
	14.5	/gi=6006006/ug=Hs.248131 /len=6122			
13237	0.040751	KIAA0635 gene product (KIAA0635),	NM 014645	Hs.185091	NP 055460
1323/	;0.040/51	1	NIVI_U 14045	П5. 100091	INP_055460
		mRNA /cds=(833,3373)	[·		
	-0 1 - 0 B	/gb=NM_014645 /gi=7662215			12 to 14
		/ug=Hs.185091 /len=5138	NII - 04-7000	11 50404	ND 000070
13245	0.029995	hypothetical protein FLJ20618	NM_017903	Hs.52184	NP_060373
		(FLJ20618), mRNA /cds=(319,726)		l	
		/gb=NM_017903 /gi=8923570		1	
		/ug=Hs.52184 /len=2213			
13247	5.79E-04	phosphoserine phosphatase (PSPH),	NM_004577	Hs.56407	NP_004568
4		mRNA /cds=(20,697) /gb=NM_004577	1	1.	1
		/gi=21614545 /ug=Hs.56407 /len=1432			
			_		1
13278	0.007107	601660815R1 NIH_MGC_72 cDNA	BE966810	Hs.336116	1
	* * *	clone IMAGE:3915843 3', mRNA			· ·
	1	sequence /clone=IMAGE:3915843			1
,		/clone_end=3' /gb=BE966810			
		/gi=11772610 /ug=Hs.336116 /len=730	1	1	1
	1	pg-11112010/4g-115.550110/1611-/50	1 .	1	1

Genes	Correspoi	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
		D scription	Gen Accession No.	Unig n	Protein Accession No.
13279	0.015895	UI-E-EJ0-ahr-e-11-0-UI s1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahr-e-11-0-UI 3', mRNA sequence /clone=UI-E-EJ0-ahr- e-11-0-UI /clone end=3' /gb=BU739063	BU739063	Hs.58668	
5#12 14 -	eren en lagr	/gi=23676884 /ug=Hs.58668 /len=1345		12	
13281	0.030249	cDNA FLJ11379 fis, clone HEMBA1000469. /gb=AK021441 /gi=10432627 /ug=Hs.200113 /len=1672	AK021441	Hs.200113	
13282	0.024732	LIS1-interacting protein NUDEL; endooligopeptidase A (NUDEL), mRNA /cds=(134,1171) /gb=NM_030808 /gi=13540599 /ug=Hs.3850 /len=2329	NM_030808	Hs.3850	NP_110435
13284	7.63E-04	FLJ21548 fis, clone COL06252 /cds=UNKNOWN /gb=AK025201 /gi=10437665 /ug=Hs.348999 /len=2019	AK025201	Hs.348999	NP_068351
13290	0.03788	cold shock domain protein A (CSDA), mRNA /cds=(195,1313) /gb=NM_003651 /gi=21359983 /ug=Hs.198726 /len=1931	NM_003651	Hs.198726	NP_003642
13301	0.003947	far upstream element (FUSE) binding protein 1 (FUBP1), mRNA /cds=(27,1961) /gb=NM_003902 /gi=17402899 /ug=Hs.118962 /len=2325	NM_003902	Hs.118962	NP_003893
13307	0.033876	FAD104 (FAD104), mRNA /cds=(58,3672) /gb=NM_022763 /gi=27477058 /ug=Hs.299883 /len=6894	NM_022763	Hs.299883	NP_073600
13315	0.002096	partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene	AJ295844		
13316	0.005325	ring finger protein 19 (RNF19), mRNA /cds=(318,2834) /gb=NM_015435 /gi=19923421 /ug=Hs.48320 /len=4357	NM_015435	Hs.48320	NP_056250
13319	0.023945	cDNA FLJ33540 fis, clone BRAMY2007613. /gb=AK090859 /gi=21749098 /ug=Hs.21213 /len=2030	AK090859	Hs.21213	
13327	0.02801	transcriptional regulator interacting with the PHS-bromodomain 2 (TRIP-Br2), mRNA /cds=(298,1242) /gb=NM_014755 /gi=7661925 /ug=Hs.77293 /len=5544	NM_014755	Hs.77293	NP_055570

Genes	Correspon	nding To Differentially Expressed Gen			
Spot	p-value	D scription	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
13328	0.006463	E1A binding protein p400, mRNA for	AB058721	Hs.306094	NP 056224
		KIAA1818 protein, partial cds			
		(AB058721.1)		**** *	
13337	0.018784	similar to putative (H.sapiens)	XM 058647		
15001	0.010704	(LOC122704), mRNA (=AL135998.6)	XIVI_000041		
13343	0.025911	hypothetical protein MGC26914	NM 144976	Hs.202974	NP 659413
13343	0.025911	(MGC26914), mRNA /cds=(148,1809)	144970	115.202914	114F_009410
1					
		/gb=NM_144976 /gi=21699059			·
20040	0.000400	/ug=Hs.202974 /len=2900	NIN 005400	11. 000047	ND 070070
13349	0.022106	capillary morphogenesis protein 1	NM_025103	Hs.288617	NP_079379
		(CMG1), mRNA /cds=(620,1927)			
,5	[/gb=NM_025103 /gi=13376668		· ·	<u>-</u>
· · ·		/ug=Hs.288617 /len=1995			
13354	9.43E-04		NM_030877	Hs.178576	NP_110517
		/cds=(95,1786) /gb=NM_030877	,		
		/gi=18644733 /ug=Hs.178576			
		/len=1900			
13355	0.013394	mRNA; cDNA DKFZp313E1815 (from	AL833098	Hs.125031	
		clone DKFZp313E1815) /gb=AL833098]
F 400		/gi=21733689 /ug=Hs.125031			1
		/len=1937			
13358	0.002337	hypothetical protein MGC17943	NM 152261	Hs.106390	NP 689474
10000	0.002007	(MGC17943), mRNA /cds=(214,564)	1	110.10000]
engille e e e	* 4 · 4 · 4	/gb=NM_152261 /gi=22748614			
130	- E	/ug=Hs 106390 /len=3167			
40000	0.042700		AK022062	Hs.287474	-
13360	0.043799	cDNA FLJ12000 fis, clone	ANUZZUOZ	IDS.20/4/4	
		HEMBB1001531. /gb=AK022062			`
		/gi=10433382 /ug=Hs.287474	-		
		/len=2675			
13380	0.00587	similar to HYPOTHETICAL 34.0 KDA	NM_033416	Hs.91579	NP_219484
		PROTEIN ZK795.3 IN CHROMOSOME			
	1	IV (MGC19606), mRNA /cds=(18,893)			
		/gb=NM_033416 /gi=15529981			
		/ug=Hs.91579 /len=1074		1	· '
				<u> </u>	
13382	0.017288	Similar to zinc finger protein 135 (clone	BC040486	Hs.5621	
	1	pHZ-17), clone IMAGE:5271431,			
		mRNA /gb=BC040486 /gi=26996848		}	1
		/ug=Hs.5621 /len=4671		l' .	
*			,		
13388	0.023945	fos-related antigen DNA, exon 4	X98050		1
13389		brain protein 44-like (BRP44L), mRNA	NM_016098	Hs.108725	NP_057182
		/cds=(123,452) /gb=NM_016098		1	
	1 .	/gi=7706368 /ug=Hs.108725 /len=988			1 -
13392	0.00303	hypothetical protein FLJ30162	NM 152731	Hs.311163	NP 689944
10092	0.00393	(FLJ30162), mRNA /cds=(272,841)	1.1111_102701	1.10.011100	
	,	/gb=NM 152731 /gi=22749448	1		
[1		
		/ug=Hs.311163 /len=2278	<u> </u>		

		nding To Differentially Expressed Gen			<u></u>
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
	·			No.	No.
3409	0.02801	EST(tc76d07.x1 Soares_NhHMPu_S1	AI383220		NP_006363
		clone IMAGE:2070541 3')		All makes who is to	
3421	0.043799	EST(zo63g01.s1 Stratagene panCReas	AA158759		
	1	(#937208) clone IMAGE:591600 3'	1		
7		contains Alu repeat)	1		
3426	0.006463	pleckstrin domain containing, family A	NM_021622	Hs.287830	NP_067635
		(phosphoinositide binding specific)			
		member 1 (PLEKHA1), mRNA			
		/cds=(67,1281) /gb=NM_021622			
		/gi=11055985 /ug=Hs.287830			
		/len=1410			
3427	0.040751	EST(zi22h02.s1 Soares fetal liver	AA676353		NP_060719
	-1	spleen 1NFLS S1 clone 431571 3')			
3441	0.040751	hypothetical protein FLJ10769	NM 018210	Hs.8083	NP 060680
		(FLJ10769), mRNA /cds=(15,1187)			1 7 7
. 5		/gb=NM 018210 /gi=8922653			
		/ug=Hs.8083 /len=2659			
3453	0.023945	mesoderm induction early response 1	NM 020948	Hs.222746	NP 065999
.0.00	0.020010	(MI-ER1), mRNA /cds=(234,1844)			-999000
		/gb=NM_020948 /gi=24308260			
	Factories and	/ug=Hs.222746 /len=4972			
13458	0.035177	EST RC3-HT0470-070100-011-g03_2	AW580534	 	11 1250 (A 11
13430	0.033177	HT0470 cDNA	744200224		
2400	0.004079		AI095772		8.8
13468	0.001878	EST qb30c09.x1	A1095772		
	1	Soares_pregnant_uterus_NbHPU			
10.470	0.005477	cDNA clone IMAGE:1697776-3'	1100470	<u></u>	
13476		EST(yw27g01.r1 clone 253488 5')	H89172		ND 070500
13478	0.002893	EST(xd92a04.x1	AW117454		NP_073592
		Soares_NFL_T_GBC_S1 clone			
		IMAGE:2605038 3')		l	
13484	0.017288	hypothetical protein FLJ10956	NM_018283	Hs.144407	NP_060753
	 , .	(FLJ10956), mRNA /cds=(181,675)			
		/gb=NM_018283 /gi=8922791			
	<u> </u>	/ug=Hs.144407 /len=2022			<u> </u>
13510	0.004827	uncharacterized hematopoietic	NM_018466	Hs.110853	NP_060936
		stem/progenitor cells protein MDS031			} •
,		(MDS031), mRNA /cds=(35,532)		1	
		/gb=NM_018466 /gi=20070304			
	<u>L</u>	/ug=Hs.110853 /len=1358			
13513	0.002337	EST(PM3-SN0020-270300-001-h08	AW865025		NP_115668
		SN0020))		
13519	0.047031	EST(zr70e01.r1 Soares_NhHMPu_S1	AA235432	1	
•		cDNA clone IMAGE:668760 5')			1
	<u> </u>	<u> </u>	 		1
13520	0.003213	EST(tz32c11.x1 NCI_CGAP_Ut2 clone	Al631079	1	INP 079436

		nding To Differentially Expressed Gen Description	Gene		D
Spot	p-value	Description	Accession No.	Unigene Accession No.	Protein Accession No.
13521	0.030249	RAP2A, member of RAS oncogene	NM 021033	Hs.301746	NP 066361
		family (RAP2A), mRNA /cds=(18,569)			[
·		/gb=NM_021033 /gi=25188202	er e la la la la la la la la la la la la la		
	. ,	/ug=Hs.301746 /len=2943		V v	
13530	9.43E-04	synaptic nuclei expressed gene 1	NM 015293	Hs.192102	NP_598411
		(SYNE-1), transcript variant beta,	9 .00		
- Q. J		mRNA /cds=(121,10086)			
		/gb=NM _: 015293 /gi=19526752		• •	
		/ug=Hs 192102 /len=10742			(\cdot,\cdot) , \cdot
13548	0.020388	EST84415 Colon adenocarcinoma IV	AA372489		
13553		EST(zw71a05.r1-Soares testis NHT	AA432328		
	0.00-1007	cDNA clone IMAGE:781616 5' similar	7 0 1402020		
	er, grand	to contains Alu repetitive element)			
13554	0.001459	cyclin M3 (CNNM3), mRNA	NM 017623	Hs.44095	NP 060093
	0.001100	/cds=(99,1247) /gb=NM_017623	11111_017020	1113.44000	141000030
30,5		/gi=20127562 /ug=Hs.44095 /len=2234			
		/gi 29121002/4g (19.44009/1011-2 <u>20</u> 4		i	
13555	0.009388	hypothetical protein FLJ10700	NM 018182	Hs.295909	NP 060652
	0.00000	(FLJ10700), mRNA /cds=(184,1872)	11111_010102	113.20000	_000002
A. 181 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		/gb=NM_018182 /gi=8922595			
		/ug=Hs.295909 /len=3434	() () () () () ()		
13561	0.015895	EST (yr44h03.s1 Soares fetal liver	H62537		
10001	0.010000	spleen 1NFLS IMAGE:208181)	11102007		
13568	0.035177	clone HQ0477 PRO0477p (LOC51204),	NM 016360	Hs.174134	NP 057444
.0000	0.000177	mRNA /cds=(201,1094)	11111_010000	113.174134	1111 _007444
		/gb=NM_016360 /gi=27545314			
		/ug=Hs.174134 /len=1491		l a participation	
13569	0.011238	EST (tu41c10.x1 NCI_CGAP_Pr28	AI686385	 	late di Pit e
	0.011200	cDNA clone IMAGE:2253618 3' similar	7.11000000		
		to contains Alu repetitive element;)			
				, ,	∫ '
13570	0.012276	601445486F1 NIH MGC 65 cDNA	BE868854	Hs.314370	
٠,٠٠٠	3.3.22,0	clone IMAGE:3849740 5', mRNA			}
		sequence /clone=IMAGE:3849740	}	}]
	. ''	/clone_end=5' /gb=BE868854	}		\
	, .	/gi=10317630 /ug=Hs.314370 /len=754			
					1
13582	0.002893	mRNA; cDNA DKFZp586M1819 (from	AL834255	Hs.355753	NP_848934
,,,,,,,	0.002000	clone DKFZp586M1819) /cds=(1,795)	1,1200 1200	113.000700	144 _040004
- 1		/gb=AL834255 /gi=21739805		•]
		/ug=Hs.355753 /len=1723			
13592	0.008566	hypothetical gene supported by	XM 074528	 	
.0002	3.000000	XM 074528 (LOC123829), mRNA	/VI_01-1020		}
13599	0.007107	mRNA; cDNA DKFZp313E1012 (from	AL832661	Hs.94694	
. 5555	0.007 107	clone DKFZp313E1012) /gb=AL832661	, 1002001	13.54054	}
		/gi=21733237 /ug=Hs.94694 /len=3233	,		}
	. '	191-211 00201 109-113.34034 11511-3233	· ·	l	Į.

Genes	Correspor	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
		Description	Gen	Unig ne	Prot in
	1		Accession No.	Accession	Accession
				No.	No.
13600	0.006463	Cdc42 guanine nucleotide exchange	NM_015185	Hs.54697	NP 056000
		factor (GEF) 9 (ARHGEF9), mRNA			
		/cds=(802,2352) /gb=NM_015185		er Paris de la secono	
		/gi=7662107 /ug=Hs.54697 /len=5413	y a second		1
13602	0.025911	UI-1-BC1p-asi-a-02-0-UI.s1	BQ011545	Hs.361171	
10001	0.0200	NCI_CGAP_Pl3 cDNA clone UI-1-BC1p			
		asi-a-02-0-UI 3', mRNA sequence			
		/clone=UI-1-BC1p-asi-a-02-0-UI		:	
		/clone_end=3' /gb=BQ011545			
in Asset		/gi=19736446 /ug=Hs.361171		. * #	
	444	/len=1143			
13608	0.043700	inositol polyphosphate-1-phosphatase	NM 002194	Hs.32309	NP_002185
13000	0.043198	(INPP1), mRNA /cds=(304,1503)	13141_002_104	1 13.02.003	141 _002 100
land the		/gb=NM_002194 /gi=4755138			
		1 T T T T			
13612	0.02700	/ug=Hs.32309 /len=1682 poly(rC) binding protein 2 (PCBP2),	NM 005016	Hs.63525	NP 114366
13012	0.03708	transcript variant 1, mRNA	LAINITONNO IO	11 15.00020	INF_1:14300
7. 7. 7.			a second second	1	t filosof e
		/cds=(89,1189) /gb=NM_005016			
	and the second	/gi=14141167 /ug=Hs.63525 /len=1362			<u> </u>
12020	0.042700	b	NIM 025079	Un 200204	NP 079354
13628	0.043799	hypothetical protein FLJ22378	NM_025078	Hs.288284	INP_0/9354
		(FLJ22378), mRNA /cds=(52,564)			}
	n e a a a angles a gal	/gb=NM_025078 /gi=13376629	in a second	ł	
1000	0.000007	/ug=Hs.288284 /len=2143	1134 445000	11- 204005	ND CEOF47
13634	0.002337	non-SMC (structural maintenance of	NM_145080	Hs.284295	NP_659547
		chromosomes) element 1 protein			, ,
A 1 4 1 1 20,41	Li Allina San	(NSE1), mRNA /cds=(24,794)			
1		/gb=NM_145080 /gi=21489972			
100.15	0.0000	/ug=Hs.284295 /len=992	1111 400070	11 004037	ND 044005
13647	0.008677	signal transducer and activator of	NM_139276	Hs.321677	NP_644805
. 1	والأعلم أبعاله	transcription 3 (acute-phase response			
		factor) (STAT3), transcript variant 1,			12
		mRNA /cds=(241,2553)			
		/gb=NM_139276 /gi=21618339			
1.0-5	1 = 2 = 3	/ug=Hs.321677 /len=3455	100 470 400	11. 04 400	ND 775300
13654	4.50E-04	hypothetical protein LOC92597	NM_173468	Hs.31422	NP_775739
		(LOC92597), mRNA /cds=(151,801)	} _.		
		/gb=NM_173468 /gi=27735028	1		1
	1	/ug=Hs.31422 /len=6956	L		NID OFFICE
13659	0.035177	hypothetical protein (HSPC016), mRNA	NM_015933	Hs.397853	NP_057017
]	/cds=(39,233) /gb=NM_015933]	<u> </u>]
		/gi=7705430 /ug=Hs.397853 /len=384)]
					
13661	0.001878	KIAA1198 protein, partial cds	AB033024	Hs.175475	
1	*	/cds=UNKNOWN /gb=AB033024	(·	}	1
{ . ·		/gi=6330393 /ug=Hs.175475 /len=6090	1.7	1	1
	<u></u>	<u></u>	L	<u> </u>	

Gen s	Correspoi	nding To Differentially Expressed Gen	es in Figur 20 -	RA	
Spot		ue D scription	Gen	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
13681	0.005325	mRNA; cDNA DKFZp547M072 (from	AL512725	Hs.300870	NP 796375
	· , , , , , , , , , , , , , , , , , , ,	clone DKFZp547M072) /gb=AL512725			-
		/gi=12224868 /ug=Hs.300870	A segular relation		
		/len=2791		,	
13699	0.001878	KIAA1593 protein, partial cds	AB046813	Hs.11123	NP 056416
1,7		/cds=UNKNOWN /gb=AB046813			
		/gi=10047260 /ug=Hs.11123			
		(=DKFZP564G092 protein)			
13700	0.002096	DJ467N11.1 protein, FLJ13127 fis,	AK023189	Hs.143917	NP 071374
		clone NT2RP3002911	THE PROPERTY OF		
		/cds=UNKNOWN /gb=AK023189			
		/gi=10435003 /ug=Hs.143917			· · · · · · · · · · · · · · · · · · ·
	- 10 Televier	/len=3073			1
13713	0.029005	heterogeneous nuclear	NM 019597	Hs.278857	NP 062543
		ribonucleoprotein H2 (H') (HNRPH2),			
		mRNA /cds=(79,1428) /gb=NM_019597			la de la la la la la la la la la la la la la
	V	/gi=14141155 /ug=Hs.278857			
		/len=2220			
13716	0.004358	chromosome 15 open reading frame 12	NM 018285	Hs.6118	NP 060755
107, 10	0.00 1000	(C15orf12), nuclear gene encoding	10.0200	1.0.01.10	-000,00
		mitochondrial protein, mRNA			
		/cds=(48,602) /gb=NM_018285			
		/gi=8922793 /ug=Hs.6118 /len=1115	P .		
13739	0.043700	hypothetical protein LOC55580	NM 017571	Hs.254122	NP 0600415
13733	0.043733	(LOC55580), mRNA /cds=(759,2987)	1400_017011	113.204122	11000041**
		/gb=NM_017571 /gi=8923837			
		/ug=Hs.254122 /len=3109			
13752	3 0/E-0/	V-ets erythroblastosis virus E26	AK001630	Hs.18063	NP 005229
13732	3.046-04	oncogene homolog 1 (avian), cDNA	1711001000	113.10003	_003223
		FLJ10768 fis, clone NT2RP4000150	en en en en e		
* ***		/cds=UNKNOWN/gb=AK001630			
		/gi=7023001 /ug=Hs.18063 /len=2833		:	
13771	0.040751	HERV-H LTR-associating 1 (HHLA1),	NM 005712	Hs.285026	NP 005703
10//1	0.0-0/31	mRNA /cds=(899,2065)	1411_000712	13.200020	
	1	/gb=NM_005712 /gi=5031738	1		
1 - 1 - 1		/ug=Hs.285026 /len=2290		1 .	
13789	0.043700	cDNA FLJ31372 fis, clone	AK055934	Hs.89388	
13103	0.040199	NB9N42000281. /gb=AK055934	, 11000004	119.09000	
		/gi=16550786 /ug=Hs.89388 /len=2606			
	7	rgi- 10000100 /ug-115.03000 /ieii-2000			
13790	0.014500	membrane-spanning 4-domains,	NM 024021	Hs.325960	NP 683876
13/90	0.014099	subfamily A, member 4 (MS4A4A),	14W_024021	113.323300	141 _003070
		transcript variant 1, mRNA	(
				}	
		/cds=(144,806) /gb=NM_024021			1
,		/gi=20070327 /ug=Hs.325960	1		√ .
	L	/len=1619		<u> </u>	<u> </u>

		nding To Differentially Expressed Gen		KA	
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No	No.
13793	0.02801	FLJ12671 Hypothetical protein, mRNA;	AL096734	Hs.301904	NP_112242
		cDNA DKFZp434M011 (from clone			
		DKFZp434M011) /cds=UNKNOWN		gere en sin	
		/gb=AL096734 /gi=5419867			1
		/ug=Hs.301904 /len=3180		- '	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
				(h
13794	0.03788	myosin VI (MYO6), mRNA	NM 004999	Hs.118483	NP 004990
		/cds=(140,3997) /gb=NM_004999			
		/gi=4826845 /ug=Hs.118483 /len=5212			
19 E.		10200 10749 110.110 100 71011 0212			
13795	0.030249	hypothetical protein FLJ21302	NM 022901	Hs.128071	NP 075052
107.00	0.0002-0	(FLJ21302), mRNA /cds=(91,1203)	14111_022001	11.5.120071	1.10,0002
		/gb=NM_022901 /gi=12597640			
The pulse and		/ug=Hs.128071 /len=3160			
13801	0.022626	proteasome (prosome, macropain)	NM_002789	Hs.251531	NP_002780
13001	0.032636	1	NIVI_002769	HS.251551	14002760
ý.		subunit, alpha type, 4 (PSMA4), mRNA]		ľ.
		/cds=(137,922) /gb=NM_002789			
		/gi=23110940 /ug=Hs.251531			
40000	3 304400	/len=1189	1111		VIE ARETA
13803	0.001193	Rho-related BTB domain containing 3	NM_014899	Hs.10432	NP_055714
•		(RHOBTB3), mRNA /cds=(336,2171)			
• "]. ···	/gb=NM_014899 /gi=7662355		<u>†</u>	
		/ug=Hs.10432 /len=4099			
13809	0.004825	likely ortholog of mouse limb-bud and	NM_030915	Hs.57209	NP_112177
	i	heart gene (LBH), mRNA			
		/cds=(213,530) /gb=NM_030915	1		1
		/gi=13569871 /ug=Hs.57209 /len=2955			
					<u> </u>
13811	0.008566	hypothetical protein FLJ20360	NM_017782	Hs.26434	NP_060252
	1	(FLJ20360), mRNA /cds=(80,2305)			
		/gb=NM_017782 /gi=8923334			
		/ug=Hs.26434 /len=3041			
13827	0.032636	proteasome (prosome, macropain) 26S	NM 002802	Hs.4745	NP_002793
		subunit, ATPase, 1 (PSMC1), mRNA	 -		_
	1	/cds=(49,1371) /gb=NM 002802			
	j	/gi=24430150 /ug=Hs.4745 /len=1586]	
		<i>g.</i> 2			
13839	0.043799	TEA domain family member 1 (SV40	AL133574	Hs.42458	NP 068780
10000	0.040755	transcriptional enhancer factor) mRNA;	1,1000111	113.42400	
		cDNA DKFZp434N1435 (from clone	1		
		DKFZp434N1435) /cds=UNKNOWN	1		
	1		}	·	
-		/gb=AL133574 /gi=6599153		1	
405	1	/ug=Hs.42458 /len=4459	100000	070010	NE 000050
13840	0.035177	FLJ11292 (FLJ11292) hypothetical	NM_018382	Hs.272246	NP_060852
		protein, mRNA /cds=(150,614)	· .		
		/gb≈NM_018382 /gi=8922980	To the second		1
		/ug=Hs.272246 /len=1948	1]	

		nding To Differentially Expressed Gen			<u> </u>
Spot	p-value	Description	Gene	Unigene	Protein
· i			Accession No.	Accession No.	Accession No.
13859	0.040751	BTB domain protein (BDPL) mRNA,	AF353674	Hs.7367	NP_150374
10000	ψ.ψ . Ψ.ν.ν.ι	partial cds /cds=UNKNOWN	, oogo, ,		1
		/gb=AF353674 /gi=13785925	e e la sala sa la sala sa sa		
•		/gg=Hs.7367 /len=1887		1	
13875	0.002802	NME7 (NME7), mRNA /cds=(93,1223)	NM_013330	Hs.274479	NP 037462
130/5	0.002093	/gb=NM 013330 /gi=7242158	14141_013330	1113.214413	_037402
		/ug=Hs.274479 /len=1475			
		/ug=ns.2/44/9/len=14/5		1	1
10070	0.000045	ACENCOLIDE 40227245	DLIESCO70	Lia 200022	
138/6	0.023945	AGENCOURT_10227215	BU536672	Hs.380933	
١		NIH_MGC_141 cDNA clone	المراواة والمعارب		
		IMAGE 6565196 5', mRNA sequence			\mathcal{L}
	[/clone=IMAGE:6565196 /clone_end=5'			
	i	/gb=BU536672 /gi=22847113			
.82	a tea sad Magazina	/ug=Hs.380933 /len=1275			
				<u> </u>	
13878	0.030249	EST(yr18g03.r1 cDNA clone 205684 5')	H63006 		
13910	0.011238	EST(wm16d01.x1 NCI_CGAP_Ut4	AI887638		
		cDNA clone IMAGE:2436097 3')			
13923	0.02801	mRNA for KIAA1754 protein, partial	AB051541	Hs.28501	NP 203755
.0020	0.0200	cds. /cds=(32,1816) /gb=AB051541			ļ
	1	/gi=12698052 /ug=Hs.28501 /len=4088			1
		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			
13933	0.025911	EST(qx14c02.x1 NCI_CGAP_Lym12	Al358712		
	0.0200	clone IMAGE:2001314 3' contains Alu			
		and MER4 repeat)			
13935	0.003213	CD68 antigen (CD68), mRNA	NM_001251	Hs.246381	NP 001242
10000	0.0002,10	/cds=(16,1080) /gb=NM_001251	00.20.		
		/gi=4557434 /ug=Hs.246381 /len=1722			
•					
13947	0.04244	5'-3' exoribonuclease 2 (XRN2), mRNA	NM 012255	Hs.268555	NP 036387
100-11	0.04244	/cds=(86,2938) /gb=NM_012255	1411_012200	113.20000	
		/gi=18860915 /ug=Hs.268555	12		
		I/len=3445			
13950	0.003803	hypothetical protein FLJ10330	NM_018061	Hs.342307	NP_060531
13930	0.002093	(FLJ10330), mRNA /cds=(77,1717)	114141_010001	115.542507	144 _00000
				1 .	1
	<u> </u>	/gb=NM_018061 /gi=8922357			
40050	0,005005	/ug=Hs.342307 /len=3239	A140000404	110 255900	
13952	0.005325	cDNA FLJ13342 fis, clone	AK023404	Hs.255890	1.
		OVARC1001950. /gb=AK023404			
		/gi=10435328 /ug=Hs.255890		1	
4000	0.055	/len=2490	144055005	11. 64665	
13955	0.035177	cDNA FLJ32123 fis, clone	AK056685	Hs.349397	1.
		PEBLM1000174. /gb=AK056685	1	1	
		/gi=16552158 /ug=Hs.349397	1	1	
	1	/len=2326	•	1	.1

		nding To Differentially Expressed Gen			<u> </u>
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
	L		.	No.	No.
13956	0.010277	zh79h09.s1	W92715	Hs.59358	
		Soares_fetal_liver_spleen_1NFLS_S1			
		cDNA clone IMAGE:418337 3', mRNA			
		sequence /clone=IMAGE:418337	No.		
		/clone_end=3' /gb=W92715		}	1
	} `	/gi=1421867 /ug=Hs.59358 /len=397			
13973	0.021	wd40a10.x1 Soares NFL T GBC S1	Al688631	Hs.224625	
		cDNA clone IMAGE:2330586 3', mRNA			1
· . • . • .		sequence /clone=IMAGE:2330586			
		/clone_end=3' /gb=Al688631			
1		/gi=4899925 /ug=Hs.224625 /len=539			
13982	0.00587	EST(nv54h12:r1 NCI_CGAP_Ew1	AA721522		
10002	0.0000	cDNA clone IMAGE:1233671)	777 2 1022	-	
13983	0.004825	EST(zh93h04.r1	AA004789	 	
13303	0.004023	Soares_fetal_liver_spleen_1NFLS_S1	AAUU4769 		
			`		
14011	0.01045	cDNA clone IMAGE:428887 5')	A1400700	11- 470040	
14011	0.01045	tm42d10.x1 NCI_CGAP_Kid11 cDNA	AI498708	Hs.170849	
		clone IMAGE:2160787.3', mRNA			
		sequence /clone=IMAGE:2160787			
		/clone_end=3' /gb=Al498708		la de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de	
		/gi=4390690 /ug=Hs.170849 /len=453	 		1
14020	0.002337	EST (EST385328 MAGE resequences,	AW973230		
		MAGM cDNA)		<u> </u>	
14021	4.50E-04	UI-E-EJ0-ahg-j-09-0-UI:r1 UI-E-EJ0	BM712784	Hs.278378	
		cDNA clone UI-E-EJ0-ang-j-09-0-UI 5',			
		mRNA sequence /clone=UI-E-EJ0-ahg-			
		j-09-0-UI /clone_end=5' /gb=BM712784			
	}	/gi=19026042 /ug=Hs.278378			
)	/len=1255			
14027	0.012276	601659091R1 NIH_MGC_70 cDNA	BE965912	Hs.394354	
		clone IMAGE:3895678 3', mRNA			
		sequence /clone=IMAGE:3895678			
		/clone_end=3' /gb=BE965912			
		/gi=11770773 /ug=Hs.394354			
		/len=1440			
14032	0.012276	cDNA sequence (cDNA sequence	AK021798		
	}	FLJ11736 fis, clone HEMBA1005468)	,	1	
14061	6.56F-04	cDNA FLJ14201 fis, clone	AK024263	Hs.193063	
	0.00,2 0 .	NT2RP3002955. /gb=AK024263	1,11(02-1200	113.10000	
	•	/gi=10436597 /ug=Hs.193063			1
		/len=4077	•		1
14062	0.019797	P1-Cdc21 mRNA /cds=(1,2774)	X74794	Uc 154442	}
14002	0.010704		14/94	Hs.154443	
		/gb=X74794 /gi=683749	100		
4.4005	0.047000	/ug=Hs 154443 /len=3273	1,404000	 	
14065	U.U1/288	EST (tg92b12.x1 NCI_CGAP_CLL1	Al401293		
		IMAGE:2116223 3')	l		

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
r . ** ')			Accession No.	Accession No.	Accession No.
14066	0.040751	cDNA sequence FLJ13663 fis, clone	AK023725		NP 003817
		PLACE1011646, highly similar to			T
		H.sapiens clone	et een		
14069	0.012276	EST np77c06.s1 NCI_CGAP_Pr2	AA622809		
		cDNA clone IMAGE:1132330 similar to			
,		contains Alu repetitive element;			
14080	0.047031	EST(af08g07.s1 Soares_testis_NHT	AA610081		
;		cDNA clone IMAGE:1031100 3')			
14087	0.003563	EST ab74g12.s1 Stratagene fetal retina	AA668159		NP_054767
		937202 H.sapiens cDNA clone			
٠.		IMAGE:852742 3'			
14092	0.005898	hypothetical protein DKFZp434K1421	NM_032141	Hs.374609	NP_115517
Ų.		(DKFZP434K1421), mRNA			
4.		/cds=(29,1705) /gb=NM_032141		<u> </u>	
		/gi=14149806 /ug=Hs.374609			
		/len≈2547		·	
14093	0.001501	v-myc myelocytomatosis viral oncogene	NM_002467	Hs.79070	NP_002458
The second		(avian) (MYC), mRNA /cds=(559,1878)			**
		/gb=NM_002467 /gi=12962934			
11 (1) 11 (1)		/ug=Hs.79070 /len=2121		.	
14102	0.001501	ribosomal protein L13a (RPL13A),	NM_012423	Hs.389335	NP_036555
		mRNA /cds=(23,634) /gb=NM_012423			
		/gi=14591905 /ug=Hs.389335			1
		/len=1142		.	
14105	0.004367	Kruppel-like factor 12 (KLF12),	NM_007249	Hs.23510	NP_057369
·	(X)	transcript variant 1, mRNA	<u></u>		
		/cds=(199,1407) /gb=NM_007249			1
		/gi=21071073:/ug=Hs:23510			4.1
		/len=10891			
14107	0.009388	601660660R1 NIH_MGC_72 cDNA	BE967103	Hs.394696	
		clone IMAGE:3915686 3', mRNA			
		sequence /clone=IMAGE:3915686			
]	/clone end=3' /gb=BE967103			
		/gi=11773230 /ug=Hs.394696 /len=842		A Company	1
	1				
14108	0.001501	EST (381219 MAGE resequences	AW969142		
		MAGK)	_	·	
14112	0.00587	BX094467 Soares fetal liver spleen	BX094467	Hs.122140	-
		1NFLS cDNA clone IMAGp998J03121,			
		mRNA sequence			
		/clone=IMAGp998J03121 ;_IMAGE:12			
		4514 /gb=BX094467 /gi=27827126		1	1
		/ug=Hs.122140 /len=805			
14121	0.032636	spindlin-like protein 2 (SPIN2), mRNA	NM 019003	Hs.82577	NP_061876
· · · · ·		/cds=(494,1192) /gb=NM_019003			
		/gi=9506850 /ug=Hs.82577 /len=2483	1	1	1 .
14127	0.032636	EST (zs23c11.r1 NCI_CGAP_GCB1	AA262101	 	NP_002712
	1,0.5,02,000	cDNA clone IMAGE:686036 5')	1 · · · ·	1 .	

Genes Corresponding To Differentially Expressed Genes in Figure 20 - RA Spot p-value Description G ne Unigene						
Spot	p-value	Description	G ne	Unigene	Protein	
			Accession No.	Accession	Accession	
4 4 4 5 6	0.000000	00.00	A1000700	No.	No.	
14133	0.002893	ox08a07.x1	AI023766	Hs.434976		
		Soares_fetal_liver_spleen_1NFLS_S1				
		cDNA clone IMAGE:1655700 3', mRNA			1	
		sequence /clone=IMAGE:1655700				
		/clone_end=3' /gb=AI023766				
	. F	/gi=3238810 /ug=Hs 434976 /len=432				
14134	0.022106	EST (602302386F1 NIH_MGC_87	BG034307		NP 001943	
		cDNA clone IMAGE:4403877.5')				
14137	0.004367	ribosomal protein S4, X-linked	NM_001007	Hs.389933	NP 000998	
		(RPS4X), mRNA /cds=(36,827)	-		-	
		/gb=NM_001007 /gi=17981705				
		/ug=Hs.389933 /len=916		} ·	}	
14144	0.020388	EST (AU143964 HEMBA1 cDNA clone	AU143964		NP_057535	
	} •	HEMBA1000519 3')			1 7	
14145	0.043799	mitochondrion, complete genome	NC_001807			
14157		EST(ye79b12.r1 Soares fetal liver	R01617	** ***********************************		
		spleen 1NFLS cDNA clone				
-, .		IMAGE:123935 5')				
14161	0.039408	EST (RC3-HT0600-130400-013-h06	BE178244	, ,		
	7, 7, 7	HT0600)				
14168	0.040751	7j81h05.x1	BF055560	Hs.298968	Transfer of the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second	
		Soares_NSF_F8_9W_OT_PA_P_S1				
		cDNA clone IMAGE:3392889 3', mRNA				
	ige v	sequence /clone=IMAGE:3392889		}		
		/clone_end=3' /gb=BF055560		j		
•		/gi=10809456 /ug=Hs.298968 /len=506		1		
		1				
14170	0.00587	EST (nf20b09.s1 NCI_CGAP_Pr1	AA572847	 	<u> </u>	
	0.0000	cDNA clone IMAGE:914297)				
14171	0.010277	nz80g08.s1 NCI_CGAP_GCB1 cDNA	AA767226	Hs.368058		
	0.010211	clone IMAGE:1301822 3', mRNA		1.0.00000		
		sequence /clone=IMAGE:1301822				
		/clone_end=3' /gb=AA767226		l l	1	
		/gi=2818241 /ug=Hs.368058 /len≑542			{·	
1/17/	0.001501	mitochondrion, complete genome	NC_001807	 		
14175		ribosomal protein, large, P1 (RPLP1),	NM 001003	Hs.424299	NP_000994	
17113	J.JUL-03	mRNA /cds=(130,474) /gb=NM_001003	l —	13.727233		
	} : ·	//gi=16905511 /ug=Hs.424299 /len=512	.			
٠.		/gi- 103000 1 1 /ug=115.424233 /ief1-012		,	1	
14177	0.014046	hypothetical protein BC008207	NM_138386	Hs.267130	NP 612395	
1417.7	1,0.014940	1 **	14141_130300	119.207 100	_012333	
	}	(LOC92345), mRNA /cds=(195,1679)		1	1	
		/gb=NM_138386 /gi=19923910	1	4	Į.	
3 4 5 5 4	0.00400	/ug=Hs.267130 /len=1919	1055763	 	 	
14184		EST(clone IMAGE:2509657 3')	Al955713	 	 	
14186	0.040747	EST (QV2-HT0577-090500-212-f02	BE175330			
	1	HT0577 cDNA)	1 1			

Genes	Correspoi	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession No.	Accession No.
14187	0.003213	EST(RC5-HT0581-210300-021-B05	BE175638	INO.	NO.
14107	0.003213	HT0581)	DE 175000		
14199	0.014599	EST(HS-1029-A1-B05-MF.abi CIT	B35426		
14100	0.014000	Genomic Sperm Library C genomic	100 120		
! 		clone)	Make the second		
14205	0.007107	hypothetical protein DKFZp761B1514	NM_032288	Hs.177537	NP 115664
14200	0.00. 10.	(DKFZp761B1514), mRNA	502250		1
		/cds=(73,1029) /gb=NM_032288			
		/gi=14150032 /ug=Hs.177537			
Art, if		/len=3453			
14209	0.020388	BX109160 Soares_NhHMPu_S1 cDNA	BX109160	Hs.308982	
		clone IMAGp998H024744, mRNA			
		sequence			
		/clone=IMAGp998H024744; IMAGE:1			
		933489 /gb=BX109160 /gi=27877586			
1.11		/ug=Hs.308982 /len=483			
14217	0.04244	similar to CG3714 gene product	NM 145201	Hs.333388	NP 660202
		(PP3856), mRNA /cds=(697,1098)			
. *		/gb=NM_145201 /gi=24475828			
		/ug=Hs.333388 /len=1198		1	
14219	0.014599	cDNA FLJ37978 fis, clone	AK095297	Hs.381207	
		CTONG2010348. /gb=AK095297			
		/gi=21754529 /ug=Hs.381207			1
		/len=3284			
14225	0.02801	clone 23933 mRNA sequence	U79273	Hs.239483	
		/gb=U79273 /gi=1710239		!	, , ,
	<u> </u>	/ug=Hs.239483 /len=1440		·)
14229	7.41E-04	EST(cDNA clone IMAGE:4705591 5')	BG574776		NP_060713
14230	0.003213	mRNA; cDNA DKFZp313K1012 (from	AL832666	Hs.99480	
		clone DKFZp313K1012) /gb=AL832666		}	
		/gi=21733242 /ug=Hs.99480 /len=3759			
			*		
14238	0.047031	UI-H-BI3-akh-b-10-0-UI.s1	AW449245	Hs.438347	
		NCI_CGAP_Sub5 cDNA clone			
		IMAGE:2734051 3', mRNA sequence			
		/clone=IMAGE:2734051 /clone_end=3'			∤ *
		/gb=AW449245 /gi=6990021		1	
	<u> </u>	/ug=Hs.438347 /len=707		<u> </u>	
14243	0.003947	cDNA FLJ36574 fis, clone	AK093893	Hs.356595	
	1	TRACH2012376. /gb=AK093893			
		/gi=21752845 /ug=Hs.356595	1	1 .	1
		/len=1952		 	ļ
14244	0.010277	cDNA FLJ11946 fis, clone	AK022008	Hs.323231	
		HEMBB1000709. /gb=AK022008	,	ļ.	}
	1	/gi=10433321 /ug=Hs.323231	1 1 2		
	1	/len=3241	<u> </u>	<u> </u>	<u> </u>

		nding To Differentially Expressed Gen			<u></u>
Spot	p-value	Description	Gene Accession No.	Unigene Accession	Protein Accession
	,			No.	No.
14245	0.017288	hypothetical protein FLJ32894	NM_144667	Hs.350668	NP 653268
		(FLJ32894), mRNA /cds=(50,550)		1	-
		/gb≋NM_144667 /gi=21389550) · · · · · · · · · · · · · · · · · · ·	*
٠ .		/ug=Hs.350668 /len=1710		} : :	
14249	0.02801	mitochondrion, complete genome	NC 001807	 	
4253		BX099231	BX099231	Hs.155766	
17200	0.001002	Soares_total_fetus_Nb2HF8_9w cDNA	D/(055201	113.100700	1
	,	clone IMAGp998J031903, mRNA			1
	!				
	1 1	sequence		1	<u> </u>
. , .		/clone=IMAGp998J031903_;_IMAGE:7	T 1		
		73090 /gb=BX099231 /gi=27843988			
	1	/ug=Hs.155766 /len=766			<u> </u>
14255	0.02801	EST wt25d05.x1 NCI_CGAP_Ut1	AI962961		
	[cDNA clone IMAGE:2508489 3' similar		1	
		to contains Alu repetitive]	}
		element;contains L1.t1; L1 repetitive		1	
		element;			
14262	0.014599	mRNA for KIAA1965 protein.	AB075845	Hs.71730	
		/cds=(1,1699) /gb=AB075845			1
		/gi=18916817 /ug=Hs.71730 /len=4299			1
14263	0.018784	mRNA, cDNA DKFZp451M2119 (from	AL833088	Hs.313295	
151200	1 0.010.04	clone DKFZp451M2119) /gb=AL833088	ľ '	110.010200	
		/gi=21733679 /ug=Hs.313295			
:		/len=5234			1
14269	0.005225	ESTs, cDNA, 5' end	BE745453	Hs.133213	-
14209	0.005325	j	DE/40400	ITS. 133213	
	∤ * .	/clone=IMAGE:3928684 /clone_end=5'			
1		/gb=BE745453 /gi=10159445			}
Ŧ.,	1	/ug=Hs.133213 /len=1196			1
	<u> </u>			<u> </u>	
14270	0.023945	clone FLC0593 /cds=UNKNOWN	AF113701	Hs.346911	NP_000974
		/gb=AF113701 /gi=6855635			1
	<u> </u>	/ug=Hs.346911 /len=1562		L	<u> </u>
14272	0.001193	nuclear protein double minute 1	NM_017440	Hs.12871	NP_064513
	}	(MDM1), mRNA /cds=(93,2237)	}	ŀ	
		/gb=NM_017440 /gi=24586654	ļ	f	1
-	1	/ug=Hs.12871 /len=2942			}
14279	0.004825	AL535026 LTI_FL013_FBrn1 cDNA	AL535026	Hs.268474	1
	,	clone CS0DF007YJ21 3 prime, mRNA			
		sequence /clone=CS0DF007YJ21			
		/clone_end=3' /gb=AL535026			1
		//gi=12798519 /ug=Hs.268474 /len=921			1
		rgi- 121 300 13 rug-115.2004 14 /ien-921			1
14000	0.000047	FOTANII MOO 77 aDNA alaaa	DCE410CC	 	
14282	0.003947	EST(NIH _MGC_77 cDNA clone	BG541966]	
	1	IMAGE:4694104 5')	1		1 .

		nding To Differentially Expressed G n			L	
Spot	p-value	Description	Gene	Unigen	Protein	
			Accession No.	Accession	Accession	
				No.	No.	
14283	0.011238	ESTs, cDNA, 5' end /clone=GLCCSC04	AV720392	Hs.293568		
		/clone_end=5' /gb=AV720392	r .	,		
11		/gi=10817544 /ug=Hs 293568 (=ESTs,				
		Weakly similar to AF116721 112			,	
		PRO2738)			• 1	
14284	7 30F 05	hypothetical protein FLJ23751	NM 152282	Hs.37443	NP 689495	
14204	7.002-00	(FLJ23751), mRNA /cds=(121,1563)	102202	113.07 440	141 _000455	
		/gb=NM 152282 /gi=22748648				
'					,	
4.4005	0.005477	/ug=Hs.37443 /len=2994	DC040670	11- 24240		
14285	0.035177	clone IMAGE:4817835, mRNA, partial	BC040679	Hs.21349		
٠		cds /cds=(1,636) /gb=BC040679			1	
		/gi=26251822 /ug=Hs.21349 /len=3331				
14286	0.003183	mRNA; cDNA DKFZp434J214 (from	AL080156	Hs.12813	NP_056323	
		clone DKFZp434J214); partial cds				
		/cds=(1,1082) /gb=AL080156				
		/gi=5262614 /ug=Hs.12813 /len=2749	· · · · · · · · · · · · · · · · · · ·	, , , , , , , , , , , , , , , , , , ,		
14288	0.001339	small acidic protein (SMAP), mRNA	NM_014267	Hs.78050	NP_055082	
		/cds=(137,688) /gb=NM_014267		1		
		/gi=20070245 /ug=Hs.78050 /len=1504				
	, " ,					
14298	0.025911	AGENCOURT_8228579	BQ893981	Hs.71719		
· :		Lupski_dorsal_root_ganglion cDNA				
		clone IMAGE:6181947 5', mRNA				
	8	sequence /clone=IMAGE:6181947				
		/clone_end=5' /gb=BQ893981				
		/gi=22285995 /ug=Hs.71719 /len=969				
14299	0.003563	cDNA FLJ12106 fis, clone	AK022168	Hs.296699	 	
14233	0.003303	HEMBB1002702. /gb=AK022168	/11022 100	1113.230033		
		/gi=10433503 /ug=Hs.296699		:		
1,.				1		
4.4202	0.002045	/len=2268	NIM 42020C	110 2004	ND 644045	
14303	0.023945	CDC26 subunit of anaphase promoting	NIVI_139200	Hs.3991	NP_644815	
		complex (CDC26), mRNA		· · · · · ·		
*		/cds=(360,617) /gb=NM_139286				
		/gi=22027503 /ug=Hs.3991 /len=885			<u> </u>	
14304	0.002337	cDNA: FLJ23111 fis, clone LNG07835.	AK026764	Hs.268231		
	ļ .	/gb=AK026764 /gi=10439690]	
		/ug=Hs.268231 /len=2263				
	<u> </u>			<u> </u>		
14305	0.009388	hh32h11.x1 NCI_CGAP_Lu24 cDNA	AW615336	Hs.281215	· F	
		clone IMAGE:2956869 3', mRNA]-]	1	
		sequence /clone=IMAGE:2956869				
		/clone_end=3' /gb=AW615336	Į.		1	
		/gi=7320522 /ug=Hs.281215 /len=391	1.		1	
14307	0.047031	EST(cDNA clone IMAGE:6104513 5'.)	BQ429184	 	 	

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
14309	0.004367	wk71e10.x1 NCI CGAP Pan1 cDNA	AI815141	Hs.230542	11 4
		clone IMAGE:2420874 3', mRNA		1.0.200012	
		sequence /clone=IMAGE:2420874		'	The second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon
					-
		/clone_end=3' /gb=Al815141		N .	
		/gi=5426356 /ug=Hs.230542 /len=357			
14316	0.03788	AV737736 CB cDNA clone CBLAAD01	AV737736	Hs.258992	
		5', mRNA sequence /clone=CBLAAD01			
		/clone_end=5' /gb=AV737736			
		/gi=10855317 /ug=Hs.258992 /len=326			
· · ·					1 1
14322	0.047031	clone IMAGE:4297077, mRNA	BC017920	Hs.375771	
		/gb=BC017920 /gi=17389820			
		/ug=Hs.375771 /len=1247			
1/225	5 11 = 04	EST(clone ADBAOB04 5')	AV705982		ND OGESS
					NP_006633
14340	0.004825	EST(cDNA clone IMAGE:2112249 3'	Al425068		NP_008869
		similar to gb:J03798 AUTOANTIGEN			
	r s	SMALL NUCLEAR	in the second second		
		RIBONUCLEOPROTEIN SM-D1)			
14342	0.002602	mRNA, cDNA DKFZp586F1418 (from	AL833819	Hs.296356	
		clone DKFZp586F1418) /gb=AL833819			
		/gi=21739144 /ug=Hs.296356			
	أوجي رزوة ميم	/len=4355		e da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da l	
14246	0.043700	cDNA clone CBLAPH08 5'	A) (720000	 	
			AV739829	11 000 400	
14348	0.007107	clone IMAGE:4704474, mRNA	BC020895	Hs.269429	
		/gb=BC020895 /gi=21595279			
151		/ug=Hs.269429 /len=1436		<u> </u>	
14353	0.007107	cDNA FLJ31303 fis, clone	AK055865	Hs.350200	
•		LIVER1000082. /gb=AK055865			
1.1		/gi=16550700 /ug=Hs.350200			
	·.	/len=2801		15.00	
14358	0.016299	nab71h02.x1	BF439932	Hs.331476	The second section
. 1000	0.0.0200	Soares NSF F8 9W OT PA P S1	D. 100002	110.001.170	
		cDNA clone IMAGE:3273435 3' similar			
- '					
".	<u>.</u> .	to contains Alu repetitive element;,			
		mRNA sequence	1]	
		/clone=IMAGE:3273435 /clone_end=3'			. :
	(/gb=BF439932 /gi=11452449			
		/ug=Hs.331476 /len≈347			
	;				
14360	0.014946	EST(RC2-BN0074-010400-016-a07	BE000916	,	NP_659412
		BN0074 cDNA, mRNA sequence)	=		
14363	0 000380	ESTs, cDNA, 3' end	AI719659	Hs.372094	
1-100	. 0.003300		 	113.372094	
	}	/clone=IMAGE:2355101 /clone_end=3'	1	and the second	[
	,	/gb=AI719659 /gi=5036915	, ·]	
	11	/ug=Hs.372094 /len=528			<u> </u>
14374	0.035177	RC4-HT0277-160200-013-d07 HT0277	BE151126	Hs.158600	
	ŀ	cDNA, mRNA sequence /gb=BE151126	(-		
		/gi=8613847 /ug=Hs.158600 /len=571			
	i .	10. 4		1	I

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
14375	0.040751	ESTs, cDNA, 3' end	AI768858	Hs.157149	NP_066012
		/clone=IMAGE:2402646 /clone_end=3'	to the second of the second		Ī
		/gb=Al768858 /gi=5235367]
		/ug=Hs.157149 /len=562			
14379	0.009388	Similar to hypothetical protein	BC039535	Hs.440840	NP 776163
		FLJ20489, clone MGC:50559			
	1	IMAGE:5744381, mRNA, complete cds			
1	1	/cds=(290,1078) /gb=BC039535			}
		/gi=24659157 /ug=Hs.440840			
		/len=2078			
14388	0.012276	cDNA FLJ13830 fis, clone	AK023892	Hs.287601	
14300	0.012270	THYRO1000637. /gb=AK023892	AR023032	1115.207001	
)	/gi=10435965 /ug=Hs.287601]
sada al		/len=1916/			
14206	0.006707	cDNA FLJ11437 fis, clone	AIC021400	110 070701	
14390	0.026797		AK021499	Hs.270791	
• •		HEMBA1001226 /cds=UNKNOWN		la de la companya de la companya de la companya de la companya de la companya de la companya de la companya de	
		/gb=AK021499 /gi=10432694			
4446	0.005477	/ug=Hs:270791	0.0007700		NE 070500
		EST(cDNA clone IMAGE:4521448 5')	BG387788		NP_073568
14414	0.035177	AV764634 MDS cDNA clone	AV764634	Hs.270532	
		MDSBZE01 5', mRNA sequence] .
. 1, 4		/clone=MDSBZE01 /clone_end=5'			
		/gb=AV764634 /gi=10922482			
		/ug=Hs.270532 /len=1289			
14415	0.032636	ESTs, cDNA, 5' end	BG292389	Hs.374490	
	, ·	/clone=IMAGE:4515481 /clone_end=5'			
		/gb=BG292389 /gi=13051140			
		/ug=Hs.374490 /len=887		1	
				<u> </u>	
14417	0.025911	proteasome (prosome, macropain)	NM_002789	Hs.251531	NP_002780
original extremely		subunit, alpha type, 4 (PSMA4), mRNA			
		/cds=(137,922) /gb=NM_002789	$\int_{\mathcal{F}}$	\	
	ľ	/gi=23110940 /ug=Hs.251531			
		/len=1189			
14424	0.035177	EST(MR0-HT0157-040500-012-d07	BE143000		
		HT0157 Homo sapiens cDNA, mRNA			
		sequence)			
14425	0.020388	wc34a07.x1 NCI_CGAP_Pr28 cDNA	AI745524	Hs.205153	
		clone IMAGE:2317044 3' similar to			
÷	1	contains element MSR1 repetitive			
	7	element ;, mRNA sequence			
	[-	/clone=IMAGE:2317044 /clone_end=3'		1	
		/gb=Al745524 /gi=5113812	ł ·	1	
		/ug=Hs.205153 /len=398		}	
14452	0.032636	No significant match	SEQ.ID.No.35	 	
14461		No significant match, ORF-2(111~269)	SEG.12.140.00	 	
7-701	0.022.00		SEQ.ID.No.84	1	
14468	0.023045	No significant match (ORF:none)	SEQ.ID.No.21	 	
1-1-100	0.020940	Ino agrinoani matori (OIXE.HORE)	DEG.ID.140.21	<u></u>	<u> </u>

		nding To Differ ntially Expressed Gen			
Spot	p-valu	Description	Gene	Unigene	Protein
e	,		Accession No.	Accession	Accession
				No.	No.
14483	0.022106	cDNA FLJ34248 fis, clone	AK091567	Hs.112461	1,30,
		FCBBF4000446. /gb=AK091567		1,16:1,151	
].	/gi=21749972 /ug=Hs.112461			
•			,		1 .
4 4 4 6 7	0 00000	/len=1623			
14497	0,002337	serine (or cysteine) proteinase inhibitor,	NM_000295	Hs.297681	NP_000286
		clade A (alpha-1 antiproteinase,			
		antitrypsin), member 1 (SERPINA1),			
		mRNA /cds=(233,1489)	* * * * * * * * * * * * * * * * * * * *		
		/gb=NM_000295 /gi=21361197			
***		/ug=Hs.297681 /len=1584			
14502	0.025911	No match, ORF+2(59~245)	SEQ.ID.No.101		
14504		No significant match (ORF:none)	SEQ.ID.No.22		
		No significant match (ORF none)	SEQ.ID.No.66		
14516	0.00587	EST (od85a05.x5 NCI_CGAP_Ov2	AI821981		
		IMAGE:1374704)			<u> </u>
14518	0.043799	cDNA FLJ36977 fis, clone	AK094296	Hs.151143	
		BRACE2006344. /gb=AK094296	, i		
		/gi=21753327 /ug=Hs.151143		(
** 515.74		/len=1678			1
14519	0.00587	ATP-binding cassette, sub-family A	NM 018672	Hs.180513	NP 758424
		(ABC1), member 5 (ABCA5), transcript	11111_010072	1.10.100010	111 _700 121
		variant 1, mRNA /cds=(1219,6147)	,		
	ļ.,				[.
, .		/gb=NM_018672 /gi=27262623			
		/ug=Hs.180513 /len=7044			
	<u> </u>				
14525	0.001501	hypothetical protein MGC13159	NM_032927	Hs 12845	NP_116316
		(MGC13159), mRNA /cds=(592,1017)			ļ .
		/gb=NM_032927:/gi=14249719	1		
		/ug=Hs.12845 /len=1759			}
14526	0.003563	EST (UI-HF-BL0-adc-e-05-0-UI.s1	AW575379		
14528		EST (EST34421 Embryo, 6 week I	AA330691		
. 1020	0.040701	cDNA 5' end similar to EST containing	/V1000001		
	<u> </u>				
4500	0.000707	L1 repeat)	41001010	ļ	
14530	0.026797	EST (Human fetal liver HA0635 cDNA	AI064840	1	1
· .		library cDNA)			<u> </u>
14541	0.021	EST tz43f04.x1 NCI_CGAP_Brn52	Al863121		
	(cDNA clone IMAGE:2291359 3' similar		'	İ
	1.	to contains Alu repetitive		;	
* .		element;contains L1.b1 L1 repetitive	· ·		1
14546	0.032636	EST (601819273F1 NIH_MGC_58	BF130672	 	NP 003655
1-10-10	0.002000	cDNA clone IMAGE:4051098 5')	Di 130072	,	-003033
1 4 5 4 7	E 44E 04		A14004504	11-004000	
14547) 0.11E-U4	cDNA FLJ11469 fis, clone	AK021531	Hs.224398	}
		HEMBA1001658. /gb=AK021531			1.
		/gi=10432731 /ug=Hs.224398		,]
		/len=1665	ļ·		ŀ
14548	0.007107	mRNA; cDNA DKFZp566P1124 (from	AL110236	Hs.321022	
		clone DKFZp566P1124) /gb=AL110236			}
]	/gi=5817178 /ug=Hs.321022 /len=2267]]

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unig ne	Protein
Ï			Accession No.	Accession	Accession
				No.	No
14550	0.017288	cDNA FLJ31626 fis, clone	AK056188	Hs.375198	
		NT2RI2003317. /gb=AK056188			
		/gi=16551523 /ug=Hs.375198			
		/len=2041			ĺ
ACCA	0.047004		A A E O 2 O 4 2		
4551	0.047031	EST (ng23f02.s1 NCI_CGAP_Ov2	AA502813		
		cDNA clone IMAGE:930267 similar to			
		contains Alu repetitive element)			
14553	0.009388	hypothetical protein H41 (H41), mRNA	NM_017548	Hs.283690	NP_060018
		/cds=(324,1100) /gb=NM_017548			1
		/gi=24475997 /ug=Hs.283690	***		
		/len=3346			
14558	0.047031	EST (7f19b11.x1 NCI CGAP CLL1	BE675960		
000).	H.sapiens cDNA clone IMAGE:3295101			∦arakan .
		31/			1
14550	0.04244	EST PROGUE AT MICH COVER THE	AW439829	 	NP_620128
14559	0.04244	EST hb88d08.x1 NCI_CGAP_Ut2	AVV439029		JINF_020128
		cDNA clone IMAGE:2890287 3'	1114 04000	46000	100 000 00
14560	2.66E-04	TRAM-like protein (KIAA0057), mRNA	NM_012288	Hs.153954	NP_036420
		/cds=(76,1188) /gb=NM_012288			
		/gi=6912449 /ug=Hs.153954 /len=6974			
14561	0.03788	mRNA; cDNA DKFZp451B1818 (from	AL832623	Hs.77554	
:		clone DKFZp451B1818) /gb=AL832623			
	i. i i	/gi=21733198 /ug=Hs.77554 /len=6240			
	1	/gi-21/00190/dg-113.//004/heii=0240			
LAECO	4 455 04	ribecomel protein James DO (DDI DO)	NM 053275	Hs.406511	NP 444505
14500	1.15E-04	ribosomal protein, large, P0 (RPLP0),	INIVI_US3275	HS.400011	JNP_444505
		transcript variant 2, mRNA			
	{	/cds=(111,1064) /gb=NM_053275		İ	
• .		/gi=16933545 /ug=Hs.406511			
	<u> </u>	/len=1148			<u> </u>
14571	0.003183	EST(xx31a10.x1 NCI_CGAP_Ut1 clone	AW571469		NP_055260
		IMAGE:2839098 3')			
14573	0.041997	hypothetical protein DKFZp434N1923	NM 030974	Hs.295866	NP_112236
		(DKFZP434N1923), mRNA			
]	/cds=(209,1372) /gb=NM_030974			
		/gi=13569949 /ug=Hs 295866			
44504	0.000040	/len=1579	414/004000		
14591		EST(wz82e11.x1 NCI_CGAP_Gas4	AW004920		
14593	0.047031	EST (oy90d09.x1	Al051247	ļ. ·	
]	Soares_fetal_liver_spleen_1NFLS_S1			
.*		cDNA clone IMAGE 1673105 3')			· .
				1	
14600	0.03788	hypothetical gene supported by	XM_046853	J	
·		AY007122 (LOC92719)		.	
14604	9.43F_0/	eukaryotic translation elongation factor	NM_001402	Hs.422118	NP_001393
1-004	J 3.43E-04	1 alpha 1 (EEF1A1), mRNA	1411 00 1702	13.722110	_001000
		/cds=(63,1451) /gb=NM_001402]
	[/gi=25453469 /ug=Hs.422118			1 .
		/len=1837	1	J .	1

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession No.	Accession No.
14612	0.006463	EST (AL536815 LTI FL013_FBrn1	AL536815	140.	110.
	-	clone CS0DF020YK05 5')			
14618	0.018784	EST (UI-H-Bl2-agh-g-08-0-UI.s1	AW291353		NP 061049
		NCI_CGAP_Sub4 cDNA clone			-
1		IMAGE:2724303 3')			
14629	0.043799	UI-H-ED1-axs-i-05-0-UI.s1	BQ014114	Hs.195045	
-		NCI_CGAP_ED1 cDNA clone	, ,		
• ;		IMAGE:5833036 3', mRNA sequence	· · · · · · · · · · · · · · · · · · ·	<u> </u>	
	;	/clone=IMAGE:5833036 /clone_end=3'] .	
		/gb=BQ014114 /gi=19739015			
		/ug=Hs.195045 /len=1024			
<u> </u>					
14637	0.025911	hypothetical protein PRO1331	NM_030778	Hs.301824	NP_110405
		(PRO1331), mRNA /cds=(423,617)	11 Sept.		
		/gb=NM_030778 /gi=13562115			
		/ug=Hs.301824 /len=1634			
14638	0.049079		BG677029	Hs.123445	
•	1	clone IMAGE:4748515 5', mRNA		1 1	
		sequence /clone=IMAGE:4748515			
		/clone_end=5' /gb=BG677029		1.	
		/gi=13908426 /ug=Hs.123445 /len=882			
14660	6.56E-04	ai18d09.s1 Soares testis NHT cDNA	AA725750	Hs.120496	
	245 S. D.	clone 1343153 3', mRNA sequence			
		/clone=1343153 /clone_end=3'			
		/gb=AA725750 /gi=2743457			
		/ug=Hs.120496 /len=425			
14666	0.017288	EST(QV4-DT0021-281299-070-a12	AW936306		
		DT0021)			
14676	3.04E-04	EST(QV0-CT0225-101299-071-b01	AW377614		NP_842565
		CT0225)			
14680	0.002602	clone IMAGE:4839532, mRNA	BC026289	Hs.7037	
	,	/gb=BC026289 /gi=20070813		, -	
		/ug=Hs.7037 /len=2326		-	<u> </u>
14688	0.012526	cDNA FLJ34825 fis, clone	AK092144	Hs.376593	
		NT2NE2008785, weakly similar to		1	l
		ANTER-SPECIFIC PROLINE-RICH			
t i k		PROTEIN APG. /gb=AK092144			
		/gi=21750666 /ug=Hs.376593			
4.4000	0.004.000	/len=2130	AKOOSSES	110 450440	<u> </u>
14690	0.001062	cDNA FLJ35033 fis, clone	AK092352	Hs.156113	1
		OCBBF2016590, weakly similar to			1.
		CELL SURFACE ANTIGEN 114/A10	1		1
		PRECURSOR. /cds=(407,934)			
	1	/gb=AK092352 /gi=21750925			1
14600	0.044500	/ug=Hs.156113 /len=2884	DC7/1500	 	
<u> 14693</u>	10.014599	EST(cDNA clone IMAGE:4780184 5')	BG741529	ا نب	J

		nding To Differentially Expressed Gen			
Spot	p-value	Description	G n Acc ssion No.	Unigene Accession No.	Protein Accession
14694	0.004367	cDNA FLJ35910 fis, clone	AK093229	Hs.348902	No.
1400 /	0.001.007	TESTI2009987./gb=AK093229 /gi=21752038 /ug=Hs.348902 /len=2035	, , , , , , , , , , , , , , , , , , , ,	113.040002	
14697	0.011238	EST00015 NCI_CGAP_Lu5 cDNA	BF707422	Hs.298289	
÷.		clone IMAGE:1568018 3', mRNA			
;		sequence /clone=IMAGE:1568018		٠	
		/clone_end=3' /gb=BF707422			
		/gi=11999083 /ug=Hs.298289 /len=858			, ,
14698	0.011816	EST(MR1-MT0282-191200-005-b11	BF904004		
14030	0.011010	MT0282 cDNA)	DI-904004		
14699	0.025911	cDNA, 5' end /clone=IMAGE:3911301	BE886472	Hs.200483	NP 079466
		/clone end=5' /gb=BE886472			
*		/gi=10340792 /ug=Hs.301486 /len=945			
14709	0.008566	Similar to hypothetical protein	BC035643	Hs.202613	W X i S
, ,		FLJ20378, clone IMAGE:5547904,			
		mRNA, partial cds /cds=(1,802)			
		/gb=BC035643 /gi=23274249	,		
		/ug=Hs.202613 /len=1653			<u> </u>
14714	0.002337	UI-E-CL1-afe-n-12-0-UI s1 UI-E-CL1	BU729525	Hs.233617	
		cDNA clone UI-E-CL1-afe-n-12-0-UI 3',			
	*	mRNA sequence /clone=UI-E-CL1-afe-			1
		n-12-0-UI /clone_end=3' /gb=BU729525			
		/gi=23652495 /ug=Hs.233617			•
		/len=1402			
14715	0.00587	ADP-ribosylation factor-like 6	NM_015161	Hs.75249	NP_055976
		interacting protein (ARL6IP), mRNA			
e de la composición de la composición de la composición de la composición de la composición de la composición d La composición de la composición de la composición de la composición de la composición de la composición de la		/cds=(70,681) /gb=NM_015161	e un une		
		/gi=24308006 /ug=Hs.75249 /len=2280			
4.4700	0.000045	DNA 51 134 400 5	ALCOCIEDA		
14/22	0.023945	cDNA FLJ11439 fis, clone	AK021501	Hs.287416	1
		HEMBA1001299. /gb=AK021501	1		
-		/gi=10432697 /ug=Hs.287416 /len=1500			
14727	0.012276	fh01f01.y1 NIH_MGC_17 cDNA clone	AW409578	Hs.279718	 `
14121	0.012276	IMAGE:2961144 3', mRNA sequence	AVV409576 		
	,	/clone=IMAGE:2961144 /clone_end=3'			
		/gb=AW409578 /gi=6935198		1	
.•	<u> </u>	/ug=Hs.279718 /len=529			
14761	0.023945	clone IMAGE:5275203, mRNA	BC041380	Hs.293782	
, -, 01	0.020340	/gb=BC041380 /gi=27370609	(113.200,02	,
	1	/ug=Hs.293782 /len=2857	1.		
14771	0.030249	FLJ31352 fis, clone MESAN2000238	AK055914	Hs.8107	NP 061329
-711	1.0002-70	/cds=UNKNOWN /gb=AK055914	, 1,000017	1.13.0.107	
	F	/gi=16550761 /ug=Hs.8107 /len=2841	1	1	1

Genes	Correspoi	nding To Differentially Expressed Gen	es in Figure 20 -	RA	
	p-valu	D scription	Gene	Unigene	Protein
_			Accession No.	Accession	Accession
				No.	No.
14778	0.001501	RC-BT164-290399-017 BT164 cDNA,	AI908188	Hs.209245	
	15 j	mRNA sequence /gb=Al908188			4 14.4
		/gi=6498868 /ug=Hs.209245 /len=508	*		
14779	0.005325	UI-H-BI2-ahk-c-12-0-UI.s1	AW294558	Hs.437134	ing in the second
		NCI CGAP Sub4 cDNA clone			
		IMAGE:2727166 3', mRNA sequence			: .
		/clone=IMAGE:2727166 /clone_end=3'			3.
		/gb=AW294558 /gi=6701194			
		/ug=Hs.437134 /len=888			
14781	0.022106	UI-1-BC1-ajq-h-10-0-UI.s1	BQ010713	Hs.281575	
		NCI CGAP PI2 cDNA clone UI-1-BC1-		1.0.20 / 5.0	
	T	ajq-h-10-0-UI 3', mRNA sequence			
g (, 11	his star	/clone=UI-1-BC1-ajg-h-10-0-UI			- i - i
		/clone_end=3' /gb=BQ010713			
		/gi=19735614 /ug=Hs.281575			
: .		/len=1108			
14810	0.013394	cDNA FLJ39046 fis, clone	AK096365	Hs.9856	
1-1010	0.010001	NT2RP7010612. /gb=AK096365	7.11.000000	113.5000	
		/gi=21755841 /ug=Hs.9856 /len=2161			
14818	0.032636	AGENCOURT 10094876	BU507049	Hs.395205	
1-010	0.002000	NIH_MGC_71 cDNA clone	00007045	113.000200	
	F	IMAGE:6500936 5', mRNA sequence			
		/clone=IMAGE:6500936 /clone end=5'			
		/gb=BU507049 /gi=22813282			
		/ug=Hs.395205 /len=964			51
		TIO. 000200 TIO. 004			
14819	0.012526	FLJ14036 fis, clone	AK024098	Hs.306663	
	0.01.2020	HEMBA1004709/cds=UNKNOWN	/1102	110.00000	
		/gb=AK024098 /gi=10436394			
		/ug=Hs.306663/len=2067			
14828	0.032636	ESTs, cDNA, 3' end	AI871745	Hs.117777	
	3.552550	/clone=IMAGE:2342469 /clone_end=3'		1.3	
		/gb=Al871745 /gi=5545717		to an included in the second	
	,	/ug=Hs.117777 /len=542			
14835	0.032636	BX115107 Soares fetal liver spleen	BX115107	Hs.431087	
		1NFLS cDNA clone IMAGp998G12373,	-/	1	1
		mRNA sequence			\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
- i		/clone=IMAGp998G12373_; IMAGE:19			
		5875 /gb=BX115107 /gi=27839238	.	100	
	.	/ug=Hs.431087 /len=758			
14844	0.007107	AGENCOURT_10555391	BU943206	Hs.209356	
		NIH_MGC_127 cDNA clone		1.10.20000	
		IMAGE:6716639 5', mRNA sequence			
		/clone=IMAGE:6716639 /clone end=5'			٠.
		/gb=BU943206 /gi=24132025			
	1	/ug=Hs.209356 /len=815			
	}*	1			
	<u> </u>		L	<u> </u>	L

Spot	p-value	Description	Gene Accession No.	Unig ne Acc ssion No.	Protein Accession No.
14851	0.02801	UI-H-BW1-amm-h-09-0-UI.s1	BF512783	Hs.443691	
		NCI_CGAP_Sub7 cDNA clone	, '		
		IMAGE:3070696 3', mRNA sequence			
		/clone=IMAGE:3070696 /clone_end=3'			
		/gb=BF512783 /gi=11597962			
		/ug=Hs.443691 /len=568			
14884	0.043799	602043661F1 NCI CGAP_Brn67 cDNA	BF528488	Hs.433462	: 1
		clone IMAGE 4181462 5', mRNA			
		sequence /clone=IMAGE:4181462			
		/clone_end=5' /gb=BF528488			
		/gi=11615851 /ug=Hs.433462 /len=885			•
14917	0.005843	No significant match,			
		ORF+2(653~838),+3(618~782)	SEQ.ID.No.6		
14922	0.020388	No significant match	34 - 34	. 71	
		(ORF:+1:1~225[225])	SEQ.ID.No.24		
14924	0.017288	No significant match, ORF-3(1~195)	SEQ.ID.No.57		
14937	0.035177	control			
14970	0.01045	BDG-29 proten (BDG-29), mRNA	NM_015144	Hs.81505	NP_055959
		/cds=(36,2885) /gb=NM_015144			
		/gi=21735418 /ug=Hs.81505 /len=6245			

	9-	TABLESN			
		TABLE 3N			
		nding To Differentially Expressed Gene			5 1 :
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
4	0.025072	tetraspan 3 (TSPAN-3), mRNA	NM_005724	Hs.100090	NP_005715
		/cds=(218,979) /gb=NM_005724		ŀ	4 .
	ļ.	/gi=21264581 /ug=Hs.100090 /len=1842			
28	0.014741	602184410T1 NIH_MGC_42 cDNA	BF569051	Hs.352114	
ľ	İ	clone IMAGE:4300347 3', mRNA			
		sequence /clone=IMAGE:4300347	; · · · · · · · · · · · · · · · · · · ·	,	
	[:	/clone_end=3' /gb=BF569051			
		/gi=11642431 /ug=Hs.352114 /len=1899			
]	
33	0.024394	methionine adenosyltransferase II,	NM 005911	Hs.77502	NP_005902
·		alpha (MAT2A), mRNA /cds=(117,1304)			_
		/gb=NM_005911 /gi=19923346			
		/ug=Hs.77502 /len=2828			
-					i
42	0.025072	hydroxyacyl-Coenzyme A	NM 000182	Hs.75860	NP_000173
'-	0.0200.2	dehydrogenase/3-ketoacyl-Coenzyme A			
1		thiolase/enoyl-Coenzyme A hydratase			
	·	(trifunctional protein), alpha subunit			
		(HADHA), mRNA /cds=(35,2326)		· · · · ·	
1		/gb=NM_000182 /gi=20127407		ļ .	
				ł	
		/ug=Hs.75860 /len=2972		1.0	
98	0.020126	mitochondrion, complete genome	NC 001807	 	·
104		proteasome (prosome, macropain)	NM 002818	Hs.433810	NP_002809
104	0.034376	activator subunit 2 (PA28 beta)	14141_002616	115.455010	147_002009
1					1
İ		(PSME2), mRNA /cds=(66,785)		,	
	1	/gb=NM_002818 /gi=4506236	į		,
154	0.004070	/ug=Hs.433810 /len=828	NIM 045303	11- 040000	ND OFCIOO
154	0.034378	hypothetical protein DJ328E19.C1.1	NM_015383	Hs.218329	NP_056198
7 -		(DJ328E19.C1.1), mRNA		,	
]] .	/cds=(18,2783) /gb=NM_015383]		
	1	/gi=7657016 /ug=Hs 218329 /len=3689			
L			 		
158	0.031002	CD36 antigen (collagen type I receptor,	NM_000072	Hs.75613	NP_000063
	<u> </u>	thrombospondin receptor) (CD36),			
		mRNA /cds=(133,1551)			
		/gb=NM_000072 /gi=4557418			
<u> </u>		/ug=Hs.75613 /len=1820			
171	0.006784	putative Rab5-interacting protein (RIP5),	NM_018840	Hs.184062	NP_061328
1	_	mRNA /cds=(183,572) /gb=NM_018840			
·		/gi=10047115 /ug=Hs.184062 /len=1104	·	}	
1		·			
178	0.01798	zinc finger protein 161 (ZNF161), mRNA	NM_007146	Hs.223754	NP_009077
		/cds=(42,1592) /gb=NM_007146			, ,
		/gi=6005967 /ug=Hs.223754 /len=2306			
	.]	7			
		<u> </u>			

Spot	p-value	Description	Gene	Unigene	Protein
•		* 7 ° MB * 7 ° 7	Accession	Accession	Accession
	,		No.	No.	No.
209	0.006784	cyclin D2 (CCND2), mRNA	NM_001759	Hs.75586	NP 001750
		/cds=(270,1139) /gb=NM_001759	- ,		-
		/gi=16950656 /ug=Hs.75586 /len=6480	e egy transfer en e		
210	0.020126	protein tyrosine phosphatase type IVA,	NM_003463	Hs.227777	NP 003454
		member 1 (PTP4A1), mRNA			-
		/cds=(650,1171) /gb=NM_003463			
		/gi=17986281 /ug=Hs 227777 /len=4394	F	:	
				_:	1
224	0.031002	ubiquitin specific protease 7 (herpes	NM_003470	Hs.78683	NP_003461
		virus-associated) (USP7), mRNA			
		/cds=(200,3508) /gb=NM_003470			
		/gi=4507856 /ug=Hs.78683 /len=4022		<u> </u>	
225	0.020126	zinc finger protein 232 (ZNF232), mRNA	NM_014519	Hs.279914	NP_055334
		/cds=(126,1379) /gb=NM_014519			
		/gi=7657704 /ug=Hs.279914 /len=1465			a transfer
					<u></u>
251	0.011228	ATPase, Ca transporting, type 2C,	NM_014382	Hs.106778	NP_055197
		member 1 (ATP2C1), mRNA		17	
1		/cds=(236,2995) /gb=NM_014382			
	,	/gi=7656909 /ug=Hs.106778 /len=3637			
					-
255	0.031002	phenylalanyl-tRNA synthetase beta-	NM_005687	Hs.9081	NP_005678
		subunit (FRSB), mRNA /cds=(14,1783)			
		/gb=NM_005687 /gi=19923332			i ' i
1		/ug=Hs 9081 /len=3118	3		
256	0.042048	KIAA0494 gene product (KIAA0494),	NM_014774	Hs.62515	NP_055589
		mRNA /cds=(978,2465)			
		/gb=NM_014774 /gi=7662159			
050	0.000400	/ug=Hs.62515 /len=5766	N.M. 045070		115 000 170
259	0.020126	ornithine decarboxylase antizyme	NM_015878	Hs.223014	NP_680479
		inhibitor (OAZIN), transcript variant 1,			
		mRNA /cds=(721,2067) /gb=NM_015878 /gi=22538416	,	ĺ	1 2 3
282	0.042049	/ug=Hs.223014 /len=2882 protein phosphatase 1, regulatory	NM_005398	Hs.303090	ND OCESOO
202	0.042040	(inhibitor) subunit 3C (PPP1R3C),	 	JUS.303080	NP_005389
		mRNA /cds=(58,1011) /gb=NM_005398	,		
		/gi=21314622 /ug=Hs.303090 /len=2524			
		/g 2+3+4022/ug-+15.505030/leff-2524 			
283	0.020126	syntaxin 7 (STX7), mRNA /cds=(80,865)	NM 003569	Hs.8906	NP_003560
200	0.020120	/gb=NM_003569 /gi=4507294	1111_000003	113.0000	-005500
		/ug=Hs.8906 /len=1614			
287	0.012669	zinc finger protein 187 (ZNF187), mRNA	NM 152736	Hs.237786	NP 689949
-	3.5.2000	/cds=(193,1170) /gb=NM_152736	1.111_102700	1.15.207700	-009049
		/gi=24211018 /ug=Hs.237786 /len=2298			,
l	•				
	<u> </u>	L 		L	<u> </u>

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
294	0.034378	mitochondrial carrier 2 (MTCH2),	NM_014342	Hs.279609	NP_055157
		nuclear gene encoding mitochondrial	-	*.	
		protein, mRNA /cds=(49,960)			
		/gb=NM_014342 /gi=7657346	•		
_		/ug=Hs.279609 /len=1104	•	ľ	
310	0.022485	kinesin family member 13B (KIF13B),	NM 015254	Hs.15711	NP 056069
		mRNA /cds=(38,5518) /gb=NM 015254	- -		
		/gi=13194196 /ug=Hs.15711 /len=8743			
	ř.	3			٠.
314	0.044138	601582740F1 NIH MGC_7 cDNA clone	BE798080	Hs.446419	
		IMAGE:3937377 5', mRNA sequence			
	٠.	/clone=IMAGE:3937377 /clone end=5'			1
		/gb=BE798080 /gi=10219278			
		/ug=Hs.446419 /len=1156			
1		7.dg 3113.440410 //en=1100			
332	0.022485	similar to rat nuclear ubiquitous casein	NM 022731	Hs.118064	NP 073568
- 002	0.022,00	kinase 2 (NUCKS), mRNA	_022101		
		/cds=(67,558) /gb=NM 022731	, ,		•
	1 1	/gi=12232386 /ug=Hs.118064 /len=1811	1		
		igi- 12232300 rag-113. 1 10004 rieji- 10 1 1 		1	
333	0.020126	chaperonin containing TCP1, subunit 8	NM 006585	Hs.15071	NP 006576
000	0.020120	(theta) (CCT8), mRNA /cds=(29,1675)		110.10071	
		/gb=NM_006585 /gi=6005726			
		/ug=Hs.15071 /len=1821			
357	0.022485	deleted in pancreatic carcinoma (DPC4)	AF045440	- 2	-
00.	0.022400	gene, exon 3	, , , , , , , , , , , , , , , , , , , ,		1
359	0.04638	plakophilin 2=X97675 plakophilin 2b	NP_004563		
	0.01000	(ORF 38%)	100 1000		
361	0.032415	THO complex 1 (THOC1), mRNA	NM 005131	Hs.1540	NP_005122
""	0.002-110	/cds=(15,1988) /gb=NM_005131		110.1010	111 _000 122
		/gi=4826881 /ug=Hs.1540 /len=2092		;	
366	0.042048	voltage-dependent anion channel 1	NM 003374	Hs.149155	NP_003365
000	0.042040	(VDAC1), mRNA /cds=(100,951)	1000014	113:149190	
[/gb=NM_003374 /gi=4507878	in the state of		
	' j	/ug=Hs.149155 /len=1806			
370	0.04638	carboxypeptidase E (CPE), mRNA	NM 001873	Hs.75360	NP_001864
0,0	1 .0.0 1000	/cds=(291,1721) /gb=NM_001873	11111_001070	110.7000	-001001
	1	/gi=4503008 /ug=Hs.75360 /len=2443			
372	0.009931	DEAD/H (Asp-Glu-Ala-Asp/His) box	NM 012141	Hs.58570	NP_036273
" -		polypeptide 26 (DDX26), mRNA	0,2,7	1.10.000,0	
1		//cds=(477,3140) /gb=NM 012141			
· ·	1 .	/gi=11024693 /ug=Hs.58570 /len=3690	·		
				• .	
380	0.031002	5'-3' exoribonuclease 2 (XRN2), mRNA	NM 012255	Hs.268555	NP_036387
	5.551002	/cds=(86,2938) /gb=NM_012255			-200007
1 .		/gi=18860915 /ug=Hs 268555 /len=3445			
	1	1/9. 100000 10 /ug-110.200000 /1611-0440	I	1	I

Spot	p-value	Description	Gene	Unigene	Protein
Opor	p value	Doddin pilon	Accession	Accession	Accession
1			No.	No.	No.
384	0.031002	ADP-ribosylation factor-like 6 interacting	NM 015161	Hs.75249	NP_055976
		protein (ARL6IP), mRNA /cds=(70,681)			
ļ i		/gb=NM_015161 /gi=24308006			
		/ug=Hs.75249 /len=2280			
385	0.042048	cyclin C (CCNC), mRNA /cds=(29,940)	NM_005190	Hs.118442	NP_005181
		/gb=NM_005190 /gi=7382485		ļ	
	-	/ug=Hs.118442 /len=1508			
<u> </u>					
390	0.038054	UDP-galactose transporter related	NM_005827	Hs.154073	NP_005818
		(UGTREL1), mRNA /cds=(88,1056)			
		/gb=NM_005827 /gi=5032212			
393	0.020126	/ug=Hs.154073 /len=1186 microsomal epoxide hydrolase (EPHX1)	ΛΕΩΕ2417 [*]	-	
393	0.020120	gene, complete cds	AF255417	1	
395	0.014265	cysteine and histidine-rich domain	NM 012124	Hs.22857	NP_036256
	0.01.1200	(CHORD)-containing, zinc binding		1113.22007	141 _030230
1. "		protein 1 (CHORDC1), mRNA			
1		/cds=(85,1083) /gb=NM_012124			
		/gi=6912303 /ug=Hs.22857 /len=2058			l
396	0.04638	hypothetical protein FLJ20445	NM 017824	Hs.343748	NP 060294
		(FLJ20445), mRNA /cds=(293,1129)			
1		/gb=NM_017824 /gi=19923500			
		/ug=Hs.343748 /len=3896			
409	0.008765	S-phase kinase-associated protein 1A	NM_006930	Hs.171626	NP_733779
1		(p19A) (SKP1A), transcript variant 1,			
		mRNA /cds=(140,622) /gb=NM_006930			
1		/gi=25777710 /ug=Hs 171626 /len=2172			
117	0.007000	LATC loss Assessment O	NIA 044570		NE SECON
417	0.027906	LATS, large tumor suppressor, 2	NM_014572	Hs.432314	NP_055387
1		(Drosophila) (LATŞ2), mRNA /cds=(375,3641) /gb=NM_014572			
1		/gi=18959199 /ug=Hs.432314 /len=4098			
		/g =109591997ug=119.4525147lef =4096 			
427	0.04638	hypothetical protein FLJ20508	NM 017850	Hs.272673	NP 060320
1		(FLJ20508), mRNA /cds=(191,802)	.		
		/gb=NM_017850 /gi=8923468			ļ
L		/ug=Hs.272673 /len=2376	,		
429	0.008765	NPD009 protein (NPD009), mRNA	NM_020686	Hs.283675	NP_065737
[.	[/cds=(1327,1677) /gb=NM_020686		_ ~	[
		/gi=24476005 /ug=Hs.283675 /len=2514			
	2 2 2 2 2				
432	0.042048	DKFZp586L081 (from clone	AL080234	Hs.8078	
	·	DKFZp586L081) /cds=UNKNOWN			:
1		/gb=AL080234 /gi=5262727			
L 422	0.00070	/ug=Hs.8078 /len=2159.	A = 4 = 0 = 0 = 0	<u></u>	
439	0.006784	COBW domain-containing protein	AF452722	Hs.434050	
	,	mRNA, complete cds /cds=(35,1222)			ľ
<u> </u>		/gb=AF452722 /gi=24850425 /ug=Hs.434050 /len=1561			
L		rug-ris.404000 /icii-1001	L,	<u> </u>	

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession No.	Accession No.
459	0.012669	X-ray repair complementing defective	NM_022550	Hs.150930	NP_072044
		repair in Chinese hamster cells 4	a de la companya de la companya de la companya de la companya de la companya de la companya de la companya de		
		(XRCC4), transcript variant 3, mRNA			
	·	/cds=(176,1180) /gb=NM_022550	4		
		/gi=12408648 /ug=Hs.150930 /len=1707			
461	0.009931	a disintegrin-like and metalloprotease	NM_006988	Hs.8230	NP_008919
		(reprolysin type) with thrombospondin			*.
		type 1 motif, 1 (ADAMTS1), mRNA			
4 4		/cds=(294,3146) /gb=NM_006988			# . T
		/gi=11038653 /ug=Hs.8230 /len=4459			
462		erg protein (ets-related gene)	M21535		NP_004440
466	0.00772	activity-dependent neuroprotector	NM_015339	Hs.3657	NP_056154
		(ADNP), mRNA /cds=(346,3654)			•
		/gb=NM_015339 /gi=12229216			
		/ug=Hs.3657 /len=4713			
512	0.027906	myosin IXB (MYO9B), mRNA	NM_004145	Hs.159629	NP_004136
		/cds=(1,6069) /gb=NM_004145			
		/gi=4758749 /ug=Hs.159629 /len=6069			
517	0.015802	galactokinase 1 (GALK1), mRNA	NM_000154	Hs.92357	NP_000145
, .		/cds=(64,1242) /gb=NM_000154			
		/gi=4503894 /ug=Hs.92357 /len=1361			
518	0.02729	small nuclear ribonucleoprotein 70kDa	NM_003089	Hs.174051	NP_003080
		polypeptide (RNP antigen) (SNRP70),	*		
1		mRNA /cds=(681,2525)			
		/gb=NM_003089 /gi=4507118			* 2
		/ug=Hs.174051 /len=2693			
573	0.034378	ancient ubiquitous protein 1 (AUP1),	NM_012103	Hs.173736	NP_036235
1		mRNA /cds=(69,1499) /gb=NM_012103			
		/gi=6912259 /ug=Hs.173736 /len=1664			
574	0.013065	mRNA for KIAA1274 protein, partial cds.	AB033100	Hs.300646	
		/cds=(265,2850) /gb=AB033100		1.	1
		/gi=20521819 /ug=Hs 300646 /len=4569			
			·		
605	0.044138	integrin, alpha 5 (fibronectin receptor,	NM_002205	Hs.149609	NP_002196
		alpha polypeptide) (ITGA5), mRNA		1	
1		/cds=(24,3173) /gb=NM_002205			
1		/gi=4504750 /ug=Hs.149609 /len=4204			
612	0.022485	Finkel-Biskis-Reilly murine sarcoma	NM_001997	Hs.177415	NP_001988
		virus (FBR-MuSV) ubiquitously			
		expressed (fox derived); ribosomal			
1		protein S30 (FAU), mRNA	ŀ	Į.	.
		/cds=(106,507) /gb=NM_001997			
		/gi=17981709 /ug=Hs.177415 /len=574			
· L	<u> </u>			<u> </u>	<u> L,</u>

Spot	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
	İ		No.	No	No.
615	0.020126	cDNA FLJ11904 fis, clone	AK021966	Hs.285519	
*		HEMBB1000048. /gb=AK021966	• *		
		/gi=10433275 /ug=Hs.285519 /len=2134			
633	0.022485	A kinase (PRKA) anchor protein 13	NM_007200	Hs.301946	NP_658913
		(AKAP13), transcript variant 2, mRNA			\
		/cds=(214,8655) /gb=NM_007200			
		/gi=21493028 /ug=Hs.301946 //en=10156			
645	0.042048	hematopoietic-derived zinc fingerprotein (RefSeq aa 1e-48)	NP_004867		
672	0.035996	C-terminal binding protein 2 (CTBP2),	NM_022802	Hs.171391	NP_073713
		transcript variant 2, mRNA			_
		/cds=(137,3094) /gb=NM_022802			
· 		/gi=12746589 /ug=Hs.171391 /len=3780			
726	0.031002	tyrosine 3-monooxygenase/tryptophan 5-	NM 012479	Hs.25001	NP_036611
	,	monooxygenase activation protein,			
l	**	gamma polypeptide (YWHAG), mRNA	· ·		(
		/cds=(192,935) /gb=NM 012479		١.	
		/gi=21464100 /ug=Hs.25001 /len=3747			
749	0.034378	ribosomal protein S24 (RPS24),	NM_033022	Hs.180450	NP_148982
		transcript variant 1, mRNA			
		/cds=(38,430) /gb=NM_033022			
		/gi=14916500 /ug=Hs 180450 /len=537	* .		
779	0.012669	myosin, heavy polypeptide 9, non-	NM_002473	Hs.146550	NP_002464
		muscle (MYH9), mRNA /cds=(1,5883)	· .		* ·
		/gb=NM_002473 /gi=22507396			
		/ug=Hs.146550 /len=7274			
802	0.025072	striated muscle contraction regulatory	M96843	Hs.296811	
		protein (Id2B) mRNA, complete cds.			
		/cds=(110,220) /gb=M96843 /gi=397775			
		/ug=Hs.296811 /len=1167	. ·		
808		PIX1 mRNA (ORF)	AF037219		NP_570854
809	0.020912	methylcrotonoyl-Coenzyme A	NM_020166	Hs.47649	NP_064551
	1	carboxylase 1 (alpha) (MCCC1), mRNA			
l		/cds=(133,2310) /gb=NM_020166			ŀ . l
		/gi=13518227 /ug=Hs.47649 /len=2528			
833	0.042048	NADH dehydrogenase (ubiquinone) 1	NM_002491	Hs.109760	NP 002482
		beta subcomplex, 3, 12kDa (NDUFB3),		[
1		mRNA /cds=(253,549) /gb=NM 002491			
		/gi=4505360 /ug=Hs.109760 /len=693			
1 .	1				1 1

Spot	p-value	Description	Gene	Unig ne	Protein
		; 	Accession No.	Accession No.	Accession
842	0.031002	sema domain, immunoglobulin domain	NM 012431	Hs.212414	No. NP_036563
		(lg), short basic domain, secreted,		· · · · · · · · · · · · · · · · · · ·	
1	** *	(semaphorin) 3E (SEMA3E), mRNA	and the second second		
	1	/cds=(467,2794) /gb=NM_012431			
		/gi=6912649 /ug=Hs.212414 /len=6474			
851	0.027906	of89c05.s1 NCI_CGAP_Li5 cDNA clone	AA894384	Hs.432123	
	!	IMAGE:1437512 3' similar to contains			• .
		Alu repetitive element;, mRNA]
		sequence /clone=IMAGE:1437512			
		/clone_end=3' /gb=AA894384	· . '		
		/gi=3030785 /ug=Hs.432123 /len=296			
877	0.027906	ring finger protein 11 (RNF11), mRNA	NM_014372	Hs.96334	NP_055187
,		/cds=(128,592) /gb=NM_014372		1	f
ļ		/gi=7657519 /ug=Hs.96334 /len=2529			
885	0.031002	mRNA for KIAA1350 protein, partial cds.	AB037771	Hs.101799	
i		/cds=(1,2737) /gb=AB037771		*	
		/gi=7243080 /ug=Hs.101799 /len=4153			
900	0.042048	RAB11A, member RAS oncogene	NM_004663	Hs.75618	NP 004654
		family (RAB11A), mRNA /cds=(104,754)			7
		/gb=NM_004663 /gi=20149549			
		/ug=Hs.75618 /len=2474			
902	0.01798	H2A histone family, member Z (H2AFZ),	NM_002106	Hs.119192	NP_002097
Į		mRNA /cds=(107,493) /gb=NM_002106			
		/gi=20336749 /ug=Hs.119192 /len=873			
903	0.038054	S100 calcium binding protein A10	NM 002966	Hs.400250	NP_002957
303	0.030034	(annexin II ligand, calpactin I, light	NW_002900	FIS.400230	NP_002957
ŀ	. 1	polypeptide (p11)) (S100A10), mRNA			
1		/cds=(112,405) /gb=NM_002966	_		
		/gi=4506760 /ug=Hs.400250 /len=649	,		[].
918	0.022485	AGENCOURT_6456859 NIH_MGC_92	BM466169	Hs.439148	
1		cDNA clone IMAGE:5576908 5', mRNA		}	1
	·	sequence /clone=IMAGE:5576908	•		1
	÷	/clone_end=5' /gb=BM466169]
1		/gi=18515211 /ug=Hs.439148 /len=1150			:
925	0.00772	OGT(O-Glc-NAc transferase)-	NM_014965	Hs.6705	NP_055780
1		interacting protein 106 KDa (OIP106),			, ,
		mRNA /cds=(217,3078)			
1		/gb=NM_014965 /gi=7662457	j .]
	-2 12 - 1 -	/ug=Hs.6705 /len=5109			
941	0.038054	polybromo 1 (PB1), mRNA	NM_018165	Hs.44143	NP_060783
}		/cds=(15,935) /gb=NM_018165]
L	L	/gi=8922564 /ug=Hs.44143 /len=3131		L	<u> </u>

Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No	No.	No.
952	0.01798	mRNA; cDNA DKFZp451O194 (from	AL832029	Hs.22559	
		clone DKFZp451O194) /gb=AL832029			
		/gi=21732569 /ug=Hs.22559 /len=5226		·	
				r e	·
953	0.04638	mRNA for KIAA0592 protein, partial cds.	AB011164	Hs.439367	
		/cds=(1,4062) /gb=AB011164			
,		/gi=3043707 /ug=Hs.439367 /len=4623	e de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de l		11.1
				1.00	
961	0.042048	SON DNA binding protein (SON),	NM_058183	Hs.92909	NP 620305
		transcript variant e, mRNA	-		
: :		/cds=(50,6376) /gb=NM_058183			
		/gi=21040317 /ug=Hs.92909 /len=8482			
4.			1 4 4 4		
966	0.031002	CGI-81 protein (DREV1), mRNA	NM_016025	Hs.279583	NP_057109
,		/cds=(249,1100) /gb=NM_016025			
		/gi=19923448 /ug=Hs.279583 /len=3163			
973	0.02015	heat shock factor binding protein 1	NM_001537	Hs.250899	NP_001528
		(HSBP1), mRNA /cds=(55,285)			
		/gb=NM_001537 /gi=4557646		*** .	
L		/ug=Hs.250899 /len=547			
987	0.038054	brain protein 44-like (BRP44L), mRNA	NM_016098	Hs.108725	NP_057182
1	l 	/cds=(123,452) /gb=NM_016098			
ļ		/gi=7706368 /ug=Hs.108725 /len=988			
995	0.034378	homeodomain-interacting protein kinase	NM_005734	Hs.30148	NP_005725
<u> </u>		3 (HIPK3), mRNA /cds=(5,3652)			
		/gb=NM_005734 /gi=11386208	ar e		
		/ug=Hs.30148 /len=3723			
1040	0.042048	NADH dehydrogenase (ubiquinone) 1	NM_004546	Hs.198272	NP_004537
] ' '		beta subcomplex, 2, 8kDa (NDUFB2),			
ļ	.	mRNA /cds=(58,375) /gb=NM_004546			
1040	0.000051	/gi=4758777 /ug=Hs 198272 /len=494	A 0007707	11. 04004	ļ
1043	0.038054	mRNA for KIAA1376 protein, partial cds.	AB037797	Hs.24684	
		/cds=(144,1457) /gb=AB037797		ŀ	
1044	0.005040	/gi=7243132 /ug=Hs.24684 /len=4131	NM 040040	11- 70040	ND 000505
1044	0.005949	par-3 partitioning defective 3 (C.	NM_019619	Hs.72249	NP_062565
l i		elegans) (PARD3), mRNA			
		/cds=(1,4071) /gb=NM_019619			
	1	/gi=21361830 /ug=Hs 72249 /len=4071			
1000	0.04620	filomin D. hato (notice binding quatering	NIM 004457	U- 04000	ND 004440
1062	0.04038	filamin B, beta (actin binding protein	NM_001457	Hs.81008	NP_001448
		278) (FLNB), mRNA /cds=(132,7940)		,	}
1		/gb=NM_001457 /gi=4503746	•		
L	<u> </u>	/ug=Hs.81008 /len=9432		1	L

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1065	0.027906	cytochrome c oxidase subunit VIa	NM_005205	Hs.250760	NP_005196
		polypeptide 2 (COX6A2), nuclear gene			
		encoding mitochondrial protein, mRNA			
		/cds=(76,369) /gb=NM_005205			
		/gi=17999529 /ug=Hs.250760 /len=425			
1066	0.038054	hypothetical protein FLJ20452	NM_017828	Hs.351327	NP_060298
		(FLJ20452), mRNA /cds=(15,614)			
		/gb=NM_017828 /gi=21361660			
		/ug=Hs.351327 /len=1948			
1068	0.025072	UPF3 regulator of nonsense transcripts	NM_023011	Hs.399740	NP_542418
		A (yeast) (UPF3A), transcript variant 1,		r a constant	
		mRNA /cds=(38,1468) /gb=NM_023011			
• • • • • •		/gi=18375523 /ug=Hs.399740 /len=2381			
	Į.				
·					
1084	0.034378	ADP-ribosylation factor-like 1 (ARL1),	NM_001177	Hs.242894	NP_001168
		mRNA /cds=(105,650) /gb=NM_001177		-	
		/gi=4755126 /ug=Hs.242894 /len=968			
1090	.0.031002	protein phosphatase methylesterase-1	NM_016147	Hs.63304	NP_057231
		(PME-1), mRNA /cds=(100,1260)			,
		/gb=NM_016147 /gi=7706644			
		/ug=Hs.63304 /len=2484			
1148	0.034378	CHLORIDE INTRACELLULAR	Q9Z1Q5		
		CHANNEL PROTEIN 1 (NUCLEAR			
		CHLORIDE ION CHANNEL 27)			
<u> </u>		(NCC27) (P64 CLCP) (aa 2e-14 92%)			
1149	0.012669	fibroblast growth factor receptor 1 (fms-	NM_023109	Hs.748	NP_075599
		related tyrosine kinase 2, Pfeiffer			
		syndrome) (FGFR1), transcript variant			
		7, mRNA /cds=(727,2715)	er e		
.,		/gb=NM_023109 /gi=13186244		•	
	<u> </u>	/ug=Hs.748 /len=4066			
1164	0.034378	suppressor of Ty 5 (S. cerevisiae)	NM_003169	Hs.70186	NP_003160
	1	(SUPT5H), mRNA /cds=(208,3471)			
		/gb=NM_003169 /gi=20149523			
		/ug=Hs.70186 /len=3762			
1171	0.025072	integrin, beta 1 (fibronectin receptor,	NM_002211	Hs.287797	NP_596867
		beta polypeptide, antigen CD29 includes			
		MDF2, MSK12) (ITGB1), transcript			* * * * * * * * * * * * * * * * * * * *
		variant 1A, mRNA /cds=(127,2523)			
-		/gb=NM_002211 /gi=19743812			
		/ug=Hs.287797 /len=3700			1
		<u>'</u>	·		· · · · · · · · · · · · · · · · · · ·
1180	0.006784	complement component 2 (C2), mRNA	NM_000063	Hs.2253	NP_000054
		/cds=(37,2295) /gb=NM_000063			
		/gi=20631970 /ug=Hs.2253 /len=2609			
L					L

Spot	p-value	D scription	Gene	Unigene	Protein
			Accession No.	Accession No.	Accession No.
1184	0.009931	mannosidase, alpha, class 1A, member	NM_006699	Hs.367638	NP_006690
		2 (MAN1A2), mRNA /cds=(521,2446)			
		/gb=NM_006699 /gi=5729912			
		/ug=Hs.367638 /len=2792			
1185	0.027906	novel protein AHNAK mRNA, partial	M80899	Hs.381240	
	•	sequence. /cds=(1,3836) /gb=M80899			
		/gi=178282 /ug=Hs.381240 /len=4051			,
1186	0.031002	ankylosis, progressive (mouse) (ANKH),	NM_054027	Hs.168640	NP_473368
1,0		transcript variant 2, mRNA	<u>.</u> .		
		/cds=(265,1743) /gb=NM_054027			1
		/gi=21536394 /ug=Hs.168640 /len=4031			ļ. ,
4000	0.044005		VVA 000500		
1200	0.014265	hypothetical gene supported by	XM_000590		
4004	0.004270	XM_000590 (LOC59176)	NM_015469	Hs.24608	ND OFCOOL
1201	0.034378	DKFZp564D177 protein	NIVI_U 15469	IDS.24608	NP_056284
		(DKFZp564D177), mRNA			
	1.	/cds=(106,849) /gb=NM_015469			. 1
		/gi=22267435 /ug=Hs.24608 /len=1664			
1206	0.042048	ATP synthase, H transporting,	NM_005174	Hs.155433	NP_005165
	0.0.2	mitochondrial F1 complex, gamma			,
		polypeptide 1 (ATP5C1), mRNA			
		/cds=(32,925) /gb=NM_005174			-
	,	/gi=4885078 /ug=Hs.155433 /len=1078		\	
		3			
1210	0.025072	NADH dehydrogenase (ubiquinone) Fe-	NM_005006	Hs 8248	NP_004997
		S protein 1, 75kDa (NADH-coenzyme Q	[Ţ
		reductase) (NDUFS1), mRNA			
		/cds=(85,2268) /gb=NM_005006			
	<u> </u>	/gi=28269700 /ug=Hs 8248 /len=2382			
1213	0.04638	heat shock 10kDa protein 1 (chaperonin	NM_002157	Hs.1197	NP_002148
		10) (HSPE1), mRNA /cds=(42,350)			
	:	/gb=NM_002157 /gi=4504522	¢ · · · · · · · · ·		
		/ug=Hs.1197 /len=538			
1214	0.005206	mRNA; cDNA DKFZp586F2423 (from	AL080209	Hs.13659	1
		clone DKFZp586F2423) /gb=AL080209			
		/gi=5262698 /ug=Hs 13659 /len=4254			
1217	0.016031	DKFZp586F1918 (from clone	AL050091		NP_056347
'2''	0.010031	DKFZp586F1918); partial cds		2	111 _00007/
1220	0.008765	mRNA; cDNA DKFZp547C244 (from	AL442093	Hs.9460	
'	0.000,00	clone DKFZp547C244) /gb=AL442093	1	, .5.5-109	
j		/gi=10241768 /ug=Hs.9460 /len=2537			
1227	0.020126	integral inner nuclear membrane protein	NM 014319	Hs.7256	NP_055134
'22'	0.020120	(MAN1), mRNA /cds=(7,2742)	1,4141_0 1,40 10	1.13.7.200	
		/gb=NM_014319 /gi=7706606	l .		
	,	/ug=Hs.7256 /len=4703			
		/ug=118.1200 /1011=4100		 	<u> </u>

Spot	p-value	D scription	G ne	Unigene	Protein
			Accession	Acc ssion	Accession
			No.	No.	No.
1238	0.031002	mRNA for KIAA1673 protein, partial cds.	AB051460	Hs.301444	1
		/cds=(69,2207) /gb=AB051460			v · ·
		/gi=12697890 /ug=Hs.301444 /len=6380			
1242	0.014265	programmed cell death 4 (neoplastic	NM_145341	Hs.326248	NP_663314
3 1		transformation inhibitor) (PDCD4),			
		transcript variant 2, mRNA	7	- 4	
		/cds=(361,1737) /gb=NM_145341			
		/gi=21735597 /ug=Hs.326248 /len=2403			
1250	0.006206	Inucleor protoin, atavia telengia tagia	NM_002519	Hs.89385	NP_002510
1250	0.005206	nuclear protein, ataxia-telangiectasia locus (NPAT), mRNA /cds=(35,4318)	114141_002518	IUS.08300	NP_002510
		/gb=NM 002519 /gi=4505430			
		/gb=NiM_0023197gl=4303430 /ug=Hs.89385 /len=5895			
1255	0.014265	protein inhibitor of activated STAT, 1	NM_016166	Hs.75251	NP_057250
'200	0.01-1200	(PIAS1), mRNA /cds=(97,2052)	10.0.00	110.70201	
		/gb=NM_016166 /gi=7706636		;	
1		/ug=Hs.75251 /len=2309			,
1261	0.010197	cDNA FLJ11971 fis, clone	AK022033	Hs.121806	
		HEMBB1001208. /gb=AK022033			
		/gi=10433350 /ug=Hs.121806 /len=2355			
				**	
1281	0.020912	tripartite motif-containing 44 (TRIM44),	NM_017583	Hs.14512	NP_060053
• .		mRNA /cds=(217,1251)			
1		/gb=NM_017583 /gi=21361638			
•		/ug=Hs.14512 /len=3091	1		
1306	0.039896	poly(A) binding protein, cytoplasmic 1	NM_002568	Hs.172182	NP_002559
		(PABPC1), mRNA /cds=(503,2404)			
ļ		/gb=NM_002568 /gi=4505574	· *		
4200	0.04000	/ug=Hs.172182 /len=2848	NINA 000770	11- 04000	ND 072040
1309	0.04038	oxysterol binding protein-like 11 (OSBPL11), mRNA /cds=(306,2549)	NM_022776	Hs.61260	NP_073613
		/gb=NM 022776 /gi=23111058	e e e		
		/ug=Hs.61260 /len=4206			
1335	0.013065	hypothetical protein MGC11316	NM 032932	Hs.7985	NP 116321
ا الجَوْدَ	3.0 10000	(MGC11316), mRNA /cds=(116,226)	1111_002002	1.3.7000	111 _ 1 10021
		/gb=NM_032932 /gi=14249729	1		
		/ug=Hs.7985 /len=781			
1336	0.04638	Novel mRNA from chromosome 1,	AL096857	Hs.69559	NP_055987
	}	which has similarities to BAT2 genes			-
	1 .	/cds=(58,8163) /gb=AL096857			
]	/gi=5541862 /ug=Hs.69559 /len=10174]
1338	0.014265	anti-oxidant protein 2 (non-selenium	NM_004905	Hs.120	NP_004896
		glutathione peroxidase, acidic calcium-	· .		
	1	independent phospholipase A2)			
1	} ·	(AOP2), mRNA /cds=(44,718))	
		/gb=NM_004905 /gi=4758637			
<u> </u>	<u> </u>	/ug=Hs.120 /len=1653	1	<u></u>	<u> </u>

Spot	p-value	Description	Gene	Unigene	Protein
•			Accession	Accession	Acc ssion
			No.	No.	No.
1339	0.031002	FLJ20398 fis, clone KAT00580, highly	AK000405	Hs.76480	NP_055050
		similar to M35604 Human glucose-6-			- · ·
J 5 -		phosphate dehydrogenase			
		/cds=UNKNOWN /gb=AK000405			
		/gi=7020471 /ug=Hs.76480 /len=2342			
,		(=FLN, ≑G6PD, ≑ubiquitin-like protein			
		(GdX))			
1342	0.04638	FLJ30731 fis, clone FEBRA2000105,	AK055293	Hs.53447	NP_612352
		moderately similar to KINESIN LIGHT			
1.		CHAIN /cds=UNKNOWN	٠		
	1	/gb=AK055293 /gi=16549995			
		/ug=Hs.53447 /len=2770		-	
1345	0.04638	WW domain binding protein 1 (WBP1),	NM_012477	Hs.7709	NP_036609
		mRNA /cds=(154,963) /gb=NM_012477		. *	* .
		/gi=24430130 /ug=Hs.7709 /len=1183			
	,	· · · · · · · · · · · · · · · · · · ·			
1355	0.032415	FLJ13418 fis, clone PLACE1002090,	AK023480	Hs.237825	NP_008878
-		highly similar to SIGNAL			-
		RECOGNITION PARTICLE 72 KD			
		PROTEIN (AK023480.1)			
1358	0.034378	tropomyosin 3 (TPM3), mRNA	NM_153649	Hs.85844	NP_705935
		/cds=(52,798) /gb=NM_153649			
,		/gi=24119202 /ug=Hs.85844 /len=2089			
4000	0.005000		NIM 040004	11004400	NID 057000
1360	0.005206	chromosome 15 open reading frame 15	NIVI_016304	Hs.284162	NP_057388
	1	(C15orf15), mRNA /cds=(144,635)			
,		/gb=NM_016304 /gi=18491027	•		
1362	0.01700	/ug=Hs.284162 /len=1487 ADP-ribosylation factor related protein 1	NINA OOQQQA	Hs.389277	NP 003215
1302	0.01790	(ARFRP1), mRNA /cds=(12,617)	11111_003224	IDS.309211	INP_003215
		/gb=NM_003224 /gi=4507448			
-	4	/ug=Hs.389277 /len=1559	1		
1366	0.016031	Rho guanine nucleotide exchange factor	NM 019555	Hs.25951	NP 062455
,,,,,,	3.0 ,000	(GEF) 3 (ARHGEF3), mRNA	1.4.40.10000	1.13.20001	
		/cds=(128,1708) /gb=NM_019555			
		/gi=9506400 /ug=Hs.25951 /len=3561			
1373	0.016031	hypothetical protein MGC14421	NM_032907	Hs.334713	NP 116296
		(MGC14421), mRNA /cds=(474,1616)			
		/gb=NM_032907 /gi=14249681		[·	·
		/ug=Hs.334713 /len=1772			
1376	0.008765	chaperonin containing TCP1, subunit 5	NM_012073	Hs.1600	NP_036205
		(epsilon) (CCT5), mRNA /cds=(92,1717)	_		-
· .		/gb=NM_012073 /gi=24307938			
		/ug=Hs.1600 /len=1961			
1386	0.020912	AGENCOURT_6424254 NIH_MGC_67	BM479954	Hs.381243	- 30 20
		cDNA clone IMAGE:5491531 5', mRNA	,		
		sequence /clone=IMAGE:5491531			
		/clone_end=5' /gb=BM479954			*
	:	/gi=18528996 /ug=Hs.381243 /len=1112			[
	·				

Spot	p-value	D scription	Gene	Unigene	Protein
			Accession	Accession	Accession
V			No.	No.	No.
1396	0.01798	enoyl Coenzyme A hydratase 1,	NM_001398	Hs.196176	NP_001389
	5.5	peroxisomal (ECH1), mRNA			
		/cds=(28,1014) /gb=NM_001398			₋ - - - - - - - - - - - - -
		/gi=4503446 /ug=Hs.196176 /len=1196			
1403	0.014265	potassium voltage-gated channel, KQT-	NM_004518	Hs.4975	NP_742107
		like subfamily, member 2 (KCNQ2),]	. "	·
		transcript variant 3, mRNA			
		/cds=(178,2712) /gb=NM_004518	* *	• *	
		/gi=26051259 /ug=Hs.4975 /len=7556			
1413	0.031002	vacuolar protein sorting 29 (yeast)	NM_057180	Hs.69192	NP_476528
	,	(VPS29) transcript variant 2, mRNA			
		/cds=(61,621) /gb=NM_057180	1		#
		/gi=17402911 /ug=Hs.69192 /len=1107			
					• •
1419	0.027906	CD74 antigen (invariant polypeptide of	NM_004355	Hs.84298	NP_004346
		major histocompatibility complex, class			
		II antigen-associated) (CD74), mRNA			• .
		/cds=(8,706) /gb=NM_004355			
		/gi=10835070 /ug=Hs.84298 /len=1304			
					· ·
1503	0.04638	retrovirus-related leucine zipper protein	138587		
		p40 - human retrotransposon L1.1			
1540	0.025072	ribosomal protein S4, X-linked (RPS4X),	NM_001007	Hs.389933	NP_000998
		mRNA /cds=(36,827) /gb=NM_001007	, t		
		/gi=17981705 /ug=Hs.389933 /len=916			
1557	0.034378	MR2-CI0186-291100-010-a06 Cl0186	BF814502	Hs.446594	
].		cDNA, mRNA sequence /gb=BF814502			
ľ		/gi=12147047 /ug=Hs.446594 /len=530			
1559	0.025072	stromal cell derived factor receptor 1	NM_012428	Hs.389371	NP_059429
		(SDFR1), transcript variant beta, mRNA			•
	-	/cds=(139,1335) /gb=NM_012428			
		/gi=6912645 /ug=Hs.389371 /len=2388			
	<u> </u>				
1564	0.027906	quiescin Q6 (QSCN6), mRNA	NM_002826	Hs.77266	NP_002817
		/cds=(76,2319) /gb=NM_002826			
		/gi=13325074 /ug=Hs.77266 /len=3314		* * * * * * * * * * * * * * * * * * *	
				ļ	, , , , , , , , , , , , , , , , , , , ,
1579	0.031002	chromosome 14 open reading frame	NM_018229	Hs.106210	NP_060699
		108 (C14orf108), mRNA			·
· .		/cds=(407,1879) /gb=NM_018229			1
		/gi=21361775 /ug=Hs.106210 /len=3088			
755			: 		
1586	0.020126	KIAA1665 protein, partial cds	AB051452	Hs.300463	NP_612211
		/cds=UNKNOWN /gb=AB051452			1
		/gi=13359202 /ug=Hs.300463 /len=4311	,		
			<u> </u>		

Spot	p-value	Description	Gene	Unigene	Protein
•	•		Accession	Accession	Accession
			No.	No.	No
1596	0.042048	mRNA for KIAA1824 protein, partial cds.	AB058727	Hs.284294	
		/cds=(7,2883) /gb=AB058727			
		/gi=14017864 /ug=Hs.284294 /len=5814			
1597	0.006784	ATPase, H transporting, lysosomal	NM_001694	Hs.389107	NP_001685
		16kDa, V0 subunit c (ATP6V0C), mRNA			
·		/cds=(153,620) /gb=NM_001694			
		/gi=19913436 /ug=Hs.389107 /len=1126			٠.
1621	0.034378	mRNA for KIAA1856 protein, partial cds.	AB058750	Hs.381163	
1021	0.004070	/cds=(1,3405) /gb=AB058759	AB030739	115.561105	
		/gi=14017928 /ug=Hs.381163 /len=5223			
		/gi //01/020/0g //00//00//00//0220			
1637	0.034378	ribosomal protein S16 (RPS16), mRNA	NM 001020	Hs.397609	NP_001011
		/cds=(53,493) /gb=NM_001020			- -
		/gi=14591912 /ug=Hs.397609 /len=570			
1667	0.009931	interleukin 1 receptor, type I (IL1R1),	NM_000877	Hs.82112	NP_000868
		mRNA /cds=(83,1792) /gb=NM_000877		,	
		/gi=27894331 /ug=Hs.82112 /len=4909		,	
4004	0.04700	uhi a sais O (UDO) - BNA	NA 004000	11- 402704	ND 00000
1684	0.01798	ubiquitin C (UBC), mRNA	NM_021009	Hs.183704	NP_066289
		/cds=(136,2193) /gb=NM_021009 /gi=20149305 /ug=Hs.183704 /len=2309			
Į		/g -20149303/ug=Hs.183/04/lell-2309 			
1685	0.042048	hypothetical protein FLJ20059	NM_017644	Hs.246875	NP 060114
		(FLJ20059), mRNA /cds=(26,1291)			
	· .	/gb=NM_017644 /gi=8923060			
		/ug=Hs.246875 /len=1817		a d	
1699	0.014265	solute carrier family 11 (proton-coupled	NM_014585	Hs.5944	NP_055400
		divalent metal ion transporters),			1
	٠.	member 3 (SLC11A3), mRNA			
		/cds=(315,2030) /gb=NM_014585			
		/gi=19923794 /ug=Hs.5944 /len=3333			
4750	0.007000	ahaanhaadaa kiisaa hata (DUKD)	NIM 000000	U- 70000	NID 000004
1753	0.027906	phosphorylase kinase, beta (PHKB), mRNA /cds=(25,3306) /gb=NM 000293	NM_000293	Hs.78060	NP_000284
1.		/gi=4505782 /ug=Hs.78060 /len=4284		•.	
ļ		/gi-4505/02/ug-115./0000/ieii-4204			
1806	0.027906	hypothetical protein FLJ10134	NM_018004	Hs.104800	NP_060474
	*, • • • • • •	(FLJ10134), mRNA /cds=(314,1141)			
1	1	/gb=NM_018004 /gi=8922242			} .
		/ug=Hs.104800 /len=1564			<u> </u>
1817	0.04638	mRNA; cDNA DKFZp761P18121 (from	AL834147	Hs.44198	
		clone DKFZp761P18121)			
	:	/cds=(127,2289) /gb=AL834147		-	. ,
}		/gi=21739620 /ug=Hs.44198 /len=4286	-		
<u> </u>	L		L		L

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1831	0.038054	mRNA; cDNA DKFZp686O1729 (from clone DKFZp686O1729) /gb=AL833498 /gi=21734141 /ug=Hs.109731 /len=2003	AL833498	Hs.109731	
1834	0.014265	cDNA FLJ14337 fis, clone PLACE4000494. /gb=AK024399 /gi=10436778 /ug=Hs.180187 /len=4588	AK024399 (Hs.180187	
1866	0.042048	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta) (PPP3CB), mRNA /cds=(117,1691) /gb=NM_021132 /gi=11036639 /ug=Hs.151531 /len=3079	NM_021132	Hs.151531	NP_066955
1889	0.027906	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide (YWHAH), mRNA /cds=(198,938) /gb=NM_003405 /gi=21464102 /ug=Hs.349530 /len=1775		Hs.349530	NP_003396
1933	0.016031	mRNA for KIAA0361 gene, KIAA0361 protein. /cds=(1,4117) /gb=AB002359 /gi=2224662 /ug=Hs.105478 /len=5338	AB002359	Hs.105478	
1973	0.00344	keratin 8 (KRT8), mRNA /cds=(60,1511) /gb=NM_002273 /gi=4504918 /ug=Hs.242463 /len=1752	NM_002273	Hs.242463	NP_002264
1999	0.011228	chromosome 20 open reading frame 40 (C20orf40), mRNA /cds=(208,396) /gb=NM_014054 /gi=7661709 /ug=Hs.105379 /len=417	NM_014054	Hs.105379	NP_054773
2001	0.042048	mRNA for KIAA0892 protein, partial cds. /cds=(1,1867) /gb=AB020699 /gi=4240272 /ug=Hs.112751 /len=4164	AB020699	Hs.112751	
2002		ANG2 (ANG2) clathrin, light polypeptide (Lcb) (CLTB), transcript variant brain, mRNA /cds=(173,862) /gb=NM_007097	AF024631 NM_007097	Hs.380749	NP_008917 NP_009028
2042	0.016031	/gi=6005994 /ug=Hs.380749 /len=1134 ARF protein (LOC51326), mRNA /cds=(88,489) /gb=NM_016632	NM_016632	Hs.264509	NP_057716
2095	0.012669	/gi=7706177 /ug=Hs.264509 /len=826 chromosome 19 open reading frame 2 (C19orf2), transcript variant 1, mRNA /cds=(31,1638) /gb=NM_003796 /gi=19924158 /ug=Hs.7943 /len=2295	NM_003796	Hs.7943	NP_604431

Spot	p-value	Description	Gene	Unigene	Protein
- 1		A Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Comp	Accession	Accession	Accession
2107	0.014265	HSPC126 protein (HSPC126), mRNA	No. NM_014166	No. Hs 181112	No. NP_054885
2101	0.014200	/cds=(26,838) /gb=NM 014166	[iAM_0 14 100	1715.101112	NF_054005
		/gi≂7661787 /ug=Hs.181112 /len=1424			
		/gi=7004707 /dg=143.101112 /icli=1424	territoria (m. 1921) 1 maioria (m. 1921)		*****
2112	0.005206	NRH:quinone oxidoreductase 2 gene	AB050248	 	
		(NQO2)			
2143	0.012669	chromosome 13 open reading frame 9	NM 016075	Hs.146324	NP 057159
		(C13orf9), mRNA /cds=(6,1166)	_		-
		/gb=NM_016075 /gi=7705639			
		/ug=Hs.146324 /len=1832		<u> </u>	<u> </u>
2160	0.016031	mannosidase, alpha, class 1A, member	NM_006699	Hs.367638	NP_006690
		2 (MAN1A2), mRNA /cds=(521,2446))	
		/gb=NM_006699 /gi=5729912			
. '		/ug=Hs.367638 /len=2792			
0.00		 		}	
2167	0.034378	copine III (CPNE3), mRNA	NM_003909	Hs.14158	NP_003900
		/cds=(121,1734) /gb=NM_003909			
2470	0.007006	/gi=4503014 /ug=Hs.14158 /len=4737	NIM 000046	11. 4005	ND 777000
2176	0.027906	proteasome (prosome, macropain) 26S	NM_002816	Hs.4295	NP_777360
١.,	·	subunit, non-ATPase, 12 (PSMD12),		1	
-		mRNA /cds=(44,1414) /gb=NM_002816 /gi=4506220 /ug=Hs.4295 /len=3548			}
		/gi=4300220 /ug=i is.4293 /ieii=3346 			
2177	0.042048	RAB34, member RAS oncogene family	NM_031934	Hs.301853	NP 114140
		(RAB34), mRNA /cds=(206,985)			[
		/gb=NM_031934 /gi=21361998			
	, ·	/ug=Hs 301853 /len=1340			∤r v F v .
					\
2178	0.031002	crystallin, zeta (quinone reductase)-like	NM_145858	Hs.330208	NP_665857
		1 (CRYZL1), transcript variant 3, mRNA			1
		/cds=(86,682) /gb=NM_145858			* *
- 1		/gi=22202615 /ug=Hs.330208 /len=2099	•		
2012					
2184	1	highly charged protein (D13S106E),	NM_005800	Hs.151236	NP_005791
·	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	mRNA /cds=(178,3456)			
		/gb=NM_005800 /gi=5031648			
2207	0.027000	/ug=Hs.151236 /len=3650	NIA 007004	11- 00700	ND 004007
2207	0.027906	nidogen 2 (osteonidogen) (NID2),	NM_007361	Hs.82733	NP_031387
		mRNA /cds=(1,4131) /gb=NM_007361			
2217	0.027006	/gi=6679055 /ug=Hs.82733 /len=4829 nebulette (NEBL), mRNA	NM_006393	Hs.5025	NP_006384
, 22 (0.021900	/cds=(398,3442) /gb=NM 006393	14141_000393	113.3025	1115_000304
		/gi=5453757 /ug=Hs.5025 /len=8034			
2221	0.038054	clone MGC:43950 IMAGE:5276217,	BC037901	Hs.262716	ļ
		mRNA, complete cds /cds=(351,392)			1
	}	/gb=BC037901 /gi=23138800		·	
<i>:</i>		/ug=Hs.262716 /len=2214	· ·		
2239	0.020126	hypothetical protein (KIAA1162)	AB032988	 	NP 066979

Spot	p-value	D scription	Gene	Unigene	Protein
1			Accession	Accession	Accession
			No.	No.	No.
2244	0.022485	F-box and leucine-rich repeat protein 5	NM_033535	Hs.5548	NP_277077
:		(FBXL5), transcript variant 2, mRNA			1
	1	/cds=(586,2283) /gb=NM_033535			
		/gi=21536439 /ug=Hs.5548 /len=3475			
2288	0.008765	Similar to hypothetical protein	BC042899	Hs.153716	NP_671512
]	1	MGC30540, clone MGC:17342			
}	1	IMAGE:4342258, mRNA, complete cds			
1	1	/cds=(216,1457) /gb=BC042899			
		/gi=27552863 /ug=Hs.153716 /len=3028		}.	
	1		·	<u> </u>	
2310	0.020126	poly(A) binding protein, cytoplasmic 1	NM_002568	Hs.172182	NP_002559
		(PABPC1), mRNA /cds=(503,2404)			\
		/gb=NM_002568 /gi=4505574		.	
· .		/ug=Hs.172182 /len=2848	·	<u> </u>	
2311	0.008765	thyroid hormone receptor-associated	NM_005119	Hs.108319	NP_005110
		protein, 150 kDa subunit (TRAP150),	**:		
		mRNA /cds=(203,3070)			
		/gb≑NM_005119 /gi=4827039			
		/ug=Hs.108319 /len=3618		<u> </u>	
2330	0.034374	eukaryotic translation elongation factor	NM_001961	Hs.75309	NP_001952
		2 (EEF2), mRNA /cds=(69,2645)		1.	
		/gb=NM_001961 /gi=25453476	į.		
		/ug=Hs.75309 /len=3148			
2358	0.016031	cDNA FLJ90297 fis, clone	AK074778	Hs.405809	
1		NT2RP2000447, moderately similar to			la de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de
	1	GOLGIN-95. /cds=(333,728)]
		/gb=AK074778 /gi=22760446	·		
<u> </u>		/ug=Hs.405809 /len=2520			
2360	0.038054	hepatocyte growth factor-like protein	U28055		
		homolog (low match)		l	
2368	0.020126	capping protein (actin filament) muscle	NM_004930	Hs.333417	NP_004921
		Z-line, beta (CAPZB), mRNA			
ľ	- }	/cds=(1,819) /gb=NM_004930	}		1
	•	/gi=4826658 /ug=Hs.333417 /len=1077	}		1 1 1
241	3 0.031002	proteasome (prosome, macropain) 26S	NM_002809	Hs.9736	NP_002800
		subunit, non-ATPase, 3 (PSMD3),			1
		mRNA /cds=(165,1769)		1 / .	, ,
	1.	/gb=NM_002809 /gi=25777611]		
		/ug=Hs.9736 /len=2174	ļ	<u> </u>	<u> </u>
243	0.01798	ribosome binding protein 1 180kDa	NM_004587	Hs.98614	NP_004578
		(dog) (RRBP1), mRNA /cds=(71,3004)	1		
		/gb=NM_004587 /gi=4759055			1
		/ug=Hs.98614 /len=3106			<u> </u>
244	0.008765	oxysterol binding protein-like 2	NM_144498	Hs.15519	NP_653081
	· ·	(OSBPL2), transcript variant 2, mRNA]		
		/cds=(203,1645) /gb=NM_144498			·
}	4.4	/gi=21450852 /ug=Hs.15519 /len=3971			1
] .	1		}		1

Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
2461	0.014265	annexin A6 (ANXA6), transcript variant	NM_001155	Hs.118796	NP_004024
		1, mRNA /cds=(171,2192)			,
		/gb=NM_001155 /gi=4809274		- 	<u>.</u>
		/ug=Hs.118796 /len=2528	<u> </u>		
2476	0.022485	MAP kinase-interacting serine/threonine	NM_003684	Hs.5591	NP_003675
		kinase 1 (MKNK1), mRNA		}	
·		/cds=(174,1571) /gb=NM_003684			
		/gi=21361100 /ug=Hs.5591 /len=2745			
<u></u>					L
2477		of human GTP-binding protein G25K	AL121737		NP_426359
2488	0.025072	likely ortholog of mouse hippocampus	NM_033055	Hs.21015	NP_149044
		abundant gene transcript 1 (HIAT1),		1.	
-		mRNA /cds=(6,1124) /gb=NM_033055			
}		/gi=24308343 /ug=Hs.21015 /len=2230			
L				, , , , , , , , , , , , , , , , , , ,	
2508	0.034378	sorting nexin 1 (SNX1), transcript	NM_003099	Hs.75283	NP_690039
)		variant 1, mRNA /cds=(13,1581)			
,		/gb=NM_003099 /gi=23111033			
		/ug=Hs.75283 /len=1984	• ;		
2520	0.002982	KIAA0164 gene product (KIAA0164),	NM_014739	Hs.80338	NP_055554
		mRNA /cds=(254,3016)		, ,	
		/gb=NM_014739 /gi=7661957	,		
	,	/ug=Hs.80338 /len=5538			
2533	0.016031	kinase substrate HASPP28 mRNA,	U26541		
		complete cds			
2545	0.031002	chromosome 8 open reading frame 1	NM_004337	Hs.40539	NP_004328
[(C8orf1), mRNA /cds=(346,1863)		ĺ	i '
}		/gb=NM_004337 /gi=4757889			
0510	0.04700	/ug=Hs.40539 /len=4199	1114 000070	11- 70700	ND 000007
2546	0.01798	vascular endothelial growth factor	NM_003376	Hs.73793	NP_003367
	}	(VEGF), mRNA /cds=(702,1277))
,		/gb=NM_003376 /gi=19923239			1
25.47	0.024002	/ug=Hs.73793 /len=3166	NM_005178	Hs.31210	NP_005169
2547	0.031002	B-cell CLL/lymphoma 3 (BCL3), mRNA	NIVI_UUD1/8	1115.51210	114-700 109
]		/cds=(42,1382) /gb=NM_005178 /gi=20336471 /ug=Hs.31210 /len=1813			
	1	/g -2033047 /ug=ms.3 2 0 /len=18 3 	1	1	1
2553	0.027006	transmembrane protein vezatin	NM 017599	Hs.24135	NP_060069
2000	0.021900	(VEZATIN), mRNA /cds=(177,1886)	14141_017399	113.24130	_000009
1		/gb=NM 017599 /gi=19923537	,		[
]		/ug=Hs.24135 /len=3949			
2568	0.011228	glycoprotein M6B (GPM6B), mRNA	NM 005278	Hs.5422	NP_005269
2000	0.011220	/cds=(255,1052) /gb=NM_005278	1.111_000270	1.10.0-122	_555255
1		//gi=24307894 /ug=Hs.5422 /len=1642			
2569	0.038054	PEST-containing nuclear protein	NM_020357	Hs.71618	NP 065090
2003	0.000004	(PCNP), mRNA /cds=(19,555)	J. 1141_020007	1.15.7 1010]555550
		/gb=NM_020357 /gi=9966826			
1	1	/ug=Hs.71618 /len=2250	4		1
L ,	Ļ	1 ag 1 13,1 10 10 11011 2200	ļ 		

Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
2583	0.014265	receptor (calcitonin) activity modifying	NM_005856	Hs.25691	NP_005847
		protein 3 (RAMP3), mRNA			
4.4		/cds=(30,476) /gb=NM_005856	*		
		/gi=5032022 /ug=Hs.25691 /len=1312			<u> </u>
2602	0.042048	fibrinogen-like 2 (FGL2), mRNA	NM_006682	Hs.351808	NP_006673
	:	/cds=(34,1353) /gb=NM_006682			1
		/gi=5730074 /ug=Hs.351808 /len=1496			
2628	0.003958	methyltransferase reductase (MTRR),	NM 024010	Hs 153792	NP 076915
		transcript variant 2, mRNA			
		/cds=(31,2208) /gb=NM_024010			1
		/gi=13325067 /ug=Hs.153792 /len=3291			
			<u> </u>		
2646	0.031002	EGF-containing fibulin-like extracellular	NM_004105	Hs.76224	NP_061489
		matrix protein 1 (EFEMP1), transcript		}	
		variant 1, mRNA /cds=(150,1631)	-	1	
		/gb=NM_004105 /gi=9665261			
		/ug=Hs.76224 /len=2742			
2674	0.005206	ring finger protein 10 (RNF10), mRNA	NM_014868	Hs.5094	NP_055683
		/cds=(448,2883) /gb=NM_014868			
		/gi=27544928 /ug=Hs.5094 /len=3129		<u> </u>	
2678	0.031002	protein-L-isoaspartate (D-aspartate) O-	NM_005389	Hs.79137	NP_005380
		methyltransferase (PCMT1), mRNA		} .	1
		/cds=(74,757) /gb=NM_005389			
·		/gi=4885538 /ug=Hs.79137 /len=1599			<u> </u>
2681	0.042048	HBS1-like (S. cerevisiae) (HBS1L),	NM_006620	Hs.221040	NP_006611
		mRNA /cds=(194,2248)			
٠,		/gb=NM_006620 /gi=24431963			
حنييت	 	/ug=Hs.221040 /len=7163		<u> </u>	L
2682	0.016031	choline phosphotransferase 1 (CHPT1),	NM_020244	Hs.171889	NP_064629
		mRNA /cds=(171,1391)			
		/gb=NM_020244 /gi=9910383			
		/ug=Hs.171889 /len=1536		1	100 004050
2698	0.031002	topoisomerase (DNA) II alpha 170kDa	NM_001067	Hs.156346	NP_001058
	}	(TOP2A), mRNA /cds=(127,4722)	}		
		/gb=NM_001067 /gi=19913405			-
-	0.044005	/ug=Hs.156346 /len=5698		11. 10000	110 00000
2719	0.014265	HMG-box containing protein 1 (HBP1),	NM_012257	Hs.10882	NP_036389
		mRNA /cds=(187,1731)			ł
-	1	/gb=NM_012257 /gi=21361410			1.
0700	0.005070	/ug=Hs.10882 /len=2857	AF054500	11- 420720	
2729	0.025072	HIC protein isoform p40 and HIC protein	AFU34389	Hs.132739	
		isoform p32 mRNAs, complete cds		1	ł
	}	/cds=(264,1331) /gb=AF054589			}
	1	/gi=3426297 /ug=Hs.132739 /len=4152			
2766	0.008765	sorting nexin 7 (SNX7), transcript	NM_015976	Hs.127241	NP_689424
2,00	1 3.000,00	variant 1, mRNA /cds=(268,1431)	,,,,,_0,,00,		
	1	/gb=NM_015976 /gi=23111053	1		1

Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
2784	0.020126	dual specificity phosphatase 14	NM_007026	Hs.91448	NP_008957
		(DUSP14), mRNA /cds=(234,830)			
4		/gb=NM_007026 /gi=5902001		,	
		/ug=Hs.91448 /len=1471			
2801	0.027906	Rattus norvegicus mitochondrial	NC_001665		
		genome			
2809	0.020126	cDNA: FLJ21874 fis, clone HEP02488.	AK025527	Hs.208334	
		/gb=AK025527 /gi=10438070			
		/ug=Hs.208334 /len=2239			
			1114 000704	1	ND 000700
2815	0.022485	proteasome (prosome, macropain)	NM_002791	Hs.410276	NP_002782
		subunit, alpha type, 6 (PSMA6), mRNA		i ·	
		/cds=(110,850) /gb=NM_002791			
		/gi=23110943 /ug=Hs.410276 /len=1035		***	
2020	0.042049	zinc finger RNA binding protein (ZFR),	NM_016107	Hs.173518	NP 057191
2820	0.042046	mRNA /cds=(44,1300) /gb=NM_016107	NIVI_U 10 10 1	П5. 173316	NP_037 19 1
.		/gi=7706372 /ug=Hs.173518 /len=2734			
ı ' [!]		/gi=//003/2/ug=(18.1/3316/left=2/34 			
2852	0.042048	prefoldin 4 (PFDN4), mRNA	NM 002623	Hs.91161	NP_002614
2002	0.042040	/cds=(1,405) /gb=NM_002623		110.01101	_002017
		/gi=12408676 /ug=Hs.91161 /len=1208	·.		2
			k e		
2875	0.034378	deubiquitinating enzyme (UNPH4)=	AF106069		NP 006304
		AF153604 ubiquitin-specific protease			
		homolog (UPH)	,		
2876	0.034378	transcriptional regulator interacting with	NM_014755	Hs.77293	NP_055570
		the PHS-bromodomain 2 (TRIP-Br2),			
		mRNA /cds=(298,1242)	- "_		
		/gb=NM_014755 /gi=7661925			
		/ug=Hs.77293 /len=5544			
2892	0.042048	t-complex 1 (TCP1), mRNA	NM_030752	Hs.4112	NP_110379
·		/cds=(22,1692) /gb=NM_030752			
		/gi=13540472 /ug=Hs.4112 /len=2019			
2944	0.027906	hypothetical protein FLJ20345	NM_017777	Hs.20558	NP_060247
		(FLJ20345), mRNA /cds=(175,1425)			
٠,		/gb=NM_017777 /gi=8923323			
00.45	0.00054	/ug=Hs.20558 /len=2081	NA 400700	11- 44000	ND COOKES
2945	0.038054	hypothetical protein BC018453	NM_138798	Hs.14222	NP_620153
-		(LOC129531), mRNA /cds=(49,798)			
	1	/gb=NM_138798 /gi=20270348	*.		
2958	0.020426	/ug=Hs.14222 /len=963 TH1-like (Drosophila) (TH1L), mRNA	NM_016397	Hs.5184	NP_057481
2900	0.020120	/cds=(8,1429) /gb=NM_016397	14141 0 10381	113.0104	111-05/401
1		//gi=7705462 /ug=Hs 5184 /len=2130			
2959	0.027006	protein (peptidyl-prolyl cis/trans	NM_006223	Hs.11774	NP_006214
2909	0.027800	isomerase) NIMA-interacting, 4	14141_000223	113.11/14	_000214
		(parvulin) (PIN4), mRNA /cds=(25,420)			
1		/gb=NM_006223 /gi=5453901			
1	1 .	1/0D=NN UUDZZ3 /OI=34339U1			

Spot	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
:			No.	No.	No.
2961	0.008765	line-1 protein ORF2 (=p150)	B28096		
3023	0.042048	apolipoprotein D (APOD), mRNA	NM_001647	Hs.75736	NP_001638
	ک د پریک میا	/cds=(62,631) /gb=NM_001647			}
		/gi=4502162 /ug=Hs.75736 /len=809			
3071	0.04638	endothelin receptor type A (EDNRA),	NM_001957	Hs.76252	NP_001948
•		mRNA /cds=(485,1768)			
	,	/gb=NM_001957 /gi=4503464			
,		/ug=Hs.76252 /len=4105			
3072	0.042048	trichorhinophalangeal syndrome I	NM_014112	Hs.26102	NP_054831
41, 41		(TRPS1), mRNA /cds=(639,4484)			
	**	/gb=NM_014112 /gi=7657658	* * * * * * * * * * * * * * * * * * *		[
		/ug=Hs.26102 /len=10011			
3090	0.025072	Similar to kinesin family member C1,	BC000712	Hs.20830	NP 002254
		clone MGC:1202 IMAGE:3506669,			
11.		mRNA, complete cds /cds=(168,2189)			
		/gb=BC000712 /gi=12653842			
		/ug=Hs.20830 /len=2400			
3185	0.020126	mRNA for repressor protein, partial cds.	D30612	Hs.58167	
• • • • • • • • • • • • • • • • • • •	0.020.20	/cds=(1,2157) /gb=D30612 /gi=2723456		1.0.00	
٠,		/ug=Hs.58167 /len=3737			
3202	0.020126	cDNA FLJ13419 fis, clone	AK023481	Hs.163443	1
3202	0.020120	PLACE1002115. /gb=AK023481	711020401	113.100440	
	,	/gi=10435427 /ug=Hs.163443 /len=2290		1	
		/g = 10455427 /dg=115.105445 /left=2250 			,
3204	0.04638	clone IMAGE:5263531, mRNA	BC037740	Hs.18016	
020.	0.01000	/gb=BC037740 /gi=22902216		1.10.100.10	
1.5		/ug=Hs.18016 /len=5036		1	} :
3241)	0.031002	brain specific protein (CGI-38), mRNA	NM_016140	Hs.279772	NP 057224
١	0.001002	/cds=(100,624) /gb=NM_016140			
	1	/gi=7706392 /ug=Hs.279772 /len=999		1	
3280	0.020126	RETROVIRUS-RELATED POL	P11369	 	
O E O O	0.020120	POLYPROTEIN			
3287	0.031002	FtsJ 1 (E. coli) (FTSJ1), mRNA	NM_012280	Hs.23170	NP_803188
020.	0.001002	/cds=(301,1290) /gb=NM_012280	1 12200	1,0.20110	
	ť	/gi=7110660 /ug=Hs.23170 /len=1867			
3288	0.005206	cyclin G2 (CCNG2), mRNA	NM 004354	Hs.79069	NP 004345
3200	0.005200	/cds=(136,1170) /gb=NM 004354	14141_004334	113.73003	111 _004040
		/gi=4757935 /ug=Hs.79069 /len=2044			
3290	0.020126	mitochondrial ribosomal protein L20	NM 017971	Hs.182698	NP 060441
3290	0.020120		11101_017971	102090	INP_000441
		(MRPL20), nuclear gene encoding			1 .
	,	mitochondrial protein, mRNA			}
]	/cds=(65,514) /gb=NM_017971		1	1
·		/gi=26638656 /ug=Hs.182698 /len=705			
2242	0.025072	ATPace H transporting hispasses	NM_003945	Hs.415629	NP 003936
3313	0.025072	ATPase, H transporting, lysosomal	INIVI_003945	113.413023	_003930
}		9kDa, V0 subunit e (ATP6V0E), mRNA			ł
]		/cds=(76,321) /gb=NM_003945			· ·
	,	/gi=19913435 /ug=Hs 415629 /len=849	».		
	1	<u> </u>	<u>L </u>	<u></u>	1

Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
·			No.	No.	No.
3322	0.04638	ribonuclease P (30kD) (RPP30), mRNA	NM_006413	Hs.139120	NP_006404
		/cds=(295,1101) /gb=NM_006413		i,	
		/gi=19923360 /ug=Hs.139120 /len=2643			
0.145	0.04000	514 515 404 4500 (6	A1 407544		
3445	0.04638	mRNA; cDNA DKFZp434A1520 (from	AL137544	Hs.406722	
		clone DKFZp434A1520); partial cds			
		/cds=(1,551) /gb=AL137544 /gi=6808224 /ug=Hs.406722 /len=2775			[
		/gi=6606224 /ug=Hs.406722 /left=2775			
3520	0.009931	mRNA; cDNA DKFZp586F2423 (from	AL080209	Hs.13659	
0020	0.000001	clone DKFZp586F2423) /gb=AL080209	712000200	113.13000	
, '		/gi=5262698 /ug=Hs.13659 /len=4254			
		1	4.4		
3524	0.020912	UI-H-DH1-awr-a-12-0-UI.s1	BQ001533	Hs.194397	
		NCI_CGAP_DH1 cDNA clone			
1 .		IMAGE:5893139 3', mRNA sequence	1]
		/clone=IMAGE:5893139 /clone_end=3'			·
		/gb=BQ001533 /gi=19726433			
		/ug=Hs 194397 /len=1039			
3539	0.012669	ubiquitin C (UBC), mRNA	NM_021009	Hs.183704	NP_066289
		/cds=(136,2193) /gb=NM_021009			
		/gi=20149305 /ug=Hs.183704 /len=2309		*	
3589	0.027906	yeast Sec31p (KIAA0905), mRNA	NM_014933	Hs.70266	NP_057295
		/cds=(54,3716) /gb=NM_014933			}
22.2	0.010010	/gi=7662369 /ug=Hs.70266 /len=4129	1	4700	115 004757
3616	0.042048	CD1D antigen, d polypeptide (CD1D),	NM_001766	Hs.1799	NP_001757
		mRNA /cds=(165,1172)	Y	1.	
		/gb=NM_001766 /gi=4502648			
3649	0.012660	/ug=Hs.1799 /len=1903 FLJ14680 fis, clone NT2RP2004242,	AK027586	Hs.334802	NP 078994
3049	0.012009	weakly similar to NEUROFILAMENT	AKU27300	115,334602 	NF_076994
		TRIPLET H PROTEIN /cds=(41,1885)		1 2 2 2 2 2 2	
	· .	/gb=AK027586 /gi=14042362			
-		/ug=Hs.334802 /len=2551		1	
3672	0.008765	cDNA PSEC0152 fis, clone	AK075459	Hs.350475	
, JO. <u>-</u>	1.555.55	PLACE1007885. /cds=(20,1144)	1		
		/gb=AK075459 /gi=22761560			
: 1		/ug=Hs.350475 /len=2130	1		
3690	0.027906	IK cytokine, down-regulator of HLA II	NM_006083	Hs.8024	NP_006074
•		(IK), mRNA /cds=(112,1785)	-		
		/gb=NM_006083 /gi=11038650			
		/ug=Hs.8024 /len=1785			
3693	0.031002	exonuclease GOR (GOR), mRNA	NM_172239	Hs.373854	NP_758439
		/cds=(628,1584) /gb=NM_172239		1	
		/gi=26665874 /ug=Hs.373854 /len=6609	1		
				<u> </u>	,

Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
0700	0.04700		No.	No.	No.
3722	0.01798	clusterin (complement lysis inhibitor, SP-	NM_001831	Hs.75106	NP_001822
J		40,40, sulfated glycoprotein 2,			
ļ		testosterone-repressed prostate			
		message 2, apolipoprotein J) (CLU),		7	
}		mRNA /cds=(48,1397) /gb=NM_001831 /gi=4502904 /ug=Hs.75106 /len=1676		} . ,	
	*	/gi=4502904 /ug=Hs./5100 /ieii=10/0			
3732	0.038054	hypothetical protein FLJ20718	NM 017939	Hs.50579	NP 060409
0,02	0.000001	(FLJ20718), mRNA /cds=(228,2012)	1		
, (A)		/gb=NM_017939 /gi=8923644			
		/ug=Hs.50579 /len=2658		1	1
3763	0.025072	UI-E-EO1-aja-c-22-0-UI.s1 UI-E-EO1	BM680199	Hs.355581	
		cDNA clone UI-E-EO1-aja-c-22-0-UI 3',			
}		mRNA sequence /clone=UI-E-EO1-aja-			
		c-22-0-UI /clone_end=3' /gb=BM680199			}
		/gi=18990095 /ug=Hs.355581 /len=1071			
					
3802	0.038054	cartilage associated protein (CRTAP),	NM_006371	Hs.155481	NP_006362
P 100		mRNA /cds=(12,1217) /gb=NM_006371			
	1. 1. 1. 1.	/gi=21536278 /ug=Hs.155481 /len=2307			
2005	0.024270	humathatian arataia EL 1402E0	NIM 019067	Hs.177596	NP 060537
3805	0.034376	hypothetical protein FLJ10350 (FLJ10350), mRNA /cds=(676,2340)	NM_018067	ms. 177590	NP_00037
	**	(FL)10350), KNA7cds=(676,2340) /gb=NM_018067 /gi=21361780			
	1	/ug=Hs.177596 /len=2811			
3889	0.008765	FLJ30635 fis, clone CTONG2002520	AK055197	Hs.351331	NP 000357
,0000	0.000700	/cds=UNKNOWN /gb=AK055197		110.001001	
· ·		/gi=16549871 /ug=Hs.351331 /len=2174			
}		3			
3972	0.01798	chitinase 3-like 1 (cartilage glycoprotein-	NM_001276	Hs.75184	NP_001267
1	1	39) (CHI3L1), mRNA /cds=(127,1278)			1
.~.	1	/gb=NM_001276 /gi=4557017			1 1
		/ug=Hs.75184 /len=1925	<u> </u>		
4038	0.020126	multiple PDZ domain protein (MPDZ),	NM_003829	Hs.169378	NP_003820
1	1	mRNA /cds=(47,6175) /gb=NM_003829			<u>{</u>
		/gi=4505230 /ug=Hs 169378 /len=6582] :
4054	0.04000	Impathul CoC hinding anatolic 2 (Dott	NIM 004000	Un 2220	ND 004092
4051	0.04638	methyl CpG binding protein 2 (Rett	NM_004992	Hs.3239	NP_004983
	•	syndrome) (MECP2), mRNA /cds=(168,1628) /gb=NM_004992			
		//gi=7710148 /ug=Hs.3239 /len=10182			j
4075	0.031002	+ 	NM_054027	Hs. 168640	NP_473368
""	1,55,50	transcript variant 2, mRNA			- 11 3336
	-	/cds=(265,1743) /gb=NM_054027		to the second	1
1.		/gi=21536394 /ug=Hs.168640 /len=4031	{		
1	1		·	<u></u>	<u> </u>
4082	0.020126	Leu zipper protein p40(61%)	1901303A	,	1901303A
4084		guanyl cyclase C gene,	U20230		
4160	0.031002	BPAG1n3 (BPAG1)	AF165191		NP_065121

Spot	p-value	Description	Gene	Unigene	Protein
1	Ĵ		Accession	Accession	Accession
			No.	No.	No.
4184	0.012669	ubiquitin-conjugating enzyme E2, J1	NM_016021	Hs.184325	NP_057420
		(UBC6 yeast) (UBE2J1), mRNA			
		/cds=(118,1095) /gb=NM_016021			
		/gi=7706311 /ug=Hs.184325 /len=1786			
1400	0.044000		NINA 000744	11-400040	ND 000705
4199	0.011228	protein phosphatase 1, regulatory	NM_002714	Hs.106019	NP_002705
		subunit 10 (PPP1R10), mRNA		1	
		/cds=(553,3375) /gb=NM_002714			
		/gi=25777670 /ug=Hs.106019 /len=4540	·		
4237	0.042048	smoothelin (SMTN), transcript variant 2,	NM_134269	Hs.149098	NP_599032
4207	0.042040	mRNA /cds=(219,2966)	14101_134203	113.143030	-399032
		/gb=NM 134269 /gi=19913395			
		/ug=Hs.149098 /len=3294			
4253	0.034374	cartilage associated protein (CRTAP),	NM 006371	Hs.155481	NP_006362
1		mRNA /cds=(12,1217) /gb=NM_006371			
٠.		/gi=21536278 /ug=Hs.155481 /len=2307			
4262	0.006784	peptidylprolyl isomerase B (cyclophilin	NM_000942	Hs.394389	NP_000933
1 :		B) (PPIB), mRNA /cds=(150,800)			
		/gb=NM_000942 /gi=20149505			
	1	/ug=Hs.394389 /len=1028			
4264	0.025072	syntrophin, alpha 1 (dystrophin-	NM_003098	Hs.31121	NP_003089
·		associated protein A1, 59kDa, acidic	. ,		
		component) (SNTA1), mRNA		1.1	
		/cds=(273,1790) /gb=NM_003098			
		/gi=18765742 /ug=Hs.31121 /len=2345			
4307	0.025072	HT015 protein (HT015)	AF223466		NP 061049
4309		aminopeptidase puromycin sensitive	NM_006310	Hs.293007	NP_006301
1 4303	0.000,000	(NPEPPS), mRNA /cds=(196,2823)		113.230007	
		/gb=NM_006310 /gi=15451906	-		
		/ug=Hs.293007 /len=4177			
4313	0.04638	chromosome 20 open reading frame	NM_052951	Hs.26213	NP 443183
		167 (C20orf167), mRNA /cds=(64,1053)	<u>-</u>	1	-
		/gb=NM_052951 /gi=16418440			
	:	/ug=Hs.26213 /len=1296			
4349		class I cytokine receptor (zcytor5)	AF178684		NP_004741
4389		ADP-ribosylation factor 3 (ARF3)	NM_001659		NP_001650
4390	0.027906	ataxia telangiectasia and Rad3 related	NM_001184	Hs.77613	NP_001175
		(ATR), mRNA /cds=(106,8040)			
		/gb=NM_001184 /gi=20143978			
1555		/ug=Hs.77613 /len=8265			115 410105
4392	0.04638	hypothetical protein MGC14697	NM_032747	Hs.171625	NP_116136
		(MGC14697), mRNA /cds=(264,440)			
		/gb=NM_032747 /gi=14249375		:]
L	1	/ug=Hs.171625 /len=581	<u>L</u>	L	<u></u>

Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
4394	0.042048	Likely ortholog of mouse tumor necrosis-	AK027807	Hs.44208	NP_078912
		alpha-induced adipose-related protein,			
		cDNA FLJ14901 fis, clone]
		PLACE1005409 (AK027807.1)	·		
4404	0.022485	KIAA1723 protein, partial cds	AB051510	Hs.8700	NP_006085
,]	/cds=UNKNOWN /gb=AB051510		'	
		/gi=12697990 /ug=Hs.8700 /len=7365			
4439	0.020126	retinoblastoma binding protein 6	NM_006910	Hs.91065	NP_008841
		(RBBP6), mRNA /cds=(92,2938)	,		}
		/gb=NM_006910 /gi=5902043			
		/ug=Hs.91065 /len=2994			
4445	0.038054	cDNA FLJ36681 fis, clone	AK094000	Hs.376416	
		UTERU2006547. /gb=AK094000			
;		/gi=21752972 /ug=Hs.376416 /len=2372			
	ľ	/g. 211020,270g 110.070110 /1011 20;2	<i>t</i>		
4452	0.010561	gene from PAC 747L4. /cds=(73,555)	AL035297	Hs.119254	n
7702	0.010001	/gb=AL035297 /gi=4200248	1.2000207	110.110204	
•		/ug=Hs.119254 /len=1155			
4453	0.022495	partial RAB18 gene for RAS-related	AJ277148		Marian and
4455	0.022465		AJ277 140		
4404	0.005070	small GTPase RAB18, exons 4-6	MOAGAG		<u> </u>
4464		suCRase-isomaltase (SI)	M84646	11- 000004	
4468	0.004545	cDNA FLJ13771 fis, clone	AK023833	Hs.288934	
		PLACE4000270. /gb=AK023833			
		/gi=10435888 /ug=Hs.288934 /len=6133			
					·
4475	0.01798	RNA binding motif protein 8B (RBM8B)	AF231512	*	
4508	0.04638	peptidyl-prolyl isomerase G (cyclophilin	NM_004792	Hs.77965	NP 004783
1000	0.0.00	G) (PPIG), mRNA /cds=(158,2422)			
		/gb=NM_004792 /gi=4758105			
		/ug=Hs.77965 /len=2695			
4514	0.038054	myeloid/lymphoid or mixed-lineage	NM 005935	 	NP 005926
4014	0.030034	leukemia (trithorax (Drosophila)	14141_000900		_003320
		homolog); translocated to, 2 (MLLT2)			· ·
AEAE	0.04000	=L13773, AF-4 mRNA,	NM 022655	Ha 212920	ND 207504
4515	0.04638	cell recognition molecule CASPR3	NM_033655	Hs.212839	NP_387504
		(CASPR3), transcript variant 1, mRNA		1	
		/cds=(408,3872) /gb=NM_033655			
		/gi=16306508 /ug=Hs.212839 /len=5017			
4521	0.04638	zinc finger protein 267 (ZNF267),	NM_003414	Hs.145498	NP_003405
· I]	transcript variant 498723, mRNA]		-
		/cds=(134,2365) /gb=NM_003414			
		/gi=24431954 /ug=Hs.145498 /len=3205			
			·		
4548	0.038054	type II integral membrane protein	AF001297		

Spot	p-value	Description	Gene	Unigene	Prot in
	p		Accession	Accession	Acc ssion
			No.	No.	Nó.
4550	0.008765	hypoxanthine phosphoribosyltransferase		Hs.82314	NP 000185
	,	1 (Lesch-Nyhan syndrome) (HPRT1),	-	9	_
	and the second	mRNA /cds=(86,742) /gb=NM_000194			
		/gi=4504482 /ug=Hs.82314 /len=1331		programme in the programme	
4567	0.00772	CD163 antigen (CD163), mRNA	NM_004244	Hs.74076	NP_004235
l . ·		/cds=(102,3572) /gb=NM_004244			
:		/gi=19923275 /ug=Hs.74076 /len=4950			
4584	0.012669	Rho-associated, coiled-coil containing	NM_005406	Hs.17820	NP_005397
	•	protein kinase 1 (ROCK1), mRNA		÷.	
		/cds=(1,4065) /gb=NM_005406			l .
		/gi=4885582 /ug=Hs.17820 /len=4065		·	
4590	0.016031	zinc finger protein 106 (ZFP106), mRNA	NM_022473	Hs.15220	NP_071918
		/cds=(336,5987) /gb=NM_022473			
		/gi=11968022 /ug=Hs.15220 /len=10487			
4595	0.027906	wc09c01.x1 NCI_CGAP_Pr28 cDNA	Al674177	Hs.200089	
·		clone IMAGE:2314656 3' similar to			
		gb:J05016 PROTEIN DISULFIDE			
		ISOMERASE-RELATED PROTEIN			÷ ,
		PRECURSOR mRNA sequence			
•	ł i	/clone=IMAGE:2314656 /clone_end=3')· 		
		/gb=Al674177 /gi=4874657			
		/ug=Hs.200089 /len=526			
4614		sperm antigen-36	AF187554		
4634	0.034378	DNAJ domain-containing (MCJ), mRNA	NM_013238	Hs.45105	NP_037370
1 4		/cds=(424,876) /gb=NM_013238		l'	
		/gi=7019452 /ug=Hs.45105 /len=1074			
,					
4661	0.005206	cDNA FLJ30561 fis, clone	AK055123	Hs 153618	
		BRAWH2004580. /gb=AK055123			
		/gi=16549782 /ug=Hs.153618 /len=2115		en en en en en en en en en en en en en e	
45.5	0.00=0.00		A1/05053	0.6555	
4668	0.027906	cDNA FLJ31439 fis, clone	AK056001	Hs.349656	
l		NT2NE2000707 /gb=AK056001]
		/gi=16550873 /ug=Hs.349656 /len=2009	ĺ .		1
			N		
4680	0.011228	U4/U6-associated RNA splicing factor	NM_004698	Hs.11776	NP_004689
	1	(HPRP3P), mRNA /cds=(73,2124)			
		/gb=NM_004698 /gi=4758555			
1 2 2 2	0.005	/ug=Hs.11776 /len=2344	NIA 000555	11 (10000	ND 00054
4689	0.025072	t-complex-associated-testis-expressed	NM_006520	Hs.446392	NP_006511
		1-like (TCTE1L), mRNA /cds=(69,419)	1, 1,	1	
1		/gb=NM_006520 /gi=5730086		1	
	- K	/ug=Hs.446392 /len=2156] :.
	<u> </u>		L	L	<u> </u>

Spot	p-valu	Description	Gene Accession	Unigene Accession	Protein Accession
4798	0.022495	Rho-associated, coiled-coil containing	No. NM 004850	No. Hs.58617	No. NP 004841
4/90	0.022465	protein kinase 2 (ROCK2), mRNA	141VI_004650	ITIS. 300 17	INF_004641
		/cds=(455,4621) /gb=NM_004850			
4000	0.000405	/gi=6633807 /ug=Hs.58617 /len=6409	NIM 016120	Un CC71	ND 057012
4800	0.022465	COP9 constitutive photomorphogenic	NM_016129	Hs.6671	NP_057213
		subunit 4 (Arabidopsis) (COPS4),			
1		mRNA /cds=(7,1224) /gb=NM_016129			1
4004	0.040040	/gi=7705844 /ug=Hs.6671 /len=1613	NINA 004720	11- 77004	ND 004704
4821	0.042048	eukaryotic translation termination factor	NM_004730	Hs.77324	NP_004721
		1 (ETF1), mRNA /cds=(136,1449)	r ,	in the second	
		/gb=NM_004730 /gi=4759033			
1055	0.040040	/ug=Hs.77324 /len=3653	VM 040400		ļ
4855		KIAA0795 protein(KIAA0795), mRNA	XM_016166	11- 205 500	ND 440400
4873	0.01/98	LAT1-3TM protein (LAT1-3TM), mRNA	NM_031211	Hs.325520	NP_112488
· .		/cds=(80,622) /gb=NM_031211			
1		/gi=13654279 /ug=Hs.325520 /len=2114			
1000			1111 00000	470070	ND 000070
4992	0.034378	tissue factor pathway inhibitor	NM_006287	Hs.170279	NP_006278
	,*	(lipoprotein-associated coagulation		•	
	,	inhibitor) (TFPI), mRNA /cds=(1,915)		Ì	1
		/gb=NM_006287 /gi=6715569			
		/ug=Hs.170279 /len=915			
5033	0.031002	actin related protein 2/3 complex,	NM_152862	Hs.83583	NP_690601
		subunit 2, 34kDa (ARPC2), transcript			
}	1	variant 1, mRNA /cds=(113,1015)			
1		/gb=NM_152862 /gi=23238210			
\		/ug=Hs.83583 /len=1462			
5072	0.008765	actin binding LIM protein 2 (ABLIM2),	NM_032432	Hs.25522	NP_115808
1	1	mRNA /cds=(123,1718)	·		
		/gb=NM_032432 /gi=27477050			
<u> </u>	ļ.,	/ug=Hs.25522 /len=3407			l
5082	0.042048	solute carrier family 9 (sodium/hydrogen	NM_004785	Hs.101813	NP_004776
	1	exchanger), isoform 3 regulatory factor		P 3 1 3	1.
		2 (SLC9A3R2), mRNA /cds=(97,1449)		1	
-		/gb=NM_004785 /gi=4759141			
1		/ug=Hs.101813 /len=1600			<u> </u>
		<u> </u>			1
5177	0.031002	eukaryotic translation initiation factor 3,	NM_003750	Hs.154796	NP_003741
'		subunit 10 theta, 150/170kDa			
1.		(EIF3S10), mRNA /cds=(114,4262)		1	
[·		/gb=NM_003750 /gi=4503508			
		/ug=Hs.154796 /len=5256		<u> </u>	1
5183	0.012669	basic transCRiption factor 2 p44	U80017		
1		(btf2p44) gene, partial cds, neuronal	[1	
		apoptosis inhibitory protein (naip) and			
	<u></u>	survival motor neuron protein (smn)	<u> </u>	<u></u>	<u> </u>

Spot	p-value	Description	Gen Acc ssion	Unigene Accession	Protein Accession
			No.	No.	No.
5184	0.016031		NM_023039	Hs.239154	NP_075526
·		2 (ANKRA2), mRNA /cds=(648,1589)	,		
		/gb=NM_023039 /gi=21362082			
		/ug=Hs.239154 /len=2048		F	
5188	0.020126	p53R2 mRNA for ribonucleotide	AB036063	Hs.94262	
		reductase, complete cds.			
		/cds=(245,1300) /gb=AB036063		4,	
		/gi=7229085 /ug=Hs 94262 /len=4955			
5204	0.020126	stathmin-like 3 (STMN3), mRNA	NM_015894	Hs.285753	NP_056978
		/cds=(83,625) /gb=NM_015894	-		_
		/gi=14670374 /ug=Hs.285753 /len=2255	,	•	
``				7	
5246	0.04638	cNA sequence (RC2-BT0389-010400-	BE069597		NP 001675
la t		013-e04 BT0389)			[-
5267	0.034378	RNA binding motif protein 6 (RBM6),	NM 005777	Hs.173993	NP 005768
		mRNA /cds=(134,3505)			_ ′
**		/gb=NM_005777 /gi=5032032			
		/ug=Hs.173993 /len=3639			
5273	0.014265	mRNA; cDNA DKFZp434A163 (from	AL110218	Hs.127401	
		clone DKFZp434A163); partial cds			
·.		/cds=(1,4964) /gb=AL110218	1.7°		
		/gi=5817150 /ug=Hs.127401 /len=5084			
	F (1)	9		}	
5279	0.031002	paternally expressed 10 (PEG10),	NM 015068	Hs.137476	NP 055883
· ·		mRNA /cds=(118,1095)			T -
		/gb=NM_015068 /gi=14149662			
		/ug=Hs.137476 /len=6253			1 .
5320	0.025072	mRNA; cDNA DKFZp564O0122 (from	AL049951	Hs.22370	
-		clone DKFZp564O0122) /gb=AL049951			
٩	,	/gi=4884198 /ug=Hs.22370 /len=1727	j		
					:
5328	0.011228	CDC20 cell division cycle 20 (S.	NM 001255	Hs.82906	NP_001246
		cerevisiae) (CDC20), mRNA			
		/cds=(111,1610) /gb=NM_001255		, i	
		/gi=4557436 /ug=Hs.82906 /len=1686			
5349	0.042048	peroxisome receptor 1 (PXR1), mRNA	NM 000319	Hs.158084	NP 000310
·	· .	/cds=(52,1947) /gb=NM_000319	_		,
		/gi=21361203 /ug=Hs.158084 /len=3227			
5388	0.016031	peroxiredoxin 1 (PRDX1), mRNA	NM_002574	Hs.180909	NP_002565
]		/cds=(61,660) /gb=NM_002574]] -
, *		/gi=4505590 /ug=Hs.180909 /len=937			
5394	0.005949	hypothetical protein FLJ11294	NM 018383	Hs.107000	NP_060853
		(FLJ11294), mRNA /cds=(160,4170)			
		/gb=NM_018383 /gi=19923528			ļ
		/ug=Hs.107000 /len=4602			

Spot	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
5399	0.042048	cyclin-dependent kinase inhibitor 1B	No. NM 004064	No. Hs.238990	No. NP_004055
5599	0.042040		NIVI_004004	118.230990	NF_004055
-		(p27, Kip1) (CDKN1B), mRNA /cds=(466,1062) /gb=NM 004064			
					·
,	*	/gi=17978497 /ug=Hs.238990 /len=2422			* **
5400	0.042048	dUTP pyrophosphatase (DUT), mRNA	NM_001948	Hs.367676	NP_001939
}.		/cds=(20,514) /gb=NM_001948	÷	,	
	! !?	/gi=21361335 /ug=Hs.367676 /len=1816		era i	
5414	0.027906	mRNA; cDNA DKFZp313L1834 (from	AL832699	Hs.336446	
		clone DKFZp313L1834) /gb=AL832699			
		/gi=21733278 /ug=Hs.336446 /len=2883			
				·	
5426	0.04638	Hypothetical protein(cDNA: FLJ23458	AK027111		NP_000976
		fis, clone HSI07327)			
5428	0.042048	proteasome (prosome, macropain)	NM_002799	Hs.433434	NP_002790
		subunit, beta type, 7 (PSMB7), mRNA			
		/cds=(18,851) /gb=NM_002799		ing the second	
		/gi=23110926 /ug=Hs.433434 /len=1012			
,					
5453	0.031002	nuclear factor (erythroid-derived 2)-like	NM_006164	Hs.155396	NP_006155
		2 (NFE2L2), mRNA /cds=(114,1931)			1
		/gb=NM_006164 /gi=20149575		1	
		/ug=Hs.155396 /len=2439			
5489	0.027906	DKFZP566H073 protein	NM_015528	Hs.7158	NP_056343
		(DKFZP566H073), mRNA			·.
		/cds=(450,1502) /gb=NM_015528			,
		/gi=14149701 /ug=Hs.7158 /len=1723			•
5505	0.027906	SECIS binding protein 2 (SBP2), mRNA	NM_024077	Hs.288141	NP_076982
		/cds=(58,2622) /gb=NM_024077			
1	1	/gi=21359954 /ug=Hs.288141 /len=3457			1
5519	0.012669	solute carrier family 4, sodium	NM_003615	Hs.132904	NP_003606
		bicarbonate cotransporter, member 7			·
1		(SLC4A7), mRNA /cds=(72,3716)			
		/gb=NM_003615 /gi=19923175			
		/ug=Hs.132904 /len=7785		<u> </u>	
5522	0.031002	transcription elongation factor B (SIII),	NM_007108	Hs.172772	NP_009039
1		polypeptide 2 (18kDa, elongin B)			
		(TCEB2), mRNA /cds=(1,357)		,	
* .		/gb=NM_007108 /gi=6005889			
		/ug=Hs.172772 /len=357			
5525	0.042048	tuftelin interacting protein 11 (TFIP11),	NM_012143	Hs.20225	NP_036275
		mRNA /cds=(264,2777)		1	
		/gb=NM_012143 /gi=8393258		1	
	<u> </u>	/ug=Hs.20225 /len=3565	L	L	

r	Spot	p-value	Description	Gene	Unigene	Protein
				Acc ssion	Accession	Accession
L		,		No	No.	No.
ſ	5529	0.031002	SWI/SNF related, matrix associated,	NM_003077	Hs.250581	NP_003068
ŀ			actin dependent regulator of chromatin,		-	
		L. 41	subfamily d, member 2 (SMARCD2),]
			mRNA /cds=(423,1850)			
1			/gb=NM_003077 /gi=21264350			
L	· · · · · · · · · · · · · · · · · · ·		/ug=Hs.250581 /len=2704			
l	5560	0.04638	insulin-like growth factor 2 receptor	NM_000876	Hs.76473	NP_000867
1	,		(IGF2R), mRNA /cds=(148,7623)	:		
1		4	/gb=NM_000876 /gi=4504610	1		1
-	5500	0.004070	/ug=Hs.76473 /len=9090	N/14 000400	11- 00004	NE 000400
١	5562	0.034378	high-mobility group box 2 (HMGB2),	NM_002129	Hs.80684	NP_002120
1			mRNA /cds=(191,820) /gb=NM_002129		• •	}
١		•	/gi=14141173 /ug=Hs.80684 /len=1277	•		
H	5596	0.01709	CDA02 protein (CDA02), mRNA	NM 032025	Hs.332404	NP 114414
I	3330	0.01730	/cds=(3,1832) /gb=NM_032025	14141_032023	15.55240 4	- -
1			/gi=14042940 /ug=Hs.332404 /len=2179	l.•		1
			14042040 /ug=113.002404 /icit=2173			
ŀ	5605	0.027906	GABA(A) receptor-associated protein-	NM_007285	Hs.6518	NP 009216
١		9.02,000	like 2 (GABARAPL2), mRNA	, <u>-</u> 00, 200		
1			/cds=(137,490) /gb=NM 007285		* +*	·
ł	-		/gi=27374999 /ug=Hs 6518 /len=1031			}
t	5665	0.020126	golgi associated, gamma adaptin ear	NM_138619	Hs.87726	NP_619525
Ì			containing, ARF binding protein 3			-
١			(GGA3), transcript variant long, mRNA			
1			/cds=(10,2181) /gb=NM_138619	,		[[
ļ	•		/gi=20336266 /ug=Hs.87726 /len=3860] .]
L						·
L	5827		PHKB gene (exon 25)	X84930		
I	5905	0.020126	protein phosphatase 2 (formerly 2A),	NM_002718	Hs.28219	NP_002709
ł		·	regulatory subunit B", alpha		1	
			(PPP2R3A), mRNA /cds=(505,3957)			
İ	*		/gb=NM_002718 /gi=19923228			
ŀ	FOOC	0.020054	/ug=Hs.28219 /len=5217	DE227126	Hs.398001	
	5906	0.038054	602034564F1 NCI_CGAP_Brn64 cDNA clone IMAGE:4182759 5', mRNA	DE 337 30	1 15.350001	[.
-			sequence /clone=IMAGE:4182759		1	.
١		,	/clone_end=5' /gb=BF337136		1 %	
1			/gi=11283240 /ug=Hs.398001 /len=1223		· .	
1			19. 1.2002-10.4g 113.00000171cH=1220		· ·	
ł	5934	0.012669	enthoprotin (ENTH), mRNA	NM 014666	Hs.132853	NP 055481
	550.7		/cds=(102,1979) /gb=NM_014666			
1			/gi=7661967 /ug=Hs.132853 /len=3336		[·	
ļ]			
ļ	5986	0.006784	zinc finger and BTB domain containing	NM_014950	Hs.372699	NP_055765
			1 (ZBTB1), mRNA /cds=(263,2197)		· ,	-
		'	/gb=NM_014950 /gi=7662437			
l			/ug=Hs.372699 /len=3990	l	1	

Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
	0.000.00	EL TEMPOS	No.	No.	No.
6026	0.022485	fibromodulin (FMOD), mRNA	NM_002023	Hs.230	NP_002014
		/cds=(21,1151) /gb=NM_002023			
	0.00770	/gi=5016093 /ug=Hs.230 /len=2863			
6040	0.00772	von Hippel-Lindau binding protein 1	NM_003372	Hs.198307	NP_003363
	,	(VBP1), mRNA /cds=(211,804)		 	1
		/gb=NM_003372 /gi=21614497			
0405	0.04000	/ug=Hs.198307 /len=1778	NA 000704	11 10500	100 00000
6125	0.04638	Sjogren's syndrome nuclear autoantigen	NIVI_003731	Hs.18528	NP_003722
		1 (SSNA1), mRNA /cds=(47,406)			ŀ
40		/gb=NM_003731 /gi=4505324			
	2 2 2 2 2 2	/ug=Hs.18528 /len=865			
6127	0.006784	zinc finger protein 76 (expressed in	NM_003427	Hs.29222	NP_003418
		testis) (ZNF76), mRNA /cds=(215,1927)	S		
		/gb=NM_003427 /gi=21361145			11
		/ug=Hs.29222 /len=2680	,		
0400	0.044005	S	NIN 000400	1	1000000
6128	0.014265	Rab acceptor 1 (prenylated) (RABAC1),	NM_006423	Hs.11417	NP_006414
٠.		mRNA /cds=(31,588) /gb=NM_006423			
	- , ,	/gi=5453959 /ug=Hs.11417 /len=770			
0404	0.040004	NASIL	NIV 04 4000	11 04547	055007
6131	0.016031	NADH dehydrogenase (ubiquinone) 1	NM_014222	Hs.31547	NP_055037
!		alpha subcomplex, 8, 19kDa (NDUFA8),	j		- 1
į l		mRNA /cds=(68,586) /gb=NM_014222		,	
	'	/gi=7657368 /ug=Hs.31547 /len=700			
6135	0.005206	cyclin-dependent kinase 4 (CDK4),	NM 000075	Hs.95577	NP 443710
0133	0.003200	transcript variant 1, mRNA	111101_000073	118.93377	NF_445/10
		/cds=(228,1139) /gb=NM_000075			
1] .	/gi=16936531 /ug=Hs.95577 /len=1474			
*.		/g =10930331 /ug=115.93377 /left=1474 			
6137	0.038054	developmentally regulated GTP binding	NM 001388	Hs.78582	NP_001379
0137	0.000004	protein 2 (DRG2), mRNA	111111_001000	1113.70002	_001373
•		/cds=(65,1159) /gb=NM_001388			
	* .	/gi=23065518 /ug=Hs.78582 /len=1897	:		
)))	
6143	0.035996	mRNA, cDNA DKFZp686G1167 (from	AL833600	Hs.7720	NP 001367
		clone DKFZp686G1167) /gb=AL833600			
		/gi=21734246 /ug=Hs.7720 /len=8355			
1			1	1	1
6180	0.038054	mRNA for KIAA0774 protein, partial cds.	AB018317	Hs.22201	<u> </u>
		/cds=(1,3492) /gb=AB018317			
1		/gi=3882268 /ug=Hs.22201 /len=4021			
6215	0.027906	splicing factor, arginine/serine-rich 2	NM_003016	Hs.73965	NP_003007
		(SFRS2), mRNA /cds=(156,821)	J =] -
		/gb=NM_003016 /gi=4506898		· .	
}		/ug=Hs.73965 /len=1879		J.	1.
6227	0.027906	splicing factor, arginine/serine-rich 4	NM_005626	Hs.76122	NP_005617
<u> </u>		(SFRS4), mRNA /cds=(107,1591)	1 -	1	
			i .	i	
		/gb=NM_005626 /gi=21361281	! .		

Spot	p-value	D scription	Gene	Unigene	Protein
			Accession	Accession	Accession
		<u></u>	No.	No.	No.
6230	0.029136	nudix (nucleoside diphosphate linked	NM_019094	Hs.355399	NP_061967
	, ,	moiety X)-type motif 4 (NUDT4), mRNA			
		/cds=(191,736) /gb=NM_019094			
		/gi=24432097 /ug=Hs.355399 /len=3652			
6256	0.020126	ribonuclease, RNase A family, 4	NM_002937	Hs.283749	NP_002928
1.		(RNASE4), mRNA /cds=(173,616)			}
		/gb=NM_002937 /gi=20070170			1
		/ug=Hs.283749 /len=1414		· .	
6263	0.034378	down-regulated in metastasis (DRIM),	NM_014503	Hs.178614	NP_055318
		mRNA /cds=(145,8502)			
		/gb=NM_014503 /gi=7657040			
		/ug=Hs.178614 /len=9017			
6307	0.035996	cDNA FLJ37296 fis, clone	AK094615	Hs.4983	1
		BRAMY2015420. /gb=AK094615			
·		/gi=21753707 /ug=Hs.4983 /len=3181			
6316		KIAA1046 protein (KIAA1046)	NM_014928		
6324	0.025072	SR rich protein (DKFZp564B0769),	NM_032870	Hs.18368	NP_116259
		mRNA /cds=(33,2450) /gb=NM_032870			
1	e 1	/gi=18699723 /ug=Hs 18368 /len=2663			
6325	0.027906	AT-binding transcription factor 1	NM_006885	Hs.101842	NP_008816
		(ATBF1), mRNA /cds=(674,11785)			
-	!	/gb=NM_006885 /gi=19923286			
		/ug=Hs.101842 /len=11893			
6347		mitochondrion, complete genome	NC_001807		
6367	0.01798	growth arrest-specific 1 (GAS1), mRNA	NM_002048	Hs.65029	NP_002039
		/cds=(411,1448) /gb=NM_002048			
		/gi=4503918 /ug=Hs.65029 /len=2828			1 1 1
6378	0.04638	signal peptidase complex (18kD)	NM_014300	Hs.9534	NP_055115
		(SPC18), mRNA /cds=(78,617)			1
,		/gb=NM_014300 /gi=7657608			
		/ug=Hs.9534 /len=1105			
6387	0.031002	epithelial protein lost in neoplasm beta	NM_016357	Hs.10706	NP_057441
	<u> </u>	(EPLIN), mRNA /cds=(102,2381)]]
		/gb=NM_016357 /gi=7705372			
0.440		/ug=Hs.10706 /len=3655	10000000	1000	115 0000/0
6419	0.016031	RNA helicase family (RNAH), mRNA	NM_006828	Hs.48295	NP_006819
	}	/cds=(39,6647) /gb=NM_006828			
ļ ·	:	/gi=24307916 /ug=Hs.48295 /len=7315			
6400	0.040000	non 2 numerons of slope (O -larger)	NIM COZOZO	Un 104245	ND 024200
6422	1 0.012669	soc-2 suppressor of clear (C. elegans)	NM_007373	Hs.104315	NP_031399
•		(SHOC2), mRNA /cds=(278,2026)			(
١.		/gb=NM_007373 /gi=6677944			
0400	0.0040=0	/ug=Hs.104315 /len=3872	NIM 000700	11- 75 447	ND 000770
6466	J U.U34378	ralA binding protein 1 (RALBP1), mRNA	NM_006788	Hs.75447	NP_006779
		/cds=(78,2045) /gb=NM_006788			
l .		/gi=21361362 /ug=Hs.75447 /len=4230]
	<u></u>	<u> </u>	<u>L </u>		1

C-			Bassing	Con	Unigene	Protein
2b	ot	p-value	Description	Gen	-	
[.	ĺ			Accession	Accession	Accession
				No.	No.	No.
646	38		reverse transcriptase related protein	1207289A		1207289A
647	71	0.042048	hydroxysteroid (11-beta)	NM_005525	Hs.275215	NP_005516
1			dehydrogenase 1 (HSD11B1), mRNA			,
			/cds=(95,973) /gb=NM_005525			
	* 4		/gi=5031764 /ug=Hs.275215 /len=1375	¥ - ++		
1	- 1					
64	77	0.012669	NIMA (never in mitosis gene a)-related	AL080111	Hs.24119	NP_598001
			kinase 7, DKFZp586G2222 (from clone			_
		100	DKFZp586G2222) (AL080111.1)]
649	98	0.006784	keratinocyte, normal	U33270	-	1 1 1 1 1 1 1
660			mitogen-activated protein kinase 14	NM 139012	Hs.79107	NP 620583
"	77.	0.927000	(MAPK14), transcript variant 2, mRNA			
1			/cds=(363,1445) /gb=NM_139012		1	
1			/gi=20986511 /ug=Hs.79107 /len=3757	in a second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of t		
1	. :				1	}
CC	00	0.020054	fibroblast growth factor 2 (basic)	NM_002006	Hs.284244	NP_001997
66	บษ	0.036034		14141_002000	ns.204244	1116 _00 1997
			(FGF2), mRNA /cds=(302,934)		1	
'	٠,		/gb=NM_002006 /gi=15451897			
<u> </u>	4.0		/ug=Hs.284244 /len=6802	D0005045		-
66	10	0.027906	Similar to RIKEN cDNA 3830613O22	BC035645	Hs.356876	
			gene, clone IMAGE:5551209, mRNA,	1.		
1 -	' :		partial cds /cds=(282,4079)		1.5	
			/gb=BC035645 /gi=23272851			
			/ug=Hs.356876 /len=4079			
66	40	0.034378	c6.1A (C6.1A), mRNA /cds=(3,953)	NM_024332	Hs.301927	NP_077308
			/gb=NM_024332 /gi=13236582			
			/ug=Hs.301927 /len=2846			
67	14	0.025072	chromosome 20 open reading frame 43	NM_016407	Hs.182281	NP_057491
1			(C20orf43), mRNA /cds=(71,991)			
			/gb=NM_016407 /gi=7705482		5	
	13		/ug=Hs.182281 /len=1639			
67	15	0.038054	KIAA0076 gene product (KIAA0076),	NM 014780	Hs.51039	NP_055595
	·		mRNA /cds=(87,5183) /gb=NM_014780	-		
			/gi=7661893 /ug=Hs.51039 /len=5253			
67	18	0.022485	nucleoporin 210 (NUP210), mRNA	NM 024923	Hs.270404	NP_079199
)	. •		/cds=(84,5747) /gb=NM_024923			
	*		/gi=27477133 /ug=Hs.270404 /len=7191			
}			191 21-11 100 10g-113.210-10-11011-1191	- 		
67	22	0.022/85	syndecan 1 (SDC1), mRNA	NM 002997	Hs.82109	NP 002988
1 "	~~	0.022400	/cds=(253,1185) /gb=NM_002997	1 1111_002331	13.52 109	14 _002300
			//gi=21359855 /ug=Hs.82109 /len=2484			
			//gi-2 1505000 /ug-115.02 105 /iefi-2404			
60	26	0.025072	UI-E-DW1-ahd-d-13-0-UI.s1 UI-E-DW1	BU737702	Hs.405983	
1 00	36	0.0250/2		BU/3//UZ	IUS:405909	
1			cDNA clone UI-E-DW1-ahd-d-13-0-UI		1	
			3', mRNA sequence /clone=UI-E-DW1-			
			ahd-d-13-0-UI /clone_end=3'	,		
1 .			/gb=BU737702 /gi=23673914			
· L		<u> </u>	/ug=Hs.405983 /len=1215	<u> </u>	1	1

Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
	·		No.	No.	No.
6847	0.031002	tropomodulin 3 (ubiquitous) (TMOD3),	NM_014547	Hs.22826	NP_055362
		mRNA /cds=(66,1124) /gb=NM_014547		,	
		/gi=7657648 /ug=Hs.22826 /len=2072			
2050	0.010010	Diver 10 1/200 (5			ND 050470
6853	0.042048	DKFZp434K098 (from clone	AL133112		NP_653172
6000	0.020054	DKFZp434K098); partial cds	NINA 042404	112 2000	ND OOCEAR
6898	0.036054	plexin B2 (PLXNB2), mRNA /cds=(26,1438) /gb=NM_012401	NM_012401	Hs.3989	NP_036533
		/gi=20270189 /ug=Hs.3989 /len=2175			
6908	0.00772	thymus expressed gene 3-like	NM 145056	Hs.134185	NP 659493
	0.00712	(MGC15476), mRNA /cds=(441,1655)	140000	11.5.10-1100	111 _505,450
		/gb=NM_145056 /gi=21450823			
		/ug=Hs.134185 /len=2544	1		
6942	0.020126	eukaryotic translation elongation factor	NM 001402	Hs.422118	NP 001393
		1 alpha 1 (EEF1A1), mRNA			_
		/cds=(63,1451) /gb=NM_001402			
. *		/gi=25453469 /ug=Hs.422118 /len=1837			
7003	0.004545	histocompatibility (minor) 13 (HM13),	NM_030789	Hs.386538	NP_848697
		mRNA /cds=(86,1219) /gb=NM_030789		- 3:	
-		/gi=23308606 /ug=Hs 386538 /len=1584			a ,
7041	0.012660	overstored hinding protein like 1.0	NM 080597	Us 050746	ND 570000
7041	0.012009	oxysterol binding protein-like 1A (OSBPL1A), transcript variant	NIVI_U0U597	Hs.252716	NP_579802
		OSBPL1A), transcript variant OSBPL1B, mRNA /cds=(175,3027)			
		/gb=NM_080597 /gi=19718740			
		/ug=Hs.252716 /len=4165			
7048	0.038054	twisted gastrulation 1 (Drosophila)	NM_020648	Hs.247302	NP 065699
• .*		(TWSG1), mRNA /cds=(106,777)	-]	_
		/gb=NM_020648 /gi=21314788			
<u> </u>		/ug=Hs.247302 /len=3693			
7064	0.020126	mitochondrial ribosomal protein L18	NM_014161	Hs.23038	NP_054880
		(MRPL18), nuclear gene encoding		1.	
		mitochondrial protein, mRNA			e de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de l
ĺ		/cds=(123,665) /gb=NM_014161	la de la companya de la companya de la companya de la companya de la companya de la companya de la companya de	[
7000	0.00770	/gi=21265079 /ug=Hs.23038 /len=989	NNA 004060	110 04746	ND: 004260
7092	0.00 <i>[]</i>	chromosome condensation 1 (CHC1), mRNA /cds=(287,1552)	NM_001269	Hs.84746	NP_001260
ļ· .		/gb=NM_001269 /gi=20149512			
		/ug=Hs.84746 /len=2559			
7103	0.042048	sialidase 1 (lysosomal sialidase)	NM 000434	Hs.118721	NP 000425
		(NEU1), mRNA /cds=(130,1377)]
		/gb=NM_000434 /gi=4557790			
		/ug=Hs.118721 /len=1894			
7112	0.027906	ubiquitination factor E4A (ÚFD2 yeast)	NM_004788	Hs.75275	NP_004779
		(UBE4A), mRNA /cds=(73,3294)			
		/gb=NM_004788 /gi=4759287	7	1	
	<u> </u>	/ug=Hs.75275 /len=6060		<u> </u>	

Spot	p-value	Description	Gene	Unigene	Protein
	*		Accession	Accession	Accession
- 105	0.044000		No.	No.	No.
7127	0.011228	actin-related protein 10 (S. cerevisiae)	NM_018477	Hs.274369	NP_060947
		(ACTR10), mRNA /cds=(81,1334)			
ļ		/gb=NM_018477 /gi=8923711			
	2 2 1 2 2 2	/ug=Hs.274369 /len=1621			
7143	0.04638	benzodiazapine receptor (peripheral)	NM_000714	Hs.202	NP_009295
		(BZRP), nuclear gene encoding			,
		mitochondrial protein, transcript variant		1	1
		PBR, mRNA /cds=(88,597)			
		/gb=NM_000714 /gi=21536444			
74.47	0.000054	/ug=Hs.202 /len=848	D0000477	11 101771	
7147	0.038054	UI-1-BB1p-aki-h-05-0-UI.s1	BQ022477	Hs.424771	-
j .		NCI_CGAP_PI6 cDNA clone UI-1-BB1p-	- 3		
		akl-h-05-0-UI 3', mRNA sequence			1
	ļ	/clone=UI-1-BB1p-akl-h-05-0-UI		}	
	1.7	/clone_end=3' /gb=BQ022477 /gi=19757756 /ug=Hs.424771 /len=1598			
1		/g =197577567ug=H\$.4247717len=1598 		1	1
7203	0.034003	KIAA1036 protein (KIAA1036), mRNA	NM 014909	Hs.155182	NP 055724
1203	0.031002	/cds=(386,1483) /gb=NM_014909	14909	ПS. 155162	INP_055/24
		/gi=7662453 /ug=Hs.155182 /len=5481			
		/g =700240374g=FIS.1001027left=0461 	*.		. !
7204	0.031002	chromosome 20 open reading frame 98	NM 024958	Hs.286128	NP 079234
1204	0.001002	(C20orf98), mRNA /cds=(134,748)	14101_024330	113.200120	141 _07 3234
		/gb=NM_024958 /gi=13376446		,	
	· .	/ug=Hs.286128 /len=2042			
7205	0.042048	ribosomal protein S20 (RPS20), mRNA	NM 001023	Hs.8102	NP 001014
		/cds=(128,487) /gb=NM_001023			
		/gi=14591915 /ug=Hs.8102 /len=539			
				,	
7250	0.038054	hemoglobin, gamma G (HBG2), mRNA	NM_000184	Hs.386655	NP 000175
		/cds=(54,497) /gb=NM_000184	7		-
		/gi=28302132 /ug=Hs 386655 /len=583			
			,		
7292	0.025072	synaptic nuclei expressed gene 1	NM_015293	Hs.192102	NP_598411
		(SYNE-1), transcript variant beta,			
5		mRNA /cds=(121,10086)			1
		/gb=NM_015293 /gi=19526752			. !
		/ug=Hs.192102 /len=10742			
7322		BM-017 (=ALEX3)	AF208859		NP_808817
7349	0.027906	dermatopontin (DPT), mRNA	NM_001937	Hs.80552	NP_001928
		/cds=(7,612) /gb=NM_001937			
		/gi=4755134 /ug=Hs.80552 /len=717			
7355	0.038054	hypothetical protein (DKFZp761P2124	AL137441	·	NP_057107
7001	0.001055	clone DKFZp761P2124)	10000000	70000	110 00000
7361	J 0.031002	SWI/SNF related, matrix associated,	NM_003072	Hs.78202	NP_003063
1		actin dependent regulator of chromatin,			
		subfamily a, member 4 (SMARCA4),			
		mRNA /cds=(277,5220)			`
}		/gb=NM_003072 /gi=21071055]
	<u> </u>	/ug=Hs.78202 /len=5681		L	

Spot	p-value	Description	G n	Unigene	Protein
			Accession	Accession	Accession
	0.00=0.00		No.	No.	No.
7366	0.027906	meningioma expressed antigen 5	NM_012215	Hs.5734	NP_036347
		(hyaluronidase) (MGEA5), mRNA			
		/cds=(396,3146) /gb=NM_012215			
		/gi=11024697 /ug=Hs.5734 /len=5147			
7382	0.04638	cortactin binding protein 2 (CORTBP2),	NM_033427	Hs.293539	NP_219499
		mRNA /cds=(93,5084) /gb=NM_033427			
		/gi=16975495 /ug=Hs.293539 /len=5975	, .	}	{
7383	0.042048	mannose receptor, C type 1 (MRC1),	NM_002438	Hs.75182	NP_002429
		mRNA /cds=(104,4474)			
	[·	/gb=NM_002438 /gi=4505244			[
		/ug=Hs.75182 /len=5185			
7398	0.034378	laminin, alpha 2 (merosin, congenital	NM_000426	Hs.75279	NP_000417
	·	muscular dystrophy) (LAMA2), mRNA			
		/cds=(50,9382) /gb=NM_000426	2		
		/gi=4557708 /ug=Hs.75279 /len=9534			
7415	0.04638	hypothetical protein FLJ12619	NM_030939	Hs.7779	NP_112201
	1	(FLJ12619), mRNA /cds=(539,1228)			
		/gb=NM_030939 /gi=21359961			
		/ug=Hs.7779 /len=2444			
7427	0.034378	tropomyosin 3 (TPM3), mRNA	NM_153649	Hs.85844	NP_705935
		/cds=(52,798) /gb=NM_153649		· ·	1
	·	/gi=24119202 /ug=Hs.85844 /len=2089			
7455	0.04638	1-acylglycerol-3-phosphate O-	NM_006412	Hs.209119	NP_006403
		acyltransferase 2 (lysophosphatidic acid			
		acyltransferase, beta) (AGPAT2),			
		mRNA /cds=(67,903) /gb=NM_006412		•	
}		/gi=6041664 /ug=Hs.209119 /len=1522			
		<u> </u>			
7459	0.020126	proteasome (prosome, macropain) 26S	NM_002817	Hs.279554	NP_787128
l · ·		subunit, non-ATPase, 13 (PSMD13),	-	1	
1 .		mRNA /cds=(70,1200) /gb=NM_002817			
i		/gi=4506222 /ug=Hs.279554 /len=1584		-	
					··
7461	0.020126	dipeptidase 1 (renal) (DPEP1), mRNA	NM_004413	Hs.109	NP_004404
[/cds=(296,1531) /gb=NM_004413	1		
		/gi=4758189 /ug=Hs 109 /len=1738			
7466	0.00772	ret finger protein (RFP), transcript	NM_006510	Hs.142653	NP_112212
j	Į.	variant alpha, mRNA /cds=(359,1900)			1
1		/gb=NM_006510 /gi=17105396			
j.	,	/ug=Hs.142653 /len=2984			<u> </u>
7495	0.034378	CASP8 and FADD-like apoptosis	NM_003879	Hs.195175	NP_003870
1		regulator (CFLAR), mRNA		1	-
		/cds=(482,1924) /gb=NM_003879			
		/gi=21361768 /ug=Hs 195175 /len=2243			
		19. = . =	1	1	

Spot	p-value	Description	Gene	Unigene	Protein
	·		Accession	Acc ssion	Accession
			No.	No.	No.
7514	0.04638	cDNA FLJ35055 fis, clone	AK092374	Hs.349303	
*		OCBBF2018563. /gb=AK092374			
]. 	/gi=21750952 /ug=Hs.349303 /len=3817			
			<u> </u>		
7517	0.00772	deoxyguanosine kinase (DGUOK),	NM_080916	Hs.432811	NP_550440
		transcript variant 1, nuclear gene	•		-
*		encoding mitochondrial protein, mRNA			
		/cds=(86,919) /gb=NM_080916			
		/gi=18426966 /ug=Hs.432811 /len=1144			
7522	0.016031	TH1-like (Drosophila) (TH1L), mRNA	NM_016397	Hs.5184	NP_057481
		/cds=(8,1429) /gb=NM_016397			
		/gi=7705462 /ug=Hs.5184 /len=2130			
7532	0.04638	a disintegrin and metalloproteinase	NM_025220	Hs.173716	NP_694882
		domain 33 (ADAM33), transcript variant			
-		1, mRNA /cds=(88,2529)	٠		
		/gb=NM_025220 /gi=24041037			
		/ug=Hs.173716 /len=3594	<u> </u>		
7544	0.039654	oxysterol binding protein-like 10	NM_017784	Hs.321622	NP_060254
}	}	(OSBPL10), mRNA /cds=(382,2676)	}	}	}
		/gb=NM_017784 /gi=23111057	· · ·	<u>'</u>	
: <u>-</u>		/ug=Hs.321622 /len=3938		***	
7549	0.00772	cDNA: FLJ21552 fis, clone COL06322.	AK025205	Hs.6634	
		/gb=AK025205 /gi=10437670			
		/ug=Hs.6634 /len=2045			
7550	0.00772	hypothetical protein FLJ20343	NM_017775	Hs.252692	NP_060245
		(FLJ20343), mRNA /cds=(19,1524)			
		/gb=NM_017775 /gi=22547158			
		/ug=Hs.252692 /len=2784			
7551	0.025072	hypothetical protein FLJ11021 similar to	NM_023012	Hs.81648	NP_075388
١,	;	splicing factor, arginine/serine-rich 4		}	
		(FLJ11021), mRNA /cds=(767,1375)			
		/gb=NM_023012 /gi=20127619			
		/ug=Hs.81648 /len=1878			<u> </u>
7552	0.006784	interferon, alpha-inducible protein (clone	NM_005101	Hs.432233	NP_005092
ŀ		IFI-15K) (G1P2), mRNA /cds=(76,573)			
		/gb=NM_005101 /gi=4826773	ĺ		
		/ug=Hs.432233 /len=634			
7574	0.023403	ubiquitin-conjugating enzyme E2N	NM_003348	Hs.75355	NP_003339
	-	(UBC13 yeast) (UBE2N), mRNA			
	1.	/cds=(64,522) /gb=NM_003348			
		/gi=4507792 /ug=Hs.75355 /len=1203	<u> </u>		<u></u>
7613	0.034378	thymosin, beta 4, X chromosome	NM_021109	Hs.75968	NP_066932
1	1.	(TMSB4X), mRNA /cds=(78,212)			
		/gb=NM_021109 /gi=11056060			
		/ug=Hs.75968 /len=556		<u> </u>	<u></u>

Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession No.	Accession No.
7620	0.027906	UI-H-EI0-ayf-a-03-0-UI.s1	No. CA447644	Hs.440691	INO.
		NCI_CGAP_EI0 cDNA clone UI-H-EI0-	****	er ·	
		ayf-a-03-0-UI 3', mRNA sequence			
		/clone=UI-H-EI0-ayf-a-03-0-UI			
		/clone_end=3' /gb=CA447644			
		/gi=24812064 /ug=Hs.440691 /len=770			
7628	0.014265	FLJ10287 fis, clone HEMBB1001387	AK001149		NP 061956
7631		mRNA for KIAA0794 protein, partial cds.	AB018337	Hs.127287	-
		/cds=(1,1473) /gb=AB018337			
	200	/gi=3882308 /ug=Hs.127287 /len=4656			
				<u> </u>	
7649	0.031002	cDNA FLJ20709 fis, clone KAIA1124,	AK000716	Hs.24697	
i ·		highly similar to D86324 mRNA for CMP]
		N-acetylneuraminic acid. /gb=AK000716			7 . T
	}	/gi=7020978 /ug=Hs.24697 /len=3488			
7004	0.04000	DVE7-704 M30	NIM OCCOO	11- 45500	ND 445050
7664	0.04638	hypothetical protein DKFZp761J139	NM_032280	Hs.15536	NP_115656
	V	(DKFZp761J139), mRNA			
	Ĺ	/cds=(3155,3970) /gb=NM_032280			
	1	/gi=14150026 /ug=Hs.15536 /len=4635			
7667	0.031002	cDNA FLJ31147 fis, clone	AK055709	Hs.6670	
		IMR322001438. /gb=AK055709			
	1000	/gi=16550504 /ug=Hs.6670 /len=1747			,
7694	0.034378	cDNA FLJ25013 fis, clone CBL01365.	AK057742	Hs.380091	
1 1		/gb=AK057742 /gi=16553667			
· · · · · · · · · · · · · · · · · · ·		/ug=Hs.380091 /len=2200			
7696	0.034378	glycine receptor, beta (GLRB), mRNA	NM_000824	Hs.32973	NP_000815
		/cds=(142,1635) /gb=NM_000824			
,		/gi=24431943 /ug=Hs.32973 /len=2649			
			· · · · · · · · · · · · · · · · · · ·	· ·	
7700	0.00772	mRNA, cDNA DKFZp564B222 (from	AL049974	Hs.100261	1.
		clone DKFZp564B222) /gb=AL049974	-		
		/gi=4884224 /ug=Hs.100261 /len=2315			
7704	0.005949	solute carrier family 35 (CMP-sialic acid	NM 006416	Hs.82921	NP 006407
		transporter), member 1 (SLC35A1),			
r		mRNA /cds=(28,1041) /gb=NM 006416		1	
		/gi=20149579 /ug=Hs.82921 /len=1883			
7715	0.027906	yw32d06.s1 Morton Fetal Cochlea	N22084	Hs.440534	
		cDNA clone IMAGE:253931 3', mRNA			
		sequence /clone=IMAGE:253931			
,		/clone_end=3' /gb=N22084 /gi=1128218		1 1 1 1 1	
		/ug=Hs.440534 /len=230	L	<u> </u>	<u> </u>

Spot	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
77.46	0.000051		No.	No.	No.
7719	0.038054	endothelial differentiation,	NM_057159	Hs.75794	NP_476500
		lysophosphatidic acid G-protein-coupled		-	
		receptor, 2 (EDG2), transcript variant 2,	p.,	} <u>.</u>	
		mRNA /cds=(394,1488)	* 5		
		/gb=NM_057159 /gi=16950637	1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1	S	
		/ug=Hs.75794 /len=2732			
7732	0.014265	hypothetical protein FLJ20265	NM_017733	Hs.7099	NP_060203
٠,		(FLJ20265), mRNA /cds=(40,1854)			
[/gb=NM_017733 /gi=8923239			
		/ug=Hs.7099 /len=2039			
7739	0.009931	hypothetical protein MGC12458	NM_032328	Hs.330664	NP_115704
		(MGC12458), mRNA /cds=(30,518)			2
		/gb=NM_032328 /gi=14150107	, * · · ·		
		/ug=Hs.330664 /len=1026	-		
7740	0.00344	tripartite motif-containing 32 (TRIM32),	NM_012210	Hs.236218	NP_036342
		mRNA /cds=(134,2095)			
		/gb=NM_012210 /gi=15208649		*	
		/ug=Hs.236218 /len=3160	 		
7748	0.031002	Hypothetical protein HSPC232, clone	BC025306	Hs.281428	NP_057572
		IMAGE:4893383, mRNA, partial cds			
		/cds=UNKNOWN /gb=BC025306			
		/gi=19263704 /ug=Hs.281428 /len=3392			
7751	0.012669	Leishmanolysin-like (metallopeptidase	AL565471	Hs.90363	NP_149018
		M8 family), cDNA			_
		/clone=CS0DF004YF03 /gb=AL565471		e, in the second	!
		/gi=12916880 /ug=Hs.90363 /len=1028	· · · · · · · · · · · · · · · · · · ·		
					7.
7755	0.005206	catenin (cadherin-associated protein),	NM_003798	Hs.58488	NP_003789
		alpha-like 1 (CTNNAL1), mRNA	W		
	· . /	/cds=(44,2248) /gb=NM_003798			
:		/gi=4503128 /ug=Hs.58488 /len=2446			
7758	0.020126	mRNA for KIAA0527 protein, partial cds.	AB011099	Hs.196647	
	· / ·	/cds=(1,2308) /gb=AB011099			
:		/gi=3043577 /ug=Hs.196647 /len=5005		100	
					<u> </u> -
7774	0.008765	leucine-rich repeat-containing 5	NM_018103	Hs.44672	NP_060573
1		(LRRC5), mRNA /cds=(917,2965)	<u></u>		
		/gb=NM_018103 /gi=24431980	l:	· ·	i .
		/ug=Hs.44672 /len=3338			
7775		fibronectin gene ED-A region	X07718		-
7791	0.01798	brain cell membrane protein 1 (BCMP1),	NM_031442	Hs:8769	NP_113630
		mRNA /cds=(10,555) /gb=NM_031442			
İ		/gi=13899272 /ug=Hs.8769 /len=3803			·
	004:55	F07/ 100 100 100	<u> </u>	<u> </u>	
7803	0.011228	EST(yi82d03.s1 Soares placenta	R77952		
J	J	Nb2HP clone IMAGE:145733 3'		,	
		gb:D00762 PROTEASOME			
L	L	COMPONENT C8)	<u> </u>	<u> </u>	L

Spot	p-value	Description	G ne	Unigene	Protein
	P		Accession	Accession	Accession
1.			No.	No.	No.
7826	0.022485	yh68a05.s1 Soares placenta Nb2HP	R32301	Hs.386871	
		cDNA clone IMAGE:134864 3', mRNA	• • •		
		sequence /clone=IMAGE:134864			1
		/clone_end=3' /gb=R32301 /gi=788144			
		/ug=Hs.386871 /len=246			
7828	0.025072	BX101939 Soares infant brain 1NIB	BX101939	Hs 269499	
1		cDNA clone IMAGp998C11163, mRNA			
		sequence			
į . ·		/clone=IMAGp998C11163_;_IMAGE:36			1
		364 /gb=BX101939 /gi=27831516	1 1		
ļ		/ug=Hs.269499 /len=493			
7840	0.025072	UI-H-EI1-azh-n-13-0-UI.s1	BQ005547	Hs.445146	
		NCI_CGAP_EI1 cDNA clone			1
		IMAGE:5848908 3', mRNA sequence			
,		/clone=IMAGE:5848908 /clone_end=3'			
1		/gb=BQ005547 /gi=19730447			
7055	0.000405	/ug=Hs.445146 /len=994	A1C20007		ND 000000
7855	0.022485	EST(tz31e10.x1 NCI_CGAP_Ut2 cDNA	AI630897		NP_008993
7865	0.00244	clone IMAGE:2290218 3')	AF086209	· · · · · · · · · · · · · · · · · · ·	ND 050047
7888		hypothetical protein (clone ZC48G09) cDNA FLJ31107 fis, clone	AK055669	Hs.405954	NP_056347
/ 000	0.034376	IMR322000152. /gb=AK055669	AKUSSOOS	FIS.405954]
		/gi=16550452 /ug=Hs.405954 /len=2250			
	1.0	/g = 10000402 /dg=113.400904 /left=2200 			
7896	0.042048	zh21a11.s1	AA722220	Hs.290553	
1.000	0.012010	Soares_pineal_gland_N3HPG cDNA	, , , , , , , , , , , , , , , , , , , ,	1.10.20000	,
		clone IMAGE:412700 3', mRNA	,		
	1	sequence /clone=IMAGE:412700			1
· ·	· .	/clone_end=3' /gb=AA722220] .]
		/gi=2739927 /ug=Hs 290553 /len=342			
7899	0.004545	UI-E-DW0-agk-i-01-0-UI.r1 UI-E-DW0	BM696546	Hs.356149	
		cDNA clone UI-E-DW0-agk-i-01-0-UI 5',			
		mRNA sequence /clone=UI-E-DW0-agk-		}	ł
		i-01-0-UI /clone_end=5' /gb=BM696546	,		
·	· · ·	/gi=19009804 /ug=Hs.356149 /len=1200	i		
7900	0.034378	EST(hi90a11.x1	AW665382		
1		Soares_NFL_T_GBC_S1 clone] .	
7555	1 2 2 2 2 2	IMAGE:2979548 3')	4.000	 	NID (10555
7908	0.04638	EST EST43399 Fetal brain I cDNA 3'	AA338448	1	NP_112577
7040	0.004055	lend	464666	1 1 1 1 1 1 1 1 1	ND 000005
7912	0.031002	EST zx48b06.r1 Soares_testis_NHT	AA454038		NP_060395
		cDNA clone IMAGE:795443 5' similar to			
		contains Alu repetitive element; contains			
		element MER13 repetitive element ;			-
7928	0.005206	hypothetical protein HSPC195	NM 016463	Hs.356509	
1,320	0.003200	(HSPC195), mRNA /cds=(293,889)	14101_010403	113.330008]
		(HSFC 195), HKNA /cds=(295,669) /gb=NM_016463 /gi=20070365		1	ļ
		/ug=Hs.356509 /len=1108	}	1 - 1	
- <u> </u>		rag ris.cocoo non- i roo	L		

Spot	p-value	Description	G ne	Unigene	Protein
•			Accession	Accession	Accession
7950	0.04639	cDNA sequence FLJ13553 fis, clone	No. AK023615	No.	No.
7950	1	PLACE1007454	ANU23015		NP_006818
7958	0.022485	enhancer of rudimentary (Drosophila)	NM_004450	Hs.433413	NP_004441
<u> </u>		(ERH), mRNA /cds=(72,386)			
		/gb=NM_004450 /gi=4758301			
		/ug=Hs.433413 /len=815			
7980	0.034378	splicing factor, arginine/serine-rich 12	NM_139168	Hs.381165	NP_631907
		(SFRS12), mRNA /cds=(342,1868)		la a la companya di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di santa di s	
		/gb=NM_139168 /gi=21040254			
		/ug=Hs.381165 /len=3811			
7981	0.046375	mRNA for KIAA1691 protein, partial cds.	AB051478	Hs.94761	
		/cds=(78,1754) /gb=AB051478			
'		/gi=20521967 /ug=Hs.94761 /len=4816		l	
7005	5 5 15 5 15				
7995	0.042048	lysophospholipase II (LYPLA2), mRNA	NM_007260	Hs.283655	NP_009191
1		/cds=(122,817) /gb=NM_007260			
		/gi=20302149 /ug=Hs.283655 /len=1648			
0004	0.000054	Landing (DNA) L(TOD4) - DNA	NIA 000000	11. 047	ND 000027
8004	0.038054	topoisomerase (DNA) I (TOP1), mRNA	NM_003286	Hs.317	NP_003277
	,	/cds=(247,2544) /gb=NM_003286			~~~
8019	0.020054	/gi=19913404 /ug=Hs.317 /len=3734 CGI-40 protein (CGI-40), mRNA	NM 015996	Hs.33724	ND 057000
0019	0.036034	/cds=(84,2621) /gb=NM _015996	1001012990	TS.33724	NP_057080
		/gi=7705756 /ug=Hs.33724 /len=3146			
8044		chromosome 14 open reading frame 10	NM 017917	Hs.49376	NP_060387
0044	0.042040	(C14orf10), mRNA /cds=(277,1638)	14141_017917	115.43370	NF_000307
		/gb=NM 017917 /gi=8923599		· .	
		/ug=Hs.49376 /len=1781			
8050		hypothetical protein FLJ22557	NM_024713	Hs.106101	NP 078989
		(FLJ22557), mRNA /cds=(87,1001)			
		/gb=NM 024713 /gi=13376012		-	·
		/ug=Hs.106101 /len=2676			
8086	0.038054	transmembrane, prostate androgen	NM 020182	Hs.83883	NP_064567
		induced RNA (TMEPAI), mRNA	_		-
		/cds=(321,1184) /gb=NM_020182	}		} . !
	,	/gi=21361840 /ug=Hs 83883 /len=4839			
			*		
8112	0.034378	ankylosis, progressive (mouse) (ANKH),	NM_054027	Hs.168640	NP_473368
		transcript variant 2, mRNA			[
		/cds=(265,1743) /gb=NM_054027]
		/gi=21536394 /ug=Hs.168640 /len=4031	· ()		
8176	0.020126	Similar to serine threonine protein	BC012085	Hs.8724	NP_009202
		kinase, clone MGC:20014			}
		IMAGE:4554884, mRNA, complete cds			
L'	<u> </u>	(BC012085.1)	<u> </u>	L	

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession No.	Accession No.
8199	0.04638	hypothetical protein MGC18216	NM_152452	Hs.104679	NP_689665
·		(MGC18216), mRNA /cds=(2207,2374)			
- 	P. J. J	/gb=NM_152452 /gi=22748948			
		/ug=Hs.104679 /len=3270			i '
8212	0.00772	mRNA; cDNA DKFZp434D193 (from	AL080129	Hs.225841	
		clone DKFZp434D193), partial cds			
		/cds=(1,2240) /gb=AL080129	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s		,
		/gi=5262567 /ug=Hs.225841 /len=3605	i i		
8222	0.022485	prefoldin 5 (PFDN5), transcript variant	NM 002624	Hs.288856	NP_665904
0222	0.022403	1, mRNA /cds=(36,500)	14141_002024	113.200000	_000304
		/gb=NM_002624 /gi=22202632	·.		
		/ug=Hs.288856 /len=661			•
8224	0.022485	hypothetical protein, MGC:7199	NM_138459	Hs.289008	NP_612468
		(LOC116150), mRNA /cds=(174,1055)			
		/gb=NM_138459 /gi=20270242			
	0.00000	/ug=Hs.289008 /len=2645			
8243	0.038054	T-cell lymphoma invasion and	NM_012454	Hs.12598	NP_036586
	·	metastasis 2 (TIAM2), mRNA /cds=(51,3284) /gb=NM_012454			
 		/gi=6912703 /ug=Hs.12598 /len=4586			,
8316	0.038054	clone IMAGE:4794726, mRNA	BC042028	Hs.367688	
		/gb=BC042028 /gi=27469506			
		/ug=Hs.367688 /len=1479			
8324	0.016031	hypothetical protein (FLJ10562 fis, clone	AK001424	7	NP_057116
	22.22	NT2RP2002701)			
8338	0.031002	cDNA FLJ14181 fis, clone	AK024243	Hs.130874	
<u> </u>		NT2RP2004300. /gb=AK024243 /gi=10436570 /ug=Hs.130874 /len=4411			
,		/gi=1043037074g=115.1308747leti=4411 	. : 1	. '	
8358	0.027906	EST from cd34 stem cells Human	AF150123		
l		sapiens cDNA clone CBCALE06			
8363	0.031002	hypothetical protein FLJ14753	NM_032558	Hs.13453	NP_115947
		(FLJ14753), mRNA /cds=(247,1095)	0.00		
}	}	/gb=NM_032558 /gi=14211858 /ug=Hs 13453 /len=2593			}.
8366	0.04638	ob70e10.s1 NCI_CGAP_GCB1 cDNA	AA809350	Hs.246180	
		clone IMAGE:1336746 3', mRNA			
		sequence /clone=IMAGE:1336746			
		/clone_end=3' /gb=AA809350			
		/gi=2878756 /ug=Hs.246180 /len=454		<u> </u>	
8402	0.04638	EST (wh75b01.x1 NCI_CGAP_CLL1	A1809166		
	[cDNA clone IMAGE:2386537 3' similar	, .		
		to gb:X69392 60S RIBOSOMAL PROTEIN L26 (HUMAN);contains L1.b3			
		L1 repetitive element ;	,		1
8438	0.022485	mRNA sequence /gb=L26969	L26969	Hs.362852	<u> </u>
		/gi=16905391 /ug=Hs.362852 /len=1738			
<u> </u>			·		<u> </u>

Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
í i			No.	No.	No.
8442	0.042048	UI-H-FL1-bgw-f-18-0-UI.s1	BU634141	Hs.32163	•
i 1		NCI_CGAP_FL1 cDNA clone UI-H-FL1-		_	
		bgw-f-18-0-UI 3', mRNA sequence			
		/clone=UI-H-FL1-bgw-f-18-0-UI	. ,	k sa company in the	
	,	/clone_end=3' /gb=BU634141		* .	
!		/gi=23301396 /ug=Hs.32163 /len=1068			
		/gi 2555 1555 /ug 115.52 /55 /icii 1555			
8443	0.031002	UI-H-EU1-bag-b-11-0-UI.s1	BQ448425	Hs.438826	
"	0.00.002	NCI_CGAP_Ct1 cDNA clone UI-H-EU1-	DQ.110120	110.100020	v
		bag-b-11-0-UI 3', mRNA sequence			
		/clone=UI-H-EU1-bag-b-11-0-UI			
		/clone_or=1-201-bag-b-11-0-01 /clone_end=3' /gb=BQ448425			
	1	/gi=21251537 /ug=Hs.438826 /len=1023			
		/gi-2125155/ /ug-ns.456626/len-1025 			
0447	0.01700	IODNA EL 120604 fin along	AV057492	Un 405445	
8447	0.01/98	cDNA FLJ32621 fis, clone	AK057183	Hs.425445	
ł	1.00	STOMA2000395. /gb=AK057183	+ 1. - 1.		
.	1	/gi=16552779 /ug=Hs.425445 /len=2648			
- 100	0.044400				
8462		reverse transcriptase (non-exact)	AAB02291		
8473	0.022485	EST(xe97d09.x1 NCI_CGAP_Brn35	AW129107		
<u></u>	<u> </u>	cDNA clone IMAGE:2616497 3')		· · · · · · · · · · · · · · · · · · ·	
8486	0.023403	cDNA, 3' end /clone=IMAGE:1935382	Al340092	Hs.327321	NP_002370
	·	/clone_end=3' /gb=Al340092	3		1
	<u></u>	/gi=4077019 /ug=Hs.327321 /len=361		<u> </u>	
8494	0.020126	UI-H-DH0-aul-j-10-0-UI.s1	BM994461	Hs.434057	
		NCI_CGAP_DH0 cDNA clone			
		IMAGE:5871081 3', mRNA sequence			
	1:	/clone=IMAGE:5871081 /clone_end=3'		,	
]	,	/gb=BM994461 /gi=19719362			
		/ug=Hs.434057 /len=2059			
8511	0.01798	EST(yx64g06.r1 clone 266554 5')	N31192		
8523		EST (0x48a03.x1	AI038291		NP 612206
		Soares_total_fetus_Nb2HF8_9wIMAGE			
		:1659532 3')			
8528	0.009931	EST (602152342F1 NIH_MGC_81	BF671599		
	1	cDNA clone IMAGE:4293442 5')			
8531	0.042048	cDNA FLJ40915 fis, clone	AK098234	Hs.207079	7 7 7
		UTERU2005450. /gb=AK098234	, (00020)	1.0.20.0.0	
}	·	/gi=21758205 /ug=Hs.207079 /len=2739		1	{
	. ,	3. = 1. 0 \(\frac{1}{2} \text{LOO (AG) (10.2010) O (OH=2100)}			
8532	0 00780	sin3-associated polypeptide, 18kDa	NM 005870	Hs.23964	NP_005861
ا محمد	0.00703	(SAP18), mRNA /cds=(65,526)	1.1.41_000070	11.0.2000	-000001
		/gb=NM_005870 /gi=23510407			
		/ug=Hs.23964 /len=2035		٠.	,
8545	0.038054	as32a11 x1 Barstead aorta HPLRB6	AI707688	Hc 360505	
0040	0.030054		171101000	Hs.369595	
[cDNA clone IMAGE:2318876 3', mRNA			
]		sequence /clone=IMAGE:2318876			
·		/clone_end=3' /gb=Al707688		,	
j		/gi=4997464 /ug=Hs.369595 /len=518].
		<u> </u>		L	<u> </u>

Spot	p-valu	Description	Gene	Unig ne	Protein
			Acc ssion	Accession	Accession
8560	0.04639	ribosomal protein L28 (RPL28), mRNA	No. NM_000991	No.	No.
0000	0.04030		 1 66000	Hs.356371	NP_000982
		/cds=(43,456) /gb=NM_000991		•	
`		/gi=13904865 /ug=Hs.356371 /len=500			
4.				<u> </u>	
8561	0.004545	UI-H-BI2-agy-f-12-0-UI.s1	AW292315	Hs.435074	
		NCI_CGAP_Sub4 cDNA clone	¥ 1		100
		IMAGE:2726158 3', mRNA sequence			٠,
		/clone=IMAGE:2726158 /clone end=3'			
		/gb=AW292315 /gi=6698951			ŀ
		/ug=Hs.435074 /len=1117			
8567	0.008070	UI-E-CL1-afg-f-16-0-UI.r1 UI-E-CL1	BM702572	Un 446404	
0307	0.000979		DIVI702372	Hs 446404	
		cDNA clone UI-E-CL1-afg-f-16-0-UI 5',	1 1 1		ļ. ·
		mRNA sequence /clone=UI-E-CL1-afg-f-			
		16-0-UI /clone_end=5' /gb=BM702572			
	4	/gi=19015830 /ug=Hs.446404 /len=1067			
8568	0.012669	EST(clone IMAGE:4733034 5')	BG619661		
8572	0.038054	UI-H-EU0-azo-d-01-0-UI.s1	BQ180851	Hs.436432	
	1	NCI_CGAP_Car1 cDNA clone IMAGE:			, ,
] . ,	.	5851344 3', mRNA sequence			
		/clone=IMAGE: 5851344 /clone end=3'			
] .]	1			
		/gb=BQ180851 /gi=20356343			1
		/ug=Hs.436432 /len=1067			
8580	0.032415	BX096173 Soares_testis_NHT cDNA	BX096173	Hs.188780	
		clone IMAGp998F151793, mRNA	* .		,
	la de la companya de la companya de la companya de la companya de la companya de la companya de la companya de	sequence			
		/clone=IMAGp998F151793_;_IMAGE:7			ŀ
·		30766 /gb=BX096173 /gi=27842669		,	
[·		/ug=Hs.188780 /len=556			
8595	0.027906	ribosomal protein L3 (RPL3), mRNA	NM 000967	Hs.119598	NP 000958
	1 0.027000	/cds=(27,1238) /gb=NM 000967	11111_000007	113.773000	141 _000000
		/gi=16507968 /ug=Hs.119598 /len=1311			
		/g = 10507 900 /ug=ns. 1 19590 /left=151 1			
0500	0.000705		D14000000	100500	
8596	0.008765	UI-E-CQ1-acq-f-05-0-UI.r1 UI-E-CQ1	BM688680	Hs.406520	
		cDNA clone UI-E-CQ1-acq-f-05-0-UI 5',			
		mRNA sequence /clone=UI-E-CQ1-acq-			
	•	f-05-0-UI /clone_end=5' /gb=BM688680	·		
ĺ		/gi=19001938 /ug=Hs.406520 /len=934			
8597	0.022485	hypothetical protein MGC23918	NM_144716	Hs.43773	NP 653317
:		(MGC23918), mRNA /cds=(17,517)			
ĺ		/gb=NM_144716 /gi=21389496			
		/ug=Hs.43773 /len=874			
0612	0.006704		Algagaes	Ho 121072	-
8613	J U.UU0/84	ESTs, cDNA, 3' end	AI039268	Hs.131973	
		/clone=IMAGE:1658128 /clone_end=3'	(1	, , , ,
'		/gb=AI039268 /gi=3278462			
<u> </u>		/ug=Hs.131973 /len=437		L	
8618	0.031002	EST(HOA (Human Osteoarthritic	BG896206		
		Cartilage) Homo sapiens cDNA)			
					

Spot	p-valu	Description	Gene	Unigene	Protein
			Acc ssion	Accession	Accession
			No.	No.	No.
8669	0.04638	cDNA FLJ10190 fis, clone	AK001052	Hs.274546	
	-	HEMBA1004753. /gb=AK001052			
		/gi=7022081 /ug=Hs.274546 /len=1318			
8670	0.006049	mRNA; cDNA DKFZp434A128 (from	AL122120	Hs.313948	
		clone DKFZp434A128); partial cds			
		/cds=(621,2888) /gb=AL122120			
		/gi=6102946 /ug=Hs.313948 /len=4493			
8675	0.04638	UI-H-EI0-ayo-a-20-0-UI.s1	BQ004581	Hs.412459	
	, ,	NCI_CGAP_EI0 cDNA clone			,
		IMAGE:5841307 3', mRNA sequence			
		/clone=IMAGE:5841307 /clone end=3'			
		/gb=BQ004581 /gi=19729481			
	!	/ug=Hs.412459 /len=1095			
8729	0.020126	cDNA FLJ30135 fis, clone	AK054697	Hs.34906	NP_776170
ŀ		BRACE2000061. /gb=AK054697			- · · · ·
		/gi=16549295 /ug=Hs.34906 /len=2024			
		, , , , , , , , , , , , , , , , , , ,		,	
8732	0.011228	UI-H-DT1-awm-l-24-0-UI.s1	BQ019127	Hs.434910	
		NCI_CGAP_DT1 cDNA clone			
		IMAGE:5891495 3', mRNA sequence		}	
) .	/clone=IMAGE:5891495 /clone_end=3'			· '
`.		/gb=BQ019127 /gi=19754404		(terminal	
,		/ug=Hs.434910 /len=896			
8769	0.042048	EST(adult brain Danio rerio cDNA clone	BI429083		
}	}	4966301 5' similar to SW:RLA1_CHICK			
· .	Y -	P18660 60S ACIDIC RIBOSOMAL	. "		, X 1
]	• •	PROTEIN P1.; contains element			. !
		MER22 repetitive element;)			}
]
8782	0.025072	mitochondrion, complete genome	NC 001807		
8791		tg51b06.x1 Soares NFL_T_GBC_S1	Al419722	Hs.161220	
		cDNA clone IMAGE:2112275 3', mRNA			
-		sequence /clone=IMAGE:2112275		i.	
[/clone end=3' /gb=Al419722			
		/gi=4265653 /ug=Hs.161220 /len=484]
	¥			* 1	
8792	0.038054	EST(cDNA clone IMAGE:2092653 3')	Al381556		
8796		ESTs, cDNA, 3' end /clone=UI-E-EJ0-aii		Hs.355029	
-,,,,,,		I-19-0-UI /clone_end=3' /gb=BM681301			ļ
		/gi=18991197 /ug=Hs.355029 /len=591		1].
		1.3	· .		
8808	0.014265	EST(cDNA clone CS0DF021YG07 5	AL535948		NP_006612
3000	1 3.5 1 7 200	prime)			
8836	0.027906	No significant match	SEQ.ID.No.33		
8856	0.01798		SEG.15.110.00	 	
8874		No significant match		 	
33,7	0.000001	(ORF:+1:256~491[237])	SEQ.ID.No.26		[
<u> </u>	Ļ	[(Ora . 1.250 -48 [[251]) .	JOEG.ID.INU.ZO		<u> </u>

apot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
8889	0.020912	No significant match			
		(ORF:+2:50~238[189], +3:90~245[156])			
<u> </u>	<u> </u>	<u> </u>	SEQ.ID.No.65	L	
8906	0.042048	apoptosis, caspase activation inhibitor	NM_020371	Hs.63168	NP_065104
	1	(AVEN), mRNA /cds=(53,1141)			
		/gb=NM_020371 /gi=9966840			
		/ug=Hs.63168 /len=1549			
8939	0.034378	hypothetical protein GL009 (GL009),	NM_032492	Hs.24054	NP_115881
	*	mRNA /cds=(78,629) /gb=NM_032492	e e e e e e e e e e e e e e e e e e e	ļ ·	
		/gi=14210501 /ug=Hs.24054 /len=1097		<u>.</u>	4
8968	0.038054	xc57a09.x1 NCI_CGAP_Eso2 cDNA	AW084739	Hs.445134	
•		clone IMAGE:2588344 3' similar to			
		contains Alu repetitive element,, mRNA			
		sequence /clone=IMAGE:2588344			
		/clone_end=3' /gb=AW084739			(
		/gi=6039891 /ug=Hs.445134 /len=509			1
	0.040004	EOT/AVGGGGGGGGGGG	A) (700070		
8969	0.016031	EST(AV730379 HTF cDNA clone	AV730379		
0070	0.005000	HTFAAA05 5')	A1700450	11- 50000	
8970	0.005206	on43h10.y5 NCI_CGAP_Co8 cDNA	AI793153	Hs.58262	
* - I	`	clone IMAGE:1559491 5', mRNA			
		sequence /clone=IMAGE:1559491			
		/clone_end=5' /gb=Al793153			
8980	0.009765	/gi=5340869 /ug=Hs.58262 /len=521 EST yq55e03.r1 Soares fetal liver	R96686		
0900	0.000763	spleen 1NFLS H sapiens cDNA clone	1130000		
1.		IMAGE:199708 5' similar to contains Alu			
!		repetitive element;		1	
9003	0.016031	hypothetical protein DKFZp434B195	NM 031284	Hs.10748	NP_112574
3003	0.010031	(DKFZP434B195), mRNA	14141_001204	1113.10740	111 _112074
	1	/cds=(514,1290) /gb=NM_031284			
		/gi=21361960 /ug=Hs.10748 /len=2262			
	(13. 13. 13. 14. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15.			
9006	0.04638	cDNA FLJ38383 fis, clone	AK095702	Hs.433517	
	3.3 1000	FEBRA2003726. /gb=AK095702		1	
	0	/gi=21755022 /ug=Hs.433517 /len=3240			
		3			
9017	0.006784	UI-H-FH1-bfk-m-06-0-UI.s1	BU618627	Hs.192435	1
		NCI CGAP FH1 cDNA clone UI-H-FH1	1, 1		
]	bfk-m-06-0-UI 3', mRNA sequence	. Ta		
	[·	/clone=UI-H-FH1-bfk-m-06-0-UI			
	1	/clone_end=3' /gb=BU618627			
		/gi=23284842 /ug=Hs.192435 /len=1099			
		1 =	1	1	· I

Spot	p-value	Description	Gene	Unigene	Protein
-	. 17		Accession	Accession	Accession
			No.	No.	No.
9041	0.005949	7l40g01.x1	BF112131	Hs.288083	
	,	Soares_NSF_F8_9W_OT_PA_P_S1			
		cDNA clone IMAGE:3524136 3', mRNA		}	
		sequence /clone=IMAGE:3524136			
,		/clone_end=3' /gb=BF112131			
		/gi=10941821 /ug=Hs.288083 /len=620			
					1
9042	0.04638	UI-CF-FN0-aeu-b-13-0-UI.s1 UI-CF-	BU689604	Hs.273830	
		FN0 cDNA clone UI-CF-FN0-aeu-b-13-0		•	
:		UI 3', mRNA sequence /clone=UI-CF-			
	·	FN0-aeu-b-13-0-UI /clone end=3'	* * * * * * * * * * * * * * * * * * * *		
		/gb=BU689604 /gi=23547505			
		/ug=Hs.273830 /len=1066			
9043	0.038054	CocoaCrisp (LOC83690), mRNA	NM 031461	Hs.182364	NP 113649
		/cds=(376,1878) /gb=NM_031461	_		
		/gi=21314740 /ug=Hs.182364 /len=2962	•		
	\tag{\sigma} \sigma \sigma \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \tag{\sigma} \ta	3	>	'	
9046	0.00772	EST(xa08a12.x1	AW074833		
	3.5,7	Soares_NFL_T_GBC_S1 cDNA clone			
		IMAGE:2567710 3')		11. 1	
9055	0.034378	zi76d12.s1	AA702930	Hs.189679	
5555	0.00	Soares_fetal_liver_spleen_1NFLS_S1			
		cDNA clone IMAGE:436727 3', mRNA	f		
	'	sequence /clone=IMAGE:436727		•	
		/clone_end=3' /gb=AA702930			
		/gi=2706043 /ug=Hs.189679 /len=478		·	
9063	0.042048	clone 23612 mRNA sequence	U90902	Hs.82141	
5000	Q.032040	/gb=U90902 /gi=1913880 /ug=Hs.82141	000002	110.02777	•
		I/len=1548			
9078	0.031002	cDNA FLJ13207 fis, clone	AK023269	Hs.14355	
307.5	0.001002	NT2RP4000023. /gb=AK023269	,	110.14000	` .
		/gi=10435128 /ug=Hs.14355 /len=2633	ļ.		
		/gi=1040012074g=113.140007iCH=2000	ļ	•	ļ
9110	0.04638	UI-E-CR1-adz-a-04-0-UI.r1 UI-E-CR1	BM706524	Hs.421063	· ·
3110	0.04030	cDNA clone UI-E-CR1-adz-a-04-0-UI 5',	D.WIT 00027	1.73.421000	
		mRNA sequence /clone=UI-E-CR1-adz-			
		a-04-0-UI /clone_end=5' /gb=BM706524		1	1
* •		/gi=19019782 /ug=Hs.421063 /len=1149			
1	1 / 1	//gi= 190 197 02 /ug=115.42 1005 /left=1 149			
9112	0.04620	 UI-1-BC1-ajs-e-06-0-UI s1	BQ010796	Hs.120770	
9112	0.04030	NCI_CGAP_PI2 cDNA clone UI-1-BC1-	150010190	1113.120110	
		ajs-e-06-0-UI 3', mRNA sequence			
		/clone=UI-1-BC1-ajs-e-06-0-UI		,	
		1	,		
·[/clone_end=3' /gb=BQ010796			
		/gi=19735697 /ug=Hs.120770 /len=904			
0114	0.012660	EST(oDNA clone IMACE:2504565 21)	AW009489	 	
9114		EST(cDNA clone IMAGE:2504565-3')	AW896077		1
Ta 158	_U.U34378	EST(cDNA.	1VAA090011	<u> </u>	<u> </u>

Spot	p-value	Description	Gen	Unigene	Prot in
Opor	p value		Accession	Accession	Acc ssion
			No.	No.	No.
9150	0.031002	EST, cDNA, 3' end	BE503107	Hs.281951	110.
	0.00	/clone=IMAGE:3214604 /clone_end=3'			
		/gb=BE503107 /gi=9705515			
		/ug=Hs.281951 /len=368		*	[· · ·]
9154	0.042048	mRNA; cDNA DKFZp564B213 (from	AL049240	Hs.380268	
		clone DKFZp564B213) /gb=AL049240			
		/gi=4499973 /ug=Hs.380268 /len=767			
9157	0.031002	mRNA; cDNA DKFZp451O1818 (from	AL832650	Hs.12396	
		clone DKFZp451O1818) /gb=AL832650		ļ	
		/gi=21733226 /ug=Hs.12396 /len=4870			
9243	0.04638	AV700621 GKC cDNA clone	AV700621	Hs.191445	
		GKCDKF09 3', mRNA sequence			
		/clone=GKCDKF09 /clone_end=3'	. · ·]	
•		/gb=AV700621 /gi=10302592		·	
		/ug=Hs.191445 /len=809			
9253	0.022485	603390782F1 NIH_MGC_87 cDNA	BI860842	Hs.112472	
		clone IMAGE:5399756 5', mRNA			
٠.	,	sequence /clone=IMAGE:5399756			
		/clone_end=5' /gb=BI860842		,	
		/gi=16001577 /ug=Hs.112472 /len=917			
9319	0.011228	No significant match			
		(ORF:+2:2~226[225]), low complexity	SEQ.ID.No.17		
9387	0.038054	RAB35, member RAS oncogene family	NM_006861	Hs.94308	NP_006852
		(RAB35), mRNA /cds=(117,722)			
		/gb=NM_006861 /gi=19923377			
		/ug=Hs.94308 /len=2887			
			1100000	-	
9424	0.014265	MCM4 (MCM4) and DNA-PKcs	U63630	1	
0.400	0.040740	(PRKDC) genes, partial cds	DC000540	110 110011	·
9426	0.048742	clone IMAGE:4130494, mRNA	BC023543	Hs.112844	
i '		/gb=BC023543 /gi=23270740		1	
0450	0.046024	/ug=Hs.112844 /len=4567 FK506 binding protein 3, 25kDa	NM 002013	Hs.379557	NP 002004
9450	V.0 10031	(FKBP3), mRNA /cds=(412,1086)	[14IVI_002013	113.013001	_002004
		/gb=NM_002013 /gi=17149845			· ·
		/ug=Hs.379557 /len=1420			
9453	0.006784	mRNA for KIAA1705 protein, partial cds.	ΔB051492	Hs.7076	
9455	0.000764	/cds=(1714,3210) /gb=AB051492	A0001492	113.7070	
		/gi=12697954 /ug=Hs.7076 /len=3949		:	- -
9463	0.022485	tropomyosin 3 (TPM3), mRNA	NM 153649	Hs.85844	NP 705935
3403	0.022700	/cds=(52,798) /gb=NM_153649		. (0.00044	-, 00000
	ŀ	/gi=24119202 /ug=Hs.85844 /len=2089	∤		
		-			
9488	0.004545	UDP-N-acteylglucosamine	NM_003115	Hs.21293	NP_003106
J	1	pyrophosphorylase 1 (UAP1), mRNA			·
	-	/cds=(312,1829) /gb=NM_003115			
	1	/gi=19923738 /ug=Hs.21293 /len=2332			
	1		<u>L</u>	<u> </u>	<u> </u>

Spot	p-value	Description	Gene	Unigene	Protein
		14 T	Accession	Accession	Accession
			No.	No.	No.
9491	0.025072	clone IMAGE:2960008, mRNA	BC017253	Hs.433345	
		/gb=BC017253 /gi=16878090			
	N	/ug=Hs.433345 /len=1405			
9548	0.027906	ubiquitin specific protease 1 (USP1),	NM_003368	Hs.35086	NP_003359
		mRNA /cds=(246,2603)	-		
1		/gb=NM_003368 /gi=21361109			
		/ug=Hs.35086 /len=3379	,		
9553	0.04638	protein phosphatase 1, catalytic subunit,	NM_002709	Hs.21537	NP_002700
		beta isoform (PPP1CB), mRNA			
		/cds=(259,1242) /gb=NM_002709			,
		/gi=4506004 /ug=Hs.21537 /len=3590	•		
<u> </u>					
9576	0.01798	collagen, type XV, alpha 1 (COL15A1),	NM_001855	Hs.83164	NP_001846
		mRNA /cds=(166,4332)			. :
		/gb=NM_001855 /gi=18641349			
		/ug=Hs.83164 /len=5222			
9586	0.020126	NRRL 4123 mitochondrial ribosomal	U29233		
		RNA, small subunit, mitochondrial gene,	* -	r .	
		partial sequence		200	<u> </u>
9594	0.01798	serine (or cysteine) proteinase inhibitor,	NM_006216	Hs.21858	NP_006207
		clade E (nexin, plasminogen activator	,		
		inhibitor type 1), member 2		Ì.	
		(SERPINE2), mRNA /cds=(210,1406)			2 4
,	,	/gb=NM_006216 /gi=24307906			
	2.040005	/ug=Hs.21858 /len=2129	111.4 000000	45404	ND 775000
9610	0.012669	nuclear DNA-binding protein (C1D),	NM_006333	Hs.15164	NP_775269
		transcript variant 1, mRNA			
		/cds=(64,489) /gb=NM_006333	·		
		/gi=27894371 /ug=Hs 15164 /len=1200			4 .
0040	0.04000	5004	NINA 000040	H- 70502	ND 000000
9612	0.04638	ubiquitin-conjugating enzyme E2G 1	NM_003342	Hs.78563	NP_003333
		(UBC7 C. elegans) (UBE2G1), mRNA	<u> </u>		1
	ļ ·	/cds=(167,679) /gb=NM_003342		·	
		/gi=21314607 /ug=Hs.78563 /len=2430			
9629	0.04629	vaccinia related kinase 1 (VRK1),	NM 003384	Hs.422789	NP_003375
9029	0.04030	mRNA /cds=(76,1266) /gb=NM 003384	INIVI_003364	ITS.422709	INF_003373
		/gi=4507902 /ug=Hs.422789 /len=1662		•	
		191-45079027ug=H5.4227097left=1002	•.		*
9669	0.048742	hypothetical protein(FLJ20378)	BAA91131		
9693		hypothetical protein LOC93380	NM_173470	Hs.110702	NP 775741
3333	0.010031	(LOC93380), mRNA /cds=(301,696)	1.314 _ 17.037.0	13.110702	1,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
1	1	/gb=NM 173470 /gi=27735036	[[
]		/ug=Hs.110702 /len=3704			
9699	0.025072	EST(zeh1487.seq.F Zebrafish	AI354098		
	0.020072	Embryonic Heart cDNA Library cDNA 5')			
		Line, joing floar convictionary conviction			
L	1	I			

Spot	p-value	Description	Gene	Unigene	Protein
1			Accession	Accession	Accession
			No.	No.	No.
9701	0.034378	DKFZP586G1517 protein	NM_015440	Hs:44155	NP_056255
		(DKFZP586G1517), mRNA			
		/cds=(127,2328) /gb=NM_015440			
·		/gi=24308062 /ug=Hs.44155 /len=2749	*.		
	· i				-
9716	0.00772	EST(EST23220 Adipose tissue, white II	AA320820	•	
		5' contains Alu repeat)			
9724	0.027906	hypothetical protein BC012010	NM_138421	Hs.183733	NP_612430
	•	(LOC113174), mRNA /cds=(30,1457)			
		/gb=NM_138421 /gi=19923942			
		/ug=Hs.183733 /len=1527			
9740	0.016031	periphilin 1 (PPHLN1), mRNA	NM_016488	Hs.281428	NP_057572
		/cds=(94,1197) /gb=NM_016488	√ - 7 × W		
	± 1 4	/gi=21361573 /ug=Hs.281428 /len=1643		٠.	* *
9747	0.022485	EST(ya49e04.r2 clone 53081 5')	R16260		
9761		hypothetical protein FLJ22557	NM 024713	Hs.106101	NP_078989
		(FLJ22557), mRNA /cds=(87,1001)	-		
		/gb=NM_024713 /gi=13376012			
		/ug=Hs.106101 /len=2676			
9804	0.038054	RNA polymerase III subunit RPC2	NM 018082	Hs.197642	NP 060552
		(RPC2), mRNA /cds=(54,3455)	0.000_		
2.7		/gb=NM_018082 /gi=24475856	•		•
		/ug=Hs.197642 /len=4102			
9805	0.025072	EST (qh12h02.x1	AI240516		
0000	0.020072	Soares_NFL_T_GBC_S1	,		
		IMAGE:1844499 3')			
9819	0.025072	EST (yq42a05.r1 Soares fetal liver	R94397	en ser i i	
3013	0.020072	spleen	100,		
9840	0.022485	hypothetical protein FLJ20244	NM 017722	Hs.158947	NP 060192
1 2040	0.022-00	(FLJ20244), mRNA /cds=(89,2068)	1111-01772	110.1000 17	
,		/gb=NM 017722 /gi=8923218			
•		/ug=Hs.158947 /len=2137			
9850	0.020126	cDNA FLJ11946 fis, clone	AK022008	Hs.323231	
9000	0.020120	HEMBB1000709. /gb=AK022008	A11022000	113.020201	
1		The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s			
	1	/gi=10433321 /ug=Hs.323231 /len=3241			
9875	0.004545	heat shock 27kDa protein 2 (HSPB2),	NM 001541	Hs.78846	NP_001532
90/3	0.004545	mRNA /cds=(70,618) /gb=NM_001541	114101_001041	18.70040	_001332
				1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	•
0000	0.00770	/gi=4504518 /ug=Hs.78846 /len=874 hypothetical protein MGC40157	NM 152350	Hs.295362	NP_689563
9903	0.00772	1 2	10233U	119.280302	UNF008303
		(MGC40157), mRNA /cds=(106,498)			
		/gb=NM_152350 /gi=22748758			
0001	0.044005	/ug=Hs.295362 /len=1250	NIM 047720	Ho 102000	ND 00000
9904	J U.U14265	O-linked mannose beta1,2-N-	NM_017739	Hs.183860	NP_060209
1		acetylglucosaminyltransferase			
		(FLJ20277), mRNA /cds=(142,2124)			
		/gb=NM_017739 /gi=8923252		1	
	<u> </u>	/ug=Hs.183860 /len=2737		ļ	J

Spot	p-value	Description	Gene	Unig ne	Protein
			Accession	Accession	Accession
			No.	No.	No.
9919	0.025072	B-cell receptor-associated protein	NM_018844	Hs.27135	NP_061332
		BAP29 (BAP29), mRNA /cds=(47,775)			
		/gb=NM_018844 /gi=9994198			
		/ug=Hs.27135 /len=1085		<u> </u>	
9936	0.038054	x 009 protein (MDS009), mRNA	NM_020234	Hs.64641	NP_064619
4		/cds=(127,534) /gb=NM_020234			
		/gi=9910425 /ug=Hs.64641 /len=1133	• .	ş	
9946	0.025072	mitogen-activated protein kinase kinase	NM_002755	Hs.3446	NP_002746
	*	1 (MAP2K1), mRNA /cds=(73,1254)			
		/gb=NM_002755 /gi=14589898			
		/ug=Hs.3446 /len=2222			
10015	0.034378	mRNA for KIAA1228 protein, partial cds.	AB033054	Hs.306867	
		/cds=(1,2534) /gb=AB033054			
	i de la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da la companya da l	/gi=20521803 /ug=Hs.306867 /len=5742			
10016	0.031002	gycosyltransferase (LOC83468), mRNA	NM_031302	Hs.159993	NP_112592
		/cds=(408,1457) /gb=NM_031302			
		/gi=21314737 /ug=Hs.159993 /len=1908			
10019	0.038054	serologically defined colon cancer	NM_005786	Hs.284217	NP_005777
		antigen 33 (SDCCAG33), mRNA			
		/cds=(295,2358) /gb=NM_005786			
-		/gi=15451922 /ug=Hs.284217 /len=2858	4000		
10025	0.002982	SPARC related modular calcium binding	NM_022138	Hs.22209	NP_071421
	* * *	2 (SMOC2), mRNA /cds=(21,1394)		ļ. · · · ·	· ·
		/gb=NM_022138 /gi=24308276		le le le le le le le le le le le le le l	
		/ug=Hs.22209 /len=2947	2		
10060	0.014065	roundabaut avan ailidanaa raaantaa 1	NIM 400004	11- 204400	ND 500004
10000	0.014265	roundabout, axon guidance receptor, 1	NM_133631	Hs.301198	NP_598334
		(Drosophila) (ROBO1), transcript variant 2, mRNA /cds=(964,5802)	·	[
	,	/gb=NM_133631 /gi=19743805			
		1 T T			
10084	0.012660	/ug=Hs.301198 /len=7475 hypothetical protein MGC11034	NM 031453	Hs.103378	NP 113641
10004	0.012009	(MGC11034), mRNA /cds=(246,641)	1401_031433	103376	113041
	* .	/gb=NM_031453 /gi=13899290		,	1
		/ug=Hs.103378 /len=3301			
10102	0.04638	hypothetical protein FLJ23445	NM_025075	Hs.288151	NP 079351
13 102	0.04000	(FLJ23445), mRNA /cds=(44,658)	1.4141_020070	13.200101	_0/3351
		/gb=NM_025075 /gi=13376622			
		/ug=Hs.288151 /len=963	·]	
10130	0.014741	UI-H-EU1-bad-c-14-0-UI.s1	BQ447141	Hs.445111	
	3.3, 7, 7,	NCI_CGAP_Ct1 cDNA clone UI-H-EU1-		1110.770111	·
		bad-c-14-0-UI 3', mRNA sequence	,		
		/clone=UI-H-EU1-bad-c-14-0-UI			
		/clone_end=3' /gb=BQ447141		·	
		/gi=21250253 /ug=Hs.445111 /len=1032		l. **	
			*-		
		<u> </u>	L:	L	L

Spot	p-value	Description	Gene	Unigene	Protein
•			Accession	Accession	Accession
			No.	No.	No.
10167	0.034378	EST(zs29d10.r1 NCI_CGAP_GCB1	AA255979	- 1- 1- 1- 1- 1- 1- 1- 1- 1- 1- 1- 1- 1-	NP_004828
		IMAGE:686611 5') short match			
10178	0.011228	EST382135 MAGE resequences,	AW970055	Hs.324815	
		MAGK cDNA, mRNA sequençe			
		/gb=AW970055 /gi=8159900			
		/ug=Hs:324815 /len=764			
10191	0.031002	EST(HSPD24973 HM3 clone	F32327		
100		s3000036E04)	_		
10215	0.012669	UI-E-EJ0-aik-i-20-0-UI r1 UI-E-EJ0	BM727413	Hs.112619	
		cDNA clone UI-E-EJ0-aik-i-20-0-UI 5',			-
		mRNA sequence /clone=UI-E-EJ0-aik-i-			
		20-0-UI /clone_end=5' /gb=BM727413		, 10	
	. *	/gi=19048746 /ug=Hs.112619 /len=1667	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1		
,				·	
10228	0.00772	hypothetical protein FLJ10342	NM_018064	Hs.101514	NP_060534
		(FLJ10342), mRNA /cds=(534,1145)			
		/gb=NM_018064 /gi=14149717			
		/ug=Hs.101514 /len=1506	•		<u> </u>
10290	0.031002	ox21f03.x1	AI038379	Hs.131865	7.3
		Soares_fetal_liver_spleen_1NFLS_S1			
		cDNA clone IMAGE:1656989 3', mRNA			
		sequence /clone=IMAGE:1656989			
1844		/clone_end=3' /gb=Al038379			
		/gi=3277573 /ug=Hs.131865 /len=516		1	
					1
10312	0.026138	TATA box binding protein (TBP)-	NM_005681	Hs.153088	NP_647603
		associated factor, RNA polymerase I, A,	1		
		48kDa (TAF1A), transcript variant 1,			
		mRNA /cds=(190,1542)			
		/gb=NM_005681 /gi=21536363			
	· · · · · · · ·	/ug=Hs.153088 /len=1893			
10316	0.022485	clone IMAGE:5295896, mRNA	BC043240	Hs.104413	
		/gb=BC043240 /gi=27695834			
		/ug=Hs.104413 /len=2136		· .	
10323	0.022485	mRNA; cDNA DKFZp434K1115 (from	AL136764	Hs.42676	,
		clone DKFZp434K1115); complete cds			·
		/cds=(97,2877) /gb=AL136764			ı ·
		/gi=12053044 /ug=Hs.42676 /len=4868			
:					*
10350	0.038054	hypothetical protein FLJ90013	NM_153365	Hs.25119	NP_699196
		(FLJ90013), mRNA /cds=(15,1703)		e	
		/gb=NM_153365 /gi=23503310			
		/ug=Hs.25119 /len=3382	· · ·		
10364	0.027906	EST (QV3-NN1023-130500-178-g10	AW902437	7.7	
		NN1023)		* - :	
10380	0.016031	Hypothetical protein(cDNA: FLJ22479	AK026132		NP_079176
	. ·	fis, clone HRC10831)			<u> </u>
10401	0.038054	EST (Clontech human aorta polyA	C14262		
		mRNA (#6572) cDNA clone GEN-			

Spot	p-value	Description	Gene	Unigene	Prot in
	F 174,44		Accession	Accession	Acc ssion
			No.	No.	No.
10423	0.04638	muscleblind-like protein MBLL39	NM_144778	Hs.283609	NP 659002
		(MBLL39), transcript variant 1, mRNA	-		
		/cds=(782,1885) /gb=NM_144778		* .	
		/gi=21464124 /ug=Hs.283609 /len=4665			
		/g/ 21101121/ag/(10.200000000000000000000000000000000000	: •		
10429	0.020126	binder of Rho GTPase 3-like	NM_145057	Hs.352987	NP 659494
		(MGC21945), mRNA /cds=(340,786)		****	-
		/gb=NM_145057 /gi=21450817		-	
	•	/ug=Hs.352987 /len=929			
10437	0.038054	UI-H-EI1-aze-c-02-0-UI.s1	BQ003590	Hs.29698	
		NCI_CGAP_EI1 cDNA clone			
		IMAGE:5847481 3', mRNA sequence		- "	
		/clone=IMAGE:5847481 /clone_end=3'	,		
		/gb=BQ003590 /gi=19728490			· ·
· · · .		/ug=Hs.29698 /len=1051			
10439	0.027906	clone IMAGE:4157625, mRNA	BC033767	Hs.271450	
10-05	0.027300	/gb=BC033767 /gi=22832873		110.27 1100	
		/ug=Hs.271450 /len=1515	*		
10454	0.038054	EST(tm27f02.x1	AI479365	10	
10434	0.050054	Soares_NFL_T_GBC_S1 cDNA clone	AIH / 9000		
		IMAGE:2157819 3')			
10475	0.025072	solute carrier family 25 (mitochondrial	NM 005984	Hs.111024	NP 005975
10475	0.023072	carrier; citrate transporter), member 1	14141_005904		NF_005975
		(SLC25A1), mRNA /cds=(100,1035)		,	
	t				
		/gb=NM_005984 /gi=21389314		C-	
10400	0.007006	/ug=Hs.111024 /len=1619	W89192	Hs.194238	
10496	0.027906	zh69e06.s1	VV09192	IDS. 194230	1
		Soares_fetal_liver_spleen_1NFLS_S1			
	r	cDNA clone IMAGE:417346 3', mRNA			
i		sequence /clone=IMAGE:417346			
*		/clone_end=3' /gb=W89192		•	
40504	0.00054	/gi=1404504 /ug=Hs.194238 /len=471	DM700454	LID 422446	
10501	0.038054	UI-E-DW0-agg-d-24-0-UI.r1 UI-E-DW0	BM706154	Hs.433446	
		cDNA clone UI-E-DW0-agg-d-24-0-UI		\$ 10 m	
		5', mRNA sequence /clone=UI-E-DW0-			
		agg-d-24-0-UI /clone_end=5'		,	
	,	/gb=BM706154 /gi=19019412			
10500	0.00704	/ug=Hs.433446 /len=1003	D0040050		ND 775000
		EST(cDNA clone IMAGE:4944078 5')	BG913252	11. 75000	NP_775882
10503	0.016031	thymosin, beta 4, X chromosome	NM_021109	Hs.75968	NP_066932
	*.	(TMSB4X), mRNA /cds=(78,212)			
		/gb=NM_021109 /gi=11056060			
4555	0.005555	/ug=Hs.75968 /len=556	00405070	110 405440	
10506	0.005206	K-EST0187941 L14ChoiCK0 cDNA	CB135678	Hs.435110	
		clone L14ChoiCK0-30-C05 5', mRNA			
		sequence /clone=L14ChoiCK0-30-C05			
		/clone_end=5' /gb=CB135678	1 1 1		
		/gi=28102621 /ug=Hs.435110 /len=419		'	
70=1=		80.00			
10512	0.016031	IPOLY A		<u> </u>	1

Spot	p-value	Description	G ne Accession No.	Unigene Accession No.	Protein Accession No.
10531	0.04638	mRNA; cDNA DKFZp686J172 (from clone DKFZp686J172) /gb=AL832206 /gi=21732751 /ug=Hs.56896 /len=6055	AL832206	Hs.56896	NO.
10539	0.038054	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003	NM_001003	Hs.424299	NP_000994
		/gi=16905511 /ug=Hs.424299 /len=512			
10540	0.004545	BX116063 NCI_CGAP_Brn23 cDNA clone IMAGp998O244959, mRNA sequence	BX116063	Hs.127872	
		/clone=IMAGp998O244959_;_IMAGE:2 016239 /gb=BX116063 /gi=27839769 /ug=Hs.127872 /len=537			
10546	0.031002	cDNA FLJ13585 fis, clone PLACE1009150. /gb=AK023647 /gi=10435632 /ug=Hs.43047 /len=3430	AK023647	Hs.43047	
10561	0.014265	wn03h10.x1 NCI_CGAP_Ut2 cDNA clone IMAGE:2444419 3', mRNA	AI924266	Hs.370113	
		sequence /clone=IMAGE:2444419 /clone_end=3' /gb=Al924266 /gi=5660230 /ug=Hs.370113 /len=514			
10566	0.008765	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
10570	0.031002	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556	NM_021109	Hs.75968	NP_066932
10578	0.025072	xj80g04.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2663574 3', mRNA	AW172661	Hs.257251	
/		sequence /clone=IMAGE:2663574 /clone_end=3' /gb=AW172661 /gi=6438609 /ug=Hs.257251 /len=451			
10610	0.025072	cDNA, 3' end /clone=IMAGE:3476408 /clone_end=3' /gb=BF058813 /gi=10812709 /ug=Hs.319312 /len=382	BF058813	Hs.319312	NP_001454
10673	0.042048	mitochondrial ribosomal protein S18C (MRPS18C), nuclear gene encoding mitochondrial protein, mRNA /cds=(60,488) /gb=NM_016067	NM_016067	Hs.3385	NP_057151
10683	0.014265	/gi=7705629 /ug=Hs 3385 /len=1014 EST388886 MAGE resequences, MAGO cDNA, mRNA sequence	AW976777	Hs 223578	
		/gb=AW976777 /gi=8168011 /ug=Hs 223578 /len=519			

Accession Accession No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No.	Spot	p-value	Description	Gene	Unigene	Protein
No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. No.	, -	ile i and			. —	
10684 0.034378 EST(cDNA clone IMAGE:4090855 3') BF447403 NP 0022 10710 0.025072 No significant match SEQ.ID.No.46						(·
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10773 0.006784 EST (RC3-CT0254-300800-022-g07 CT0254) 10779 0.034378 EST (ADB cDNA clone ADBAKA02 5') AV704531 10790 0.016031 similar to zinc finger protein 22 (KOX 15) (LOC166793), mRNA /cds=(1401,2147) /gb=NM_145291 Hs.94013 NP_660.						
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10805 0.031002 EST(ak84d11.s1 Barstead spleen HPLRB2 cDNA clone IMAGE:1414581 3' similar to contains MER10.t3 MER10 repetitive element) 10806 0.016031 EST (qj86f09.x1 NCI_CGAP_Kid3 cDNA clone IMAGE:1866377.3' similar to contains MER30.t3 MER30 repetitive element) 10807 0.042048 methyltransferase like 3 (METTL3), mRNA /cds=(87,1829) /gb=NM_019852 /gi=21361826 /ug=Hs.268149 /len=1959 NM_019852 /gi=21361826 /ug=Hs.268149 /len=1959 Hs.268149 NP_062i /gb=AL355688 /gi=7799136 /ug=Hs.6655 /len=1831 10839 0.00772 calcium binding protein Cab45 /gb=AL355688 /gi=7799136 /ug=Hs.6655 /len=1831 10839 0.00772 calcium binding protein Cab45 /gb=NM_016547 /gi=7706572 /ug=Hs.42806 /len=2092 10841 0.01798 zinc finger protein 306 (ZNF306), mRNA /cds=(294,1340) /gb=NM_016547 /gi=7706572 /ug=Hs.66774 /len=2242 10867 0.022485 7k59b12.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3479758.3', mRNA RA845289 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320 Ala44320					1	ą ·
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/gi=21361826 /ug=Hs.268149 /len=1959 10811		7				
10811 0.025072 EST from clone 208499, full insert /gb=AL355688 /gi=7799136 /ug=Hs.6655 /len=1831						
/gb=AL355688 /gi=7799136 /ug=Hs.6655 /len=1831 10839						
/gb=AL355688 /gi=7799136 /ug=Hs.6655 /len=1831 10839	10811	0.025072	EST from clone 208499, full insert	AL355688	Hs.6655	
10839						
10839 0.00772 calcium binding protein Cab45 precursor (Cab45), mRNA /cds=(294,1340) /gb=NM_016547 /gi=7706572 /ug=Hs.42806 /len=2092						i -
precursor (Cab45), mRNA /cds=(294,1340) /gb=NM_016547 /gi=7706572 /ug=Hs.42806 /len=2092 10841	10839	0.00772		NM 016547	Hs.42806	NP 057631
/cds=(294,1340) /gb=NM_016547 /gi=7706572 /ug=Hs.42806 /len=2092 10841 0.01798 zinc finger protein 306 (ZNF306), mRNA NM_024493 Hs.66774 NP_0778 /cds=(149,1765) /gb=NM_024493 /gi=24308296 /ug=Hs.66774 /len=2242 10867 0.022485 7k59b12.x1 NCI_CGAP_GC6 cDNA BF059412 Hs.319320 clone IMAGE:3479758 3', mRNA						-
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10841 0.01798 zinc finger protein 306 (ZNF306), mRNA NM_024493				*		
/cds=(149,1765) /gb=NM_024493 /gi=24308296 /ug=Hs.66774 /len=2242 10867 0.022485 7k59b12.x1 NCI_CGAP_GC6 cDNA BF059412 Hs.319320 clone IMAGE:3479758 3', mRNA	10841	0.01798		NM 024493	Hs.66774	NP 077819
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			sequence /clone=IMAGE:3479758			[
/clone_end=3' /gb=BF059412						
/gi=10813230 /ug=Hs.319320 /len=453					1	
				· .		
10894 0.042048 C1q and tumor necrosis factor related NM_030945 Hs.171929 NP_852	10894	0.042048	C1q and tumor necrosis factor related	NM_030945	Hs.171929	NP_852100
protein 3 (C1QTNF3), mRNA			protein 3 (C1QTNF3), mRNA	_		- .
/cds=(84,824) /gb=NM_030945					,	
/gi=13569918 /ug=Hs.171929 /len=1710						1
10910 0.042048 EST (tg92b06.x1 NCI_CGAP_CLL1 Al401289	10910	0.042048	EST (tg92b06.x1 NCI_CGAP_CLL1	Al401289		
cDNA clone IMAGE:2116211 3' similar	'		cDNA clone IMAGE:2116211 3' similar		·	
to contains Alu repetitive element;)			to contains Alu repetitive element;)			

Spot	p-value	Description	Gene	Unigene	Protein
÷			Accession	Accession	Accession
7 - 2 7 - 2			No.	No.	No.
10917		activated RNA polymerase II	NM_006713	Hs.349506	NP_006704
<i>(</i> 1)		transcription cofactor 4 (PC4), mRNA			
		/cds=(57,440) /gb=NM_006713		ALKERT STATE	
• •		/gi=19923783 /ug=Hs.349506 /len=1336			
10930	0.031002	Similar to RIKEN cDNA 2810004N23	BC036800	Hs.390881	
		gene, clone MGC:46269			
		IMAGE:5589128, mRNA, complete cds			
	•	/cds=(57,905) /gb=BC036800	1.1		
٠		/gi=22477333 /ug=Hs.390881 /len=1468			
10942	0.04638	EST(ze42c06.r1 Soares retina N2b4HR	W96264		
		Homo sapiens cDNA clone			
		IMAGE:361642 5')			
10946	0.031002	of yeast long chain polyunsaturated fatty	NM_021814	Hs.250175	NP 068586
		acid elongation enzyme 2 (HELO1),	_		
		mRNA /cds=(345,1244)			
	ļ., ·	/gb=NM_021814 /gi=21361903			
		/ug=Hs.250175 /len=3011			
10949	0.022485	yo73e02.s1 Soares breast 3NbHBst	H44042	Hs.391565	# 55 F.S
		cDNA clone IMAGE:183578 3', mRNA			
		sequence /clone=IMAGE:183578			4,
•		/clone_end=3' /gb=H44042 /gi=920094			
		/ug=Hs.391565 /len=417			
10958	0.011228	FLJ30424 fis, clone BRACE2008881,	AK054986	Hs.21423	
	# 1	weakly similar to ZINC FINGER			
		PROTEIN 195 /cds=UNKNOWN			
•		/gb=AK054986 /gi=16549625			
	,	/ug=Hs.21423 /len=2144			
10989	0.04638	BX102645 NCI_CGAP_Brn23 cDNA	BX102645	Hs.146883	
		clone IMAGp998L144327, mRNA			
		sequence			
		/clone=IMAGp998L144327_;_IMAGE:17	7.7		
		03965 /gb=BX102645 /gi=27831887			
		/ug=Hs.146883 /len=786			
11006	0.005206	ab12g02.s1 Stratagene lung (#937210)	AA487969	Hs.96692	
		cDNA clone IMAGE:840626 3', mRNA	1		٠.
		sequence /clone=IMAGE:840626			
		/clone_end=3' /gb=AA487969			
		/gi=2215400 /ug=Hs.96692 /len=466			
11020	0.025072	UI-H-DH0-aul-j-10-0-UI.s1	BM994461	Hs.434057	
		NCI_CGAP_DH0 cDNA clone	1 ,] .
		IMAGE:5871081 3', mRNA sequence	Í		
		/clone=IMAGE:5871081 /clone_end=3'			
		/gb=BM994461 /gi=19719362			
		/ug=Hs.434057 /len=2059			
11027	0.034378	cDNA FLJ12885 fis, clone	AK022947	Hs.36093	
		NT2RP2003988. /gb=AK022947	1		
*		/gi=10434630 /ug=Hs.36093 /len=2000		· .	

Spot	p-value	Description	Gene	Unig ne	Protein
-			Accession	Acc ssion	Accession
			No.	No.	No.
11030	0.022485	ESTs, cDNA, 3' end	AI671885	Hs.110855	
		/clone=IMAGE:2308223 /clone_end=3'	. ,		
		/gb=Al671885 /gi=4851616		2	
		/ug=Hs.110855 /len=593			
11032	0.029136	nj38c05.s1 NCI_CGAP_AA1 cDNA	AA548630	Hs.105848	
4. N		clone IMAGE:994760 3' similar to			
		gb:M62424 THROMBIN RECEPTOR			
Ť.	1	PRECURSOR mRNA seguence			
		/clone=IMAGE:994760 /clone end=3'			
		/gb=AA548630 /gi=2318912	.,		
		/ug=Hs.105848 /len=555			
11033	0.016031	FLJ30661 fis, clone DFNES2000526	AK055223	Hs.265540	NP_057178
	0.0.00	/cds=UNKNOWN /gb=AK055223	, ,, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		
		/gi=16549904 /ug=Hs.265540 /len=2514			
		7gi 100400047ag 113.2000407icii 2014			* .
11044	0.034378	EST(fetal liver spleen 1NFLS Homo	H90418	Tile Tile of the	
' ' ' ' '	0.00-1970	sapiens cDNA clone IMAGE:241467 3')	1130-110		
		Sapiens CDNA Cione INIAGE.241407 3 7			
11055	0.038054	UI-E-CL1-aez-f-02-0-UI.r1 UI-E-CL1	BM695854	Hs.21509	
1,1052	0.030034	cDNA clone UI-E-CL1-aez-f-02-0-UI 5',	DIVIO93034	115.21309	
ľ					
		mRNA sequence /clone=UI-E-CL1-aez-f			•
		02-0-UI /clone_end=5' /gb=BM695854			
		/gi=19009112 /ug=Hs.21509 /len=1260			
11050	0.04700	aDNIA. EL 122050 for along HED00454	AK025703	Un 472705	
11056	0.01798	cDNA: FLJ22050 fis, clone HEP09454.	AKU257U3	Hs.173705	
		/gb=AK025703 /gi=10438305			
	*	/ug=Hs.173705 /len=1990		i .	
11067	0.000430	ECT- aDNA Flored	DC0E2000	11- 400004	NID FOAF7C
11067	0.029136	ESTs, cDNA, 5' end	BG253800	Hs.128894	NP_524576
		/clone=IMAGE:4474821 /clone_end=5'			
		/gb=BG253800 /gi=12763616			*
11000	0.004000	/ug=Hs.128894 /len=950	11.050440	11. 04004	
11068	0.031002	mRNA; cDNA DKFZp586G1520 (from	AL050148	Hs.31834	
l		clone DKFZp586G1520) /gb=AL050148			
		/gi=4884359 /ug=Hs.31834 /len=3030			
14000		FOT: OLIVE	A1700507		- 742 /
11069	0.00/72	ESTs, Stratagene ovarian cancer	AI732587		
		(#937219 cDNA clone IMAGE:595374 3'		2	1
		similar to TR:Q13129 Q13129 ZN-15			
1455		RELATED ZINC FINGER PROTEIN;	D.V.00.46.55		
11091	0.042048	BX091936 Soares placenta Nb2HP	BX091936	Hs.24598	
		cDNA clone IMAGp998N02193;			
		IMAGE:135745, mRNA sequence			·.
	, ,	/clone=IMAGp998N02193_;_IMAGE:13		[N 4	
	,	5745 /gb=BX091936 /gi=27822661			1
	<u> </u>	/ug=Hs.24598 /len=688			<u>L </u>
11110	0.020126	cDNA FLJ37125 fis, clone	AK094444	Hs.12030	Ţ.
		BRACE2022638. /gb=AK094444	1	,	
	1	/gi=21753507 /ug=Hs.12030 /len=2720		I	1
		/gi-21/3330/ /ug-118.12030/lef1-2/20	1		

Spot	p-value	Description	Gene	Unigen	Protein
			Accession	Accession	Accession
ļ			No.	No.	No.
11118	0.025072	BX100041 Soares pineal gland	BX100041	Hs.446061	
		3NbHPG cDNA clone			
		IMAGp998D02466, mRNA sequence			
		/clone=IMAGp998D02466_;_IMAGE:23		* * *	
		1505 /gb=BX100041 /gi=27830398			
		/ug=Hs.446061-/len=718			
11166	0.010197	ym53e05.s1 Soares infant brain 1NIB	H24464	Hs.417814	
``.	41	cDNA clone IMAGE:51803 3', mRNA			, .
		sequence /clone=IMAGE:51803			1
		/clone_end=3' /gb=H24464 /gi=893,159			
		/ug=Hs.417814 /len=487			
11168	0.042048	hv66b12.x1 NCI_CGAP_Lu24 cDNA	BE220031	Hs.192491	
		clone IMAGE:3178367 3', mRNA			
		sequence /clone=IMAGE:3178367			
	•	/clone_end=3' /gb=BE220031			
		/gi=8907349 /ug=Hs.192491 /len=379			
11193	0.038054	control			
11198	0.013065	cDNA FLJ23679 fis, clone HEP09084.	AK074259	Hs.351597	
,		/gb=AK074259 /gi=18676812			
		/ug=Hs.351597 /len=2006			
11200	0.04638	EST(cDNA clone IMAGE:3087494 3')	BF509784		
11224	0.034378	No significant match	SEQ.ID.No.93	4	
11238	0.027906	nebulin mRNA, partial cds. /gb=U35637	U35637	Hs.83870	NP_004534
	٠	/gi=1205988 /ug=Hs.83870 /len=9443			-
					4
11257	0.04638	mRNA for FLJ00086 protein, partial cds.	AK024487	Hs.343828	NP_835461
	·.	/cds=(1951,3150) /gb=AK024487			, 7
		/gi=10440487 /ug=Hs.343828 /len=4456			
11261	0.009931	hypothetical protein MGC14480	NM_144998	Hs.37616	NP_659435
		(MGC14480), mRNA /cds=(18,209)	<u> </u>		
		/gb=NM_144998 /gi=21450710			
		/ug=Hs.37616 /len=844			
11263	0.027906	KIAA1804 protein, partial cds	AB058707	Hs.50883	NP_115811
		/cds=UNKNOWN /gb=AB058707			
		/gi=14017824 /ug=Hs.50883	·		
11297	0.022485	farnesyl diphosphate synthase (farnesyl	NM_002004	Hs.335918	NP 001995
		pyrophosphate synthetase,			_
		dimethylallyltranstransferase,	• ,		
	ļ.	geranyltranstransferase) (FDPS),			
	1	mRNA /cds=(115,1374)			e e e e e e e e e e e e e e e e e e e
		/gb=NM_002004 /gi=4503684	[
].		/ug=Hs.335918 /len=1430			
11313	0.027459	NADH dehydrogenase (ubiquinone) 1	NM_004541	Hs.74823	NP 004532
'		alpha subcomplex, 1, 7.5kDá		 -	
		(NDUFA1), nuclear gene encoding		*	
		mitochondrial protein, mRNA			
1		/cds=(143,355) /gb=NM_004541			
	I ⁺	L === (· · = , = = / · 3 = · · · · · _ ~ ~ · · · · · ·	I .	1 .	I

Spot	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
			No.	No	No.
11324	0.01798	endoplasmic reticulum stress-inducible,	NM_014685	Hs.146393	NP_055500
		ubiquitin-like domain member 1			,
		(HERPUD1), mRNA /cds=(96,1271)			
		/gb=NM_014685 /gi=7661869			
		/ug=Hs.146393 /len=1884	:		
11325	0.027906	tetratricopeptide repeat domain 8	NM 144596	Hs.55158	NP 653197
		(TTC8), mRNA /cds=(53,1648)			_
, ,	a ,	/gb=NM_144596 /gi=21389382			
		/ug=Hs.55158 /len=2241			
11335	0.020126	COX11 cytochrome c oxidase assembly	NM 004375	Hs.241515	NP_004366
		protein (yeast) (COX11), nuclear gene			55 /555
		encoding mitochondrial protein, mRNA			
	~	/cds=(48,878) /gb=NM_004375	9		1.00
	45.4	/gi=17921983 /ug=Hs.241515 /len=2717			,
		[
11337	0.020126	dihydropyrimidine dehydrogenase	NM 000110	Hs.1602	NP 000101
		(DPYD), mRNA /cds=(102,3179)			
		/gb=NM 000110 /gi=4557874			
		/ug=Hs.1602 /len=4407			
11338	0.011228	Similar to SRY-box containing gene 5,	BC014929	Hs.383009	
		clone IMAGE:3919439, mRNA			
		/gb=BC014929 /gi=15928923			
•		/ug=Hs.383009 /len=652			
11349	0.022485	hypothetical nuclear factor SBBI22	NM 020395	Hs.432952	NP 065128
	****	(LOC57117), mRNA /cds=(207,1595)	11111_020000	110.102002	-000120
		/gb=NM_020395 /gi=21361850			
		/ug=Hs.432952 /len=1716			
11369	0.04638	clone IMAGE:5301545, mRNA	BC041951	Hs.177781	
11000	0.04000	/gb=BC041951 /gi=27469737	10041001	113,177701	
100		/ug=Hs.177781 /len=2155			
11371	0.01798	FLJ13700 fis, clone PLACE2000216,	AK023762	Hs.324648	NP 842565
	3.31730	highly similar to SPECTRIN BETA	,	1.0.02.7070	-0-72000
	l · · · ·	CHAIN, BRAIN /cds=UNKNOWN			
		/gb=AK023762 /gi=10435792			
		/ug=Hs.324648 /len=3334			
11374	0.014265	peptidyl-prolyl isomerase G (cyclophilin	NM 004792	Hs.77965	NP 004783
	0.011200	G) (PPIG), mRNA /cds=(158,2422)	14101_0047.02	113.77300	-004700
		/gb=NM_004792 /gi=4758105			
		/ug=Hs.77965 /len=2695		,	i
11394	0.016031	hypothetical protein CL25022	NM 015702	Hs.5324	NP_056517
11334	0.010031	(CL25022), mRNA /cds=(158,1048)	11101_013/02	113.0024	- 000017
		/gb=NM 015702 /gi=7661547	* 1		·
					[
11404	0.038054	/ug=Hs.5324 /len=1416 hypothetical protein MGC3067	NIM 024205	Uc 202114	NID 077074
11404	0.030034	1 * .	NM_024295	Hs.323114	NP_077271
		(MGC3067), mRNA /cds=(140,895)			
,		/gb=NM_024295 /gi=13236515			
L	l	/ug=Hs.323114 /len=1203	<u> </u>	L	<u></u>

Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No
11411	0.034378	DKFZP434D1335 protein	NM_015578	Hs.8258	NP_056393
'		(DKFZP434D1335), mRNA	4	1	[
		/cds=(78,1469) /gb=NM_015578	the state of the		
		/gi=24308092 /ug=Hs.8258 /len=3389			
11433	0.01798	annexin A7 (ANXA7), transcript variant	NM_004034	Hs.386741`	NP_004025
		2, mRNA /cds=(61,1527)		}	
		/gb=NM_004034 /gi=4809278			
		/ug=Hs.386741 /len=2176			
11444	0.034378	coproporphyrinogen oxidase	NM_000097	Hs.89866	NP_000088
		(coproporphyria, harderoporphyria)			
	, i	(CPO), mRNA /cds=(68,1432)			
	·	/gb=NM_000097 /gi=20127405			
		/ug=Hs.89866 /len=2691			
11446	0.04638	ornithine decarboxylase antizyme 1	NM_004152	Hs.281960	NP_004143
		(OAZ1), mRNA /gb≃NM_004152			}
		/gi=9845504 /ug=Hs.281960 /len=986			<u> </u>
11472	0.012669	similar to RIKEN cDNA 1110018M03,	BC026873	Hs.32478	
	1.5	clone MGC:24932 IMAGE:4938507,			[No. 1
		mRNA, complete cds /cds=(218,853)		1	
		/gb=BC026873 /gi=20073062			
_	<u> </u>	/ug=Hs.32478 /len=1826			
11473	0.04638	hypothetical protein BC013035	NM_138436	Hs.10018	NP_612445
		(LOC114926), mRNA /cds=(128,430)			
1		/gb=NM_138436 /gi=19923964			(
L		/ug=Hs.10018 /len=836			
11476	0.009931	clone IMAGE:3866125, mRNA	BC035467	Hs.301226	
}		/gb=BC035467 /gi=22028050			
		/ug=Hs.301226 /len=2297		<u> </u>	
11480	0.031002	hypothetical protein FLJ23751	NM_152282	Hs.37443	NP_689495
	.	(FLJ23751), mRNA /cds=(121,1563)			
		/gb=NM_152282 /gi=22748648			1
		/ug=Hs.37443 /len=2994			
11481	0.042048	eps8 binding protein e3B1 mRNA,	AF006516		NP_005461
		complete cds	<u> </u>		
11482	0.04638	clone IMAGE:5271722, mRNA	BC038786	Hs.190456	
1		/gb=BC038786 /gi=24270905			1
<u></u>		/ug=Hs.190456 /len=1535			<u> </u>
11484	0.034378	casein alpha s1 (CSN1S1), mRNA	NM_001890	Hs.3155	NP_001881
2		/cds=(50,607) /gb=NM_001890			
<u> </u>		/gi=4503084 /ug=Hs.3155 /len=981			
11497	0.034378	FK506 binding protein 14, 22 kDa	NM_017946	Hs.264636	NP_060416
1]	(FKBP14), mRNA /cds=(146,781)		;	}
)		/gb=NM_017946 /gi=8923658			
		/ug=Hs.264636 /len=2248	 	ļ <u> </u>	<u> </u>
		creatine kinase, brain (Ckb), mRNA	NM_021273	 	NP_067248
11513	0.020126	sulfatase SULF1 precursor, mRNA,	AF545571	Hs.70823	NP_055985
1	1	complete cds /cds=(707,3322)		}	
1		/gb=AF545571 /gi=28191289		1	
L	L	/ug=Hs.70823 /len=5699	<u>l </u>	<u> </u>	<u></u>

11517 O. 11518 O. 11520 O.	.002982	602943821F1 NIH_MGC_19 cDNA clone IMAGE:5091917 5', mRNA sequence /clone=IMAGE:5091917 /clone_end=5' /gb=BI194863 /gi=14649883 /ug=Hs.444288 /len=863 fasciculation and elongation protein zeta 1 (zygin I) (FEZ1), transcript variant 1, mRNA RAB22A, member RAS oncogene family (RAB22A), mRNA /cds=(241,825) /gb=NM_020673 /gi=10190713 /ug=Hs.288968 /len=1728 MYLE protein (MYLE), mRNA /cds=(12,299) /gb=NM_014015 /gi=13384596 /ug=Hs.11902 /len=1120	NM_020673	No. Hs. 444288 Hs. 288968 Hs. 11902	NP_072043 NP_065724 NP_054734
11517 O. 11518 O. 11520 O.	.002982	clone IMAGE:5091917 5', mRNA sequence /clone=IMAGE:5091917 /clone_end=5' /gb=BI194863 /gi=14649883 /ug=Hs.444288 /len=863 fasciculation and elongation protein zeta 1 (zygin I) (FEZ1), transcript variant 1, mRNA RAB22A, member RAS oncogene family (RAB22A), mRNA /cds=(241,825) /gb=NM_020673 /gi=10190713 /ug=Hs.288968 /len=1728 MYLE protein (MYLE), mRNA /cds=(12,299) /gb=NM_014015	NM_005103 NM_020673	Hs.288968	NP_065724
11518 0. 11520 0.	.002982	sequence /clone=IMAGE:5091917 /clone_end=5' /gb=BI194863 /gi=14649883 /ug=Hs.444288 /len=863 fasciculation and elongation protein zeta 1 (zygin I) (FEZ1), transcript variant 1, mRNA RAB22A, member RAS oncogene family (RAB22A), mRNA /cds=(241,825) /gb=NM_020673 /gi=10190713 /ug=Hs.288968 /len=1728 MYLE protein (MYLE), mRNA /cds=(12,299) /gb=NM_014015	NM_020673		NP_065724
11518 O. 11520 O.	.002982 .025072 .022485	/clone_end=5' /gb=BI194863 /gi=14649883 /ug=Hs.444288 /len=863 fasciculation and elongation protein zeta 1 (zygin I) (FEZ1), transcript variant 1, mRNA RAB22A, member RAS oncogene family (RAB22A), mRNA /cds=(241,825) /gb=NM_020673 /gi=10190713 /ug=Hs.288968 /len=1728 MYLE protein (MYLE), mRNA /cds=(12,299) /gb=NM_014015	NM_020673		NP_065724
11518 O. 11520 O.	.002982	/gi=14649883 /ug=Hs.444288 /len=863 fasciculation and elongation protein zeta 1 (zygin l) (FEZ1), transcript variant 1, mRNA RAB22A, member RAS oncogene family (RAB22A), mRNA /cds=(241,825) /gb=NM_020673 /gi=10190713 /ug=Hs.288968 /len=1728 MYLE protein (MYLE), mRNA /cds=(12,299) /gb=NM_014015	NM_020673		NP_065724
11518 O. 11520 O.	.025072	1 (zygin I) (FEZ1), transcript variant 1, mRNA RAB22A, member RAS oncogene family (RAB22A), mRNA /cds=(241,825) /gb=NM_020673 /gi=10190713 /ug=Hs.288968 /len=1728 MYLE protein (MYLE), mRNA /cds=(12,299) /gb=NM_014015	NM_020673		NP_065724
11520 0.	.025072	mRNA RAB22A, member RAS oncogene family (RAB22A), mRNA /cds=(241,825) /gb=NM_020673 /gi=10190713 /ug=Hs.288968 /len=1728 MYLE protein (MYLE), mRNA /cds=(12,299) /gb=NM_014015	 		<u> </u>
11520 0.	.025072	RAB22A, member RAS oncogene family (RAB22A), mRNA /cds=(241,825) /gb=NM_020673 /gi=10190713 /ug=Hs.288968 /len=1728 MYLE protein (MYLE), mRNA /cds=(12,299) /gb=NM_014015	 		<u> </u>
11520 0.	.022485	family (RAB22A), mRNA /cds=(241,825) /gb=NM_020673 /gi=10190713 /ug=Hs.288968 /len=1728 MYLE protein (MYLE), mRNA /cds=(12,299) /gb=NM_014015	 		<u> </u>
	.022485	/gb=NM_020673 /gi=10190713 /ug=Hs.288968 /len=1728 MYLE protein (MYLE), mRNA /cds=(12,299) /gb=NM_014015		Hs.11902	NP_054734
	.022485	/ug=Hs.288968 /len=1728 MYLE protein (MYLE), mRNA /cds=(12,299) /gb=NM_014015	NM_014015	Hs.11902	NP_054734
	.022485	MYLE protein (MYLE), mRNA /cds=(12,299) /gb=NM_014015	NM_014015	Hs.11902	NP_054734
		/cds=(12,299) /gb=NM_014015	NM_014015	Hs.11902	NP_054734
		/cds=(12,299) /gb=NM_014015	NM_014015	Hs.11902	NP_054734
11536	N				
11536		/gi=13384596 /ug=Hs.11902 /len=1120			
11536	0.04630		I	1	
110301 (EST(yh89e10.r1 cDNA clone 136938 5')	D20464	 	NP 001002
		8e-06 match	K3040 I		INP_001002
11570 0.		clone IMAGE:5295896, mRNA	BC043240	Hs.104413	
11970 0.		/gb=BC043240 /gi=27695834	DC043240	113.104413	
		/ug=Hs.104413 /len=2136			
11587 0.		EST(ga18c02.x1 NCI_CGAP_Brn23	AI094920	1	NP 001685
11007 0.		clone IMAGE:1687106 3' gb:M62762			
		VACUOLAR ATP SYNTHASE 16 KD			
		PROTEOLIPID SUBUNIT)			
11588 0		EST(oz13e06.x1	AI078464		
. 1	į	Soares_fetal_liver_spleen_1NFLS_S1			
, ·		clone IMAGE:1675234 3')			
11590 0	.038054	UI-E-EJ0-aig-j-08-0-UI.s1 UI-E-EJ0	BM682503	Hs.446242	
	,	cDNA clone UI-E-EJ0-aig-j-08-0-UI 3',			1
	9	mRNA sequence /clone=UI-E-EJ0-aig-j-			
	£ 100	08-0-UI /clone_end=3' /gb=BM682503			
	,	/gi=18992399 /ug=Hs.446242 /len=1052	<u> </u>		· ·
			<u> </u>	 	
11597 0	0.020126	EST HUM517A08B Clontech human	D63277		,
	*	placenta polyA mRNA (#6572) Human			·
		sapiens cDNA clone GEN-517A08 5'			
11640 0	024270	The 2 mDNA complete add	AF441770	Hs.16411	
11612 0	1.034378	Tho2 mRNA, complete cds	AF441//U	115.10411	
·		/cds=(1,4437) /gb=AF441770			
		/gi=20799317 /ug=Hs.16411 /len=4452		, .	İ
11657	0.04638	hypothetical protein FLJ23320	NM_024672	Hs.85910	NP 078948
1100/	V.U -1 U30	(FLJ23320), mRNA /cds=(117,2195)	11111_02-7072	1. 15.000 10	10,0040
		/gb=NM_024672 /gi=13375933			,
		/ug=Hs 85910 /len=2337	į.		

ì	Spot	p-value	Description	Gene	Unigene	Protein
		ž.		Accession	Accession	Accession
F	44704	0.040040	af in a line of a major and maked father	No.	No. Hs.250175	No.
1	11701	0.042048	of yeast long chain polyunsaturated fatty	NIVI_UZ 10 14	IU8.500112	NP_068586
١		of The Superior	acid elongation enzyme 2 (HELO1),			
1			mRNA /cds=(345,1244)			
۱			/gb=NM_021814 /gi=21361903			1
ŀ	11702	0.04639	/ug=Hs.250175 /len=3011 eukaryotic translation elongation factor	NM 001402	Hs.422118	NP 001393
1	11702	0.04036	1 alpha 1 (EEF1A1), mRNA	14101_001402	113.422110	ME_001393
1		: 1	/cds=(63,1451) /gb=NM_001402			·
1			/gi=25453469 /ug=Hs.422118 /len=1837		iner in the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the seco	
1			/gi=25455465 /dg=i15.422 i 16 /icii=1657			
ŀ	11703	0.016031	hypothetical protein MGC3295	NM_025246	Hs.101257	NP 079522
١		0.010001	(MGC3295), mRNA /cds=(510,1748)		· · · · · · · · · · · · · · · · · · ·	
ı			/gb=NM_025246 /gi=13376859			i
			/ug=Hs.101257 /len=1958			
Ì	11704	0.014265	solute carrier family 1 (neutral amino	NM 005628	Hs.183556	NP 005619
1			acid transporter), member 5 (SLC1A5),		,	_
1			mRNA /cds=(591,2216)			
	:		/gb=NM_005628 /gi=5032092			}
1			/ug=Hs.183556 /len=2856			
ſ	11707	0.020126	transmembrane 4 superfamily member	NM_004615	Hs.82749	NP_004606
			2 (TM4SF2), mRNA /cds=(62,811)			
1		1	/gb=NM_004615 /gi=21265103			}
	·		/ug=Hs.82749 /len=1813			
	11767	0.04638	Purkinje cell protein 4 (PCP4), mRNA	NM_006198	Hs.80296	NP_006189
ľ			/cds=(58,246) /gb=NM_006198			1
ŀ			/gi=5453857 /ug=Hs.80296 /len=540	11/25/020	11 04400	
	11774	0.027906	FLJ30424 fis, clone BRACE2008881,	AK054986	Hs.21423]. :]
1			weakly similar to ZINC FINGER			
1			PROTEIN 195 /cds=UNKNOWN	1.		
1	* .		/gb=AK054986 /gi=16549625			1
}	11775	0.011228	/ug=Hs.21423 /len=2144 UI-E-CQ1-acq-f-05-0-UI.r1 UI-E-CQ1	BM688680	Hs.406520	
-	11//3	0.011220	cDNA clone UI-E-CQ1-acq-f-05-0-UI 5',	DIVIOGOOOO	115.400520	
1			mRNA sequence /clone=UI-E-CQ1-acq-			
1			f-05-0-UI /clone_end=5' /gb=BM688680			
-			/gi=19001938 /ug=Hs.406520 /len=934			
١	•		1500 1500 7dg 15. 150020 1511 501			
ł	11780	0.014265	mRNA for KIAA1559 protein, partial cds.	AB046779	Hs.35524	
1			/cds=(61,1695) /gb=AB046779		1	}
١			/gi=10047182 /ug=Hs.35524 /len=5659]
١						
Ì	11787	0.022485	inhibitor of Bruton's tyrsoine kinase	NM_015525	Hs.306425	NP_056340
1			(IBTK), mRNA /cds=(420,1031)			{
١		1	/gb=NM_015525 /gi=24308082	,		
١	·		/ug=Hs.306425 /len=2240	<u> </u>		<u> </u>
-	11810	0.016031	egl nine 3 (C. elegans) (EGLN3), mRNA	NM_022073	Hs.18878	NP_203130
ł			/cds=(327,1046) /gb=NM_022073			1
			/gi=11545786 /ug=Hs.18878 /len=2770			 `
		<u> </u>		<u> </u>	<u></u>	

	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11818	0.04638	clone 23698 mRNA sequence	AF052094	Hs.8136	
		/gb=AF052094 /gì=3360400			
		/ug=Hs.8136 /len=1264			
11822	0.038054	protein phosphatase 2, regulatory	NM_002719	Hs.171734	NP_848703
		subunit B (B56), gamma isoform			
	. `	(PPP2R5C), mRNA /cds=(89,1633)		**	
		/gb=NM_002719 /gi=4506022			
		/ug=Hs.171734 /len=4064			
11840	0.04638	mitogen-activated protein kinase kinase	NM_006609	Hs.28827	NP_006600
		kinase 2 (MAP3K2), mRNA			
- 1		/cds=(102,1964) /gb=NM_006609			
		/gi=21735555 /ug=Hs.28827 /len=3336	Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Salah Sa	}	
			<u>i</u>		
11843	0.012669	kinesin family member 13B (KIF13B),	NM_015254	Hs.15711	NP_056069
		mRNA /cds=(38,5518) /gb=NM_015254		o.	
		/gi=13194196 /ug=Hs.15711 /len=8743			
		4 4			
11859	0.027906	hypothetical protein FLJ13590	NM_024840	Hs.183390	NP_079116
		(FLJ13590), mRNA /cds=(465,2210)			
	la di	/gb=NM_024840 /gi=21362002		la de la companya de la companya de la companya de	} '
		/ug=Hs.183390 /len=2225			
11922	0.025072	Hypothetical protein MGC30022, cDNA	AK022894	Hs.179852	NP_689490
		FLJ12832 fis, clone NT2RP2003137			- 1
İ		/cds=UNKNOWN /gb=AK022894			
		/gi=10434551 /ug=Hs.179852 /len=2540			
					·
11927	0.031002	CCR4-NOT transcription complex,	NM_004779	Hs.26703	NP_004770
	. ,	subunit 8 (CNOT8), mRNA		}	
		/cds=(245,1123) /gb=NM_004779	*		
		/gi=24496777 /ug=Hs.26703 /len=2489			
			<u> </u>		
11932	0.034378	LIN-7 protein 3, cDNA: FLJ21887 fis,	AK025540	Hs.91393	NP_060832
		clone HEP03135, highly similar to	٠.		
1.5		AF090900 Homo sapiens clone			
1.		HQ0189 PRO0189 mRNA			
		/cds=UNKNOWN /gb=AK025540		}	ť
		/gi=10438087 /ug=Hs.91393 /len=2440			
	,				
11947	0.042048	polymerase (RNA) II (DNA directed)	NM_006232	Hs.432574	NP_006223
		polypeptide H (POLR2H), mRNA		1	mar f
(·		/cds=(88,540) /gb=NM_006232	,		[-
ļ		/gi=14589952 /ug=Hs.432574 /len=821		}	Į.
	<u> </u>		L		
11962	0.038054	aquaporin 3 (AQP3), mRNA	NM_004925	Hs.234642	NP_004916
]		/cds=(63,941) /gb=NM_004925		j	
1	1	/gi=22165421 /ug=Hs.234642 /len=1835	ŀ		
		1/91-22 10342 1 /ug-113.234042 /1611-1033	!		İ

Spot	p-valu	Description	Gene	Unigene	Protein
37			Accession	Accession	Accession
			No.	No.	No.
11968	0.025072	likely ortholog of mouse Mak3p (S.	NM_025146	Hs.288932	NP 079422
		cerevisiae) (MAK3P), mRNA	_		':
		/cds=(301,810) /gb=NM_025146	la de la companya de la companya de la companya de Mangana de la companya de la companya de la companya de la companya de la companya de la companya de la companya		
		/gi=13376734 /ug=Hs.288932 /len=3576			
		, g. 1, c. 2, g. 1, g. 2, g. 2, g. 2, s. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1, g. 1			
12005	0.04638	EST(no44e03.s1 NCI CGAP Pr23	AA622352		
12,000		cDNA clone IMAGE:1103548)	7 1022002		
12064	0.012669	oq82d05.x5 NCI_CGAP_Kid6 cDNA	AI733421	Hs.337206	
	0.0.2000	clone IMAGE:1592841 3', mRNA	,, 60 ,,	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
		sequence /clone=IMAGE:1592841]_
		/clone_end=3' /gb=AI733421			
		/gi=5054534 /ug=Hs.337206 /len=508			
12067	0.012660	UI-H-ED1-axq-o-07-0-UI.s1	CA445564	Hs.243319	
12007	0.012003	NCI_CGAP_ED1 cDNA clone UI-H-ED1-	C/440004	118.240019	
		axg-o-07-0-UI 3', mRNA sequence			
		/clone≃UI-H-ED1-axq-o-07-0-UI			
		/clone end=3' /gb=CA445564			
	. ,				
		/gi=24809984 /ug=Hs.243319 /len=539		· .	
12077	0.024270	QV0-LT0015-180200-127-c04 LT0015)	A1A100E464	<u></u>	ND 000044
			AW835461		NP_006241
12147	0.020126	cDNA sequence(cDNA sequence	AL050376		1
		DKFZp586J101 (from clone cDNA		٠.	
10170	0.000054	sequence DKFZp586J101))	101.400474		NID 570 400
12176	0.038054	engulfment and cell motility 2 (ced-12 C.	NW_1331/1	Hs.96560	NP_573403
		elegans) (ELMO2), transcript variant 1,			•
		mRNA /cds=(141,2303)			
		/gb=NM_133171 /gi=19718768		*	1
10100		/ug=Hs.96560 /len=3630			115 25/152
12187	0.031002	myeloid/lymphoid or mixed-lineage	NM_018682	Hs.333300	NP_061152
٠. ١		leukemia 5 (trithorax Drosophila)			
		(MLL5), mRNA /cds=(202,5778)			
:		/gb=NM_018682 /gi=23503326			
		/ug=Hs.333300 /len=6543			
12190	0.011228	oxysterol binding protein-like 11	NM_022776	Hs.61260	INP_073613
·	,	(OSBPL11), mRNA /cds=(306,2549)			
		/gb=NM_022776 /gi=23111058			1
		/ug=Hs.61260 /len=4206			
12201	0.012669	EST (Soares placenta Nb2HP	R76686	1	
		IMAGE:143740 3')			
12202	0.034378	F-box and leucine-rich repeat protein 3A	NM_012158	Hs.7540	NP_036290
	1	(FBXL3A), mRNA /cds=(298,1584)		14 · · · · · ·	
[/gb=NM_012158 /gi=16306583		ĺ	
		/ug=Hs.7540 /len=3489			
12231	0.042048	EST (UI-H-BI3-akf-b-05-0-UI.s1	AW449060		NP_061174
) ·	1.	NCI_CGAP_Sub5 clone			1
		IMAGE:2734017 3')		1 5	
12233	0.042048	chemokine-like factor super family 3	NM_144601	Hs.7773	NP_653202
,		(CKLFSF3), mRNA /cds=(527,1075)			1
1	}	/gb=NM_144601 /gi=21389400	}		1
		/ug=Hs.7773 /len=2318			<u> </u>

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12237	0.016031	EST (602496405F1 NIH_MGC_75	BG433151		1.75.
		clone IMAGE:4610376 5')			·
12238	0.020126	hypothetical protein LOC115286	NM 173471	Hs.379386	NP 775742
1 -		(LOC115286), mRNA /cds=(189,740)			_
	. '	/gb=NM_173471 /gi=27735034		•	
		/ug=Hs.379386 /len=1873			
12249	0.041895	7g24c01.x1 NCI CGAP GC6 cDNA	BF222857	Hs.331205	
· · · · · ·		clone IMAGE:3699073 3', mRNA		—	-
		sequence /clone=IMAGE 3699073			
		/clone_end=3' /gb=BF222857			1.
		/gi=11130034 /ug=Hs.331205 /len=503			-
12262	0.031002	EST (IL3-ET0114-281000-318-C11	BF870398		NP_037364
	5.55.652	ET0114)		· .	
12264	0.04638	clone IMAGE:3909104, mRNA	BC015719	Hs.8852	4.0
12201	0.01000	/gb=BC015719 /gi=16041698	200.01.0		£ .
	√ 37 €	/ug=Hs.8852 /len=3169			. •
12266	0.022485	DC2 protein (DC2), mRNA	NM 021227	Hs.103180	NP 067050
12200	0.022.100	/cds=(60,509) /gb=NM_021227	02 .2	11.9.100100	
		/gi=24308270 /ug=Hs.103180 /len=1090			
	,				
12268	0.027906	EST (ys15b03.r1 Soares fetal liver	H74096		
	· · · · · · · · · · · · · · · · · · ·	spleen IMAGE:214829 5')		-	·
12275	0.027906	EST(601885028F1 NIH_MGC_57 cDNA	BF218874		NP 003109
		clone IMAGE:4103479 5')	,		
12294	0.034378	EST(7e58a12.x1	BE644843		NP 006845
		Soares_NSF_F8_9W_OT_PA_P_S1			_
		cDNA clone IMAGE:3286654 3')			
12301	0.027906	UI-H-EZ1-bbc-h-11-0-UI.s1	BQ574842	Hs.235026	
		NCI CGAP Ch2 cDNA clone UI-H-EZ1-	, ,		•
		bbc-h-11-0-UI 3', mRNA sequence			٢.
		/clone=UI-H-EZ1-bbc-h-11-0-UI	s e		
		/clone_end=3' /gb=BQ574842			
٠.		/gi=21478159 /ug=Hs.235026 /len=1065			
		.			
12309	0.020126	junctional adhesion molecule 3 (JAM3),	NM 032801	Hs.334703	NP 116190
		mRNA /cds=(25,1092) /gb=NM_032801	<u>-</u> 		
		/gi=21704285 /ug=Hs.334703 /len=3675			
٠					
12327	0.022485	wr27c02.x1 NCI_CGAP_Pr28 cDNA	AI971263	Hs.166959	
		clone IMAGE:2488898 3' similar to			1
		WP:F31E8.2 CE02711 SNT-1:			1
		SYNAPTOTAGMIN;, mRNA sequence			
		/clone=IMAGE:2488898 /clone_end=3'		1	ĺ
·		/gb=Al971263 /gi=5768089		+	1
ŀ					

Spot	p-value	Description	Gen	Unigene	Protein
			Accession No.	Accession No.	Accession No.
12339	0.029136	collagen, type III, alpha 1 (Ehlers-	NM 000090	Hs.119571	NP 000081
		Danios syndrome type IV, autosomal			
		dominant) (COL3A1), mRNA			
		/cds=(118,4518) /gb=NM_000090			* *
		/gi=15149480 /ug=Hs.119571 /len=5489	* .		
. 1	÷.	, , , , , , , , , , , , , , , , , , ,			
12345	0.04638	ESTs, cDNA, 3' end	BG236123	Hs.127325	NP 009173
		/clone=IMAGE:4141713 /clone_end=3'			_
	•	/gb=BG236123 /gi=12749970	,	· .	
		/ug=Hs.127325 /len=489			
12370	0.022485	mRNA; cDNA DKFZp586N2424 (from	AL157503	Hs.27552	
	01022100	clone DKFZp586N2424) /gb=AL157503			₹
		/gi=7018553 /ug=Hs.27552 /len=2220			
		79. 10.0000 / 49.10.2002 / 10.10.10.10.10.10.10.10.10.10.10.10.10.1			1
12384	0.012669	FLJ31039 fis, clone HSYRA2000221	AK055601	Hs.311977	
	J, 10 1 m 0 0 0	/cds=UNKNOWN /gb=AK055601	, ,	1	·
		/gi=16550371 /ug=Hs.311977 /len=2770			
		, g			i .
12404	0.035996	clone IMAGE:5301545, mRNA	BC041951	Hs.177781	
		/gb=BC041951 /gi=27469737			, £
		/ug=Hs.177781 /len=2155			
12408	0.048742	cDNA MR1-FN0010-290700-007-g10	BE834948	1720 472 123	NP 803133
		FN0010 (=AC099562.1 Homo sapiens			
		chromosome 1 clone RP11-213P13,			
		WORKING DRAFT SEQUENCE, 3			
:		unordered pieces)			
12413	0.020126	cDNA FLJ14244 fis, clone	AK024306	Hs.397378	
	-,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	OVARC1000802. /gb=AK024306			
1		/gi=10436654 /ug=Hs.397378 /len=1889		Ì	
		g	,		
12418	0.048742	yw19d08.r1 Morton Fetal Cochlea cDNA	H87947	Hs.188912	
		clone IMAGE:252687 5', mRNA			, .
		sequence /clone=IMAGE:252687	* .		
		/clone_end=5' /gb=H87947 /gi=1069526			**
		/ug=Hs.188912 /len=411			
12438	0.016598	AV686223 GKC cDNA clone	AV686223	Hs.221642	
		GKCGXH11 5', mRNA sequence			
		/clone=GKCGXH11 /clone_end=5'			
		/gb=AV686223 /gi=10288086			
		/ug=Hs.221642 /len=916			<i>,</i>
12473	0.042048	xc09d01.x1 NCI_CGAP_Co21 cDNA	AW083503	Hs.311987	
		clone IMAGE:2583745 3' similar to			
		contains MER14.t2 MER14 repetitive			
[l	[element ,, mRNA sequence	1 :		
		/clone=IMAGE:2583745 /clone_end=3'			
	ļ.	/gb=AW083503 /gi=6038579	1		
		page and to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr			

Snot	p-value	Description	Gen	Unigene	Protein
Opor	p-value	Comption	Accession	Accession	Accession
			No.	No.	No.
12519	0.04638	EST(cDNA clone IMAGE:1637714 3'	AI000800	110.	1
		similar to contains Alu repetitive	<i>j</i>		
		element;contains L1.t1 L1 repetitive			
	0	element;)			
12550	0.025072	clone IMAGE:5019705, mRNA	BC021287	Hs.184544	
		/gb=BC021287 /gi=18204277			
		/ug=Hs.184544 /len=2121	,		
12555	0.022485	ESTs, cDNA, 5' end	BG698090	Hs.12876	* **
		/clone=IMAGE:4802969 /clone_end=5'		•	
		/gb=BG698090 /gi=13965026			
		/ug=Hs.12876 /len=985			
12580		No significant match	SEQ.ID.No.34		
12581	0.048742	no significant match, ORF+3(108~209)			
			SEQ.ID.No.40		
12582		No significant match	SEQ.ID.No.47		
12644	0.005206	EST (RC0-HT0297-301099-011-a06	BE151529		
		HT0297)			
12647	0.034378	EST(tm39b03.x1 NCI_CGAP_Kid11	Al478484		
		clone IMAGE:2160461 3' contains L1.b3		· ·	
		L1 repeat)			
12668	0.042048	hypothetical protein FLJ13110	NM_022912	Hs.7358	NP_075063
		(FLJ13110), mRNA /cds=(145,750)			
		/gb=NM_022912 /gi=12597656		1	
10000	0.040004	/ug=Hs.7358 /len=3856	NIN 450005	11.04400	NID 000500
12669	0.016031	hypothetical protein FLJ31438	NM_152385	Hs.24423	NP_689598
		(FLJ31438), mRNA /cds=(347,2107)			
		/gb=NM_152385 /gi=22748824	3		
12677	0.049640	/ug=Hs.24423 /len=2266 hypothetical protein MGC12981	NM 032357	Hs.104203	NP_115733
12077	0.010049	(MGC12981), mRNA /cds=(225,767)	INIVI_U32337	IDS. 104203	NP_115735
		/gb=NM_032357 /gi=21362049			
, .	6.5%	/ug=Hs.104203 /len=1644		*	1
12687	0.031002	wr41b04.x1 NCI_CGAP_Pr28 cDNA	AI972618	Hs.370369	
12007	0.031002	clone IMAGE:2490223 3', mRNA	A137 20 10	113.570303	
		sequence /clone=IMAGE:2490223		- "	
		/clone end=3'/gb=Al972618			
		/gi=5769444 /ug=Hs.370369 /len=225			
12711	0.005206	EST(ne80b06.s1 NCI CGAP Ew1	AA491607		
' '		cDNA clone IMAGE:910547)			
12712	0.025072	EST(xg51d02.x1 NCI_CGAP_Ut4 cDNA	AW150422		
		clone IMAGE:2631843 3' similar to			
		contains Alu repetitive element)			
12721	0.031002	EST (wg23f05.x1	AI740626		
		Soares_NSF_F8_9W_OT_PA_P_S1			
		cDNA clone IMAGE:2365953 3'			
		•			·

Spot	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
			No.	No.	No.
12762	0.022485	wd19h11.x1 Soares NFL T GBC S1	Al674745	Hs.377373	NO.
1 1		cDNA clone IMAGE:2328645 3', mRNA		,	
		sequence /clone=IMAGE:2328645			ļ
,		/clone_end=3' /gb=AI674745			1 .
		/gi=4875225 /ug=Hs.377373 /len=347			
	•				~
12767	0.025072	EST (602326911F1 NIH_MGC_91	BG036175	4	
		IMAGE:4428291 5')			
12782	0.025072	EST (CM3-LT0042-271299-060-c05	AW837690		
		LT0042 cDNA)			
12822	0.034378	yu41a04.y5 Soares ovary tumor NbHOT	Al820819	Hs.193116	
		cDNA clone IMAGE:236334 5' similar to			
		contains Alu repetitive element;, mRNA			
·		sequence /clone=IMAGE:236334			1
		/clone_end=5' /gb=Al820819			
		/gi=5439898 /ug=Hs.193116 /len=567	,		
12024	0.004545		1114 000040	70500	110 00000
12824	0.004545	ubiquitin-conjugating enzyme E2G 1	NM_003342	Hs.78563	NP_003333
		(UBC7 C. elegans) (UBE2G1), mRNA			
		/cds=(167,679) /gb=NM_003342			
•.	*	/gi=21314607 /ug=Hs.78563 /len=2430		A CHARLES	
12855	0.01798	UI-E-EJ0-aik-i-20-0-UI r1 UI-E-EJ0	BM727413	Hs.112619	
.2000	9.017.00	cDNA clone UI-E-EJ0-aik-i-20-0-UI 5',	B.W. 27 4 10	113.112013	
		mRNA sequence /clone=UI-E-EJ0-aik-i-			
		20-0-UI /clone_end=5' /gb=BM727413			
	-	/gi=19048746 /ug=Hs.112619 /len=1667		`	· ·
12861	0.034378	cDNA FLJ25876 fis, clone CBR02529.	AK098742	Hs.375841	
		/gb=AK098742 /gi=21758849			
		/ug=Hs.375841 /len=1877			
12875	0.038054	clone FLB3344 PRO0845 mRNA,	AF130048	Hs.6390	
		complete cds /gb=AF130048			
		/gi=11493402 /ug=Hs.6390 /len=2171			
12881	0.016031	UI-E-CK1-abp-g-01-0-UI.s1 UI-E-CK1	BM661590	Hs.229338	
-		cDNA clone UI-E-CK1-abp-g-01-0-UI 3',			
* :	•	mRNA sequence /clone=UI-E-CK1-abp-			
		g-01-0-UI /clone_end=3' /gb=BM661590			
1 4		/gi=18965457 /ug=Hs.229338 /len=1447			1
40057	0.00=0==				*
12957	0.025072	xj85e09.x1 Soares_NFL_T_GBC_S1	AW173284	Hs.370871	
		cDNA clone IMAGE:2664040 3', mRNA	,		
		sequence /clone=IMAGE:2664040			- ,
		/clone_end=3' /gb=AW173284	-	***	
		/gi=6439232 /ug=Hs.370871 /len=548			
				1	L

Spot	p-valu	Description	Gene Accession	Unigene Accession	Protein Accession
			No.	No.	No.
12965		UI-H-ED1-axy-n-13-0-UI.s1	BQ009853	Hs.438790	
		NCI_CGAP_ED1 cDNA clone			
		IMAGE:5835468 3', mRNA sequence		•	-1,
		/clone=IMAGE:5835468 /clone_end=3'			
		/gb=BQ009853 /gi=19734754			
		/ug=Hs.438790 /len=1069			*
13003		BX108813 Soares retina N2b4HR cDNA	BX108813	Hs.144186	
		clone IMAGp998E03436, mRNA	* .		,
		sequence			· I
		/clone=IMAGp998E03436_;_IMAGE:22	,		
		0010 /gb=BX108813 /gi=27877460		3 4 1	
		/ug=Hs.144186 /len=668			
13040		UI-E-EJ1-aji-d-10-0-UI.s1 UI-E-EJ1	BM684333	Hs.17910	- 4.
		cDNA clone UI-E-EJ1-aji-d-10-0-UI 3',	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s		4
		mRNA sequence /clone=UI-E-EJ1-aji-d-			
$\mathcal{D}(X_i)$		10-0-UI /clone_end=3' /gb=BM684333			
		/gi=18994229 /ug=Hs.17910 /len=1036			
			in an english		
	0.038054		SEQ.ID.No.30		
13069		EST(PM1-HT0422-160300-009-a12	BE160886		
	1	HT0422 Homo sapiens cDNA, MRNA			
		sequence)		•	
13076		UI-H-BI1-abw-h-07-0-UI.s1	AW138111	Hs.436560	
		NCI_CGAP_Sub3 cDNA clone			
		IMAGE:2713572 3', mRNA sequence			
		/clone=IMAGE:2713572 /clone_end=3'			1
		/gb=AW138111 /gi=6142429			
		/ug=Hs.436560 /len=800			
		No significant match, ORF-1(155~328)	SEQ.ID.No.81		
13139	0.027906	chromosome 1 open reading frame 8	NM_004872	Hs.416495	NP_004863
		(C1orf8), mRNA /cds=(251,1222)	100		
		/gb=NM_004872 /gi=27545320			
		/ug=Hs.416495 /len=1709			
13170	0.011228	nucleolar protein family 6 (RNA-	NM_022917	Hs.183253	NP_631981
		associated) (NOL6), transcript variant			
		alpha, mRNA /cds=(61,3501)	. :		,
		/gb=NM_022917 /gi=22212928			
<u></u>		/ug=Hs.183253 /len=4854			
13197		similar to rat nuclear ubiquitous casein	NM_022731	Hs.118064	NP_073568
		kinase 2 (NUCKS), mRNA	4		
	. 1	/cds=(67,558) /gb=NM_022731			
		/gi=12232386 /ug=Hs.118064 /len=1811			
13212	0.026138	hypothetical protein FLJ20060	NM_017645	Hs 54617	NP_060115
	,	(FLJ20060), mRNA /cds=(72,2078)	•		'
		/gb=NM_017645 /gi=24431978			
		/ug=Hs.54617 /len=2884			

Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
	-		No.	No.	No.
13237	0.042048	KIAA0635 gene product (KIAA0635),	NM_014645	Hs.185091	NP_055460
•		mRNA /cds=(833,3373)			
		/gb=NM_014645 /gi=7662215			
		/ug=Hs.185091 /len=5138		·,;	
13274	0.031002	TAF7 RNA polymerase II, TATA box	NM_005642	Hs.155188	NP_005633
		binding protein (TBP)-associated factor,			
		55kDa (TAF7), mRNA /cds=(741,1790)			
		/gb=NM_005642 /gi=14717406			
*!		/ug=Hs.155188 /len=2310			
13278	0.008765	601660815R1 NIH_MGC_72 cDNA	BE966810	Hs 336116	
		clone IMAGE:3915843 3', mRNA		1	
		sequence /clone=IMAGE:3915843	*	1 2	
		/clone end=3' /gb=BE966810			
		/gi=11772610 /ug=Hs.336116 /len=730			
13283	0.02729	SEC24 related gene family, member D	NM 014822	Hs.19822	NP 055637
		(S. cerevisiae) (SEC24D), mRNA	7		,
		/cds=(201,3299) /gb=NM_014822	4.4		
		/gi=7662658 /ug=Hs.19822 /len=3988			
13303	0.012669	xf50g03.x1 NCI_CGAP_Gas4;cDNA	AW130421	Hs.329722	
		clone IMAGE:2621524 3' similar to			
		contains element MER4 repetitive		7	
	·	element ;, mRNA sequence			3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
		/clone=IMAGE:2621524 /clone_end=3'			
	1	/gb=AW130421 /gi=6132026			
		/ug=Hs.329722 /len=719			
13317	0.038054	Mannosidase, alpha, class 1A, member	AK024588	Hs.25253	NP_005898
, , ,	0.44040 /	1, cDNA: FLJ20935 fis, clone			
		ADSE01534 (AK024588.1)	· · · · · · · · · · · · · · · · · · ·		
13335	0.031002	hypothetical protein FLJ12118	NM 024537	Hs.381043	NP 078813
.0000	0.00,002	(FLJ12118), mRNA /cds=(24,1718)	0_ 1001		
		/gb=NM 024537 /gi=13375694			
		/ug=Hs.381043 /len=1843			
13336	0.031002	EST388184 MAGE resequences,	AW976075	Hs.401959	ř .
1.0000	0.007002	MAGN cDNA, mRNA sequence	,, ,,	1,0,10,000	
	-	/gb=AW976075 /gi=8167298			
		/ug=Hs.401959 /len=698	. **		
13341	0.04638	leucine aminopeptidase 3 (LAP3),	NM_015907	Hs.182579	NP_056991
	0.01000	mRNA /cds=(187,1746)	0.000.	1.10.102010	
		/gb=NM 015907 /gi=7705687			
		/ug=Hs.182579 /len=2147			,
13347	0.042048	general transcription factor IIB (GTF2B),	NM 001514	Hs.258561	NP_001505
100,7	3.072070	mRNA /cds=(39,989) /gb=NM 001514	1101_001014	1.13.203307	-00 1000
· .	:	/gi=13435384 /ug=Hs.258561 /len=1268		• * • • • • • • • • • • • • • • • • • •	
		10-10-000-749=115.20000171611-1200			
13348	0.01708	hypothetical protein FLJ14153	NM_022736	Hs:7503	NP_073573
,,,,,,,	0.01730	(FLJ14153), mRNA /cds=(31,1428)	, <u>022</u>	13.7505	_0,00,0
	1.5	/gb=NM_022736 /gi=12232392			
		/ug=Hs.7503-/len=2161	+		
		1/49 113.7000 /ICII-2 10 1	ļ	 	

	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13354	0.016031	catenin, beta like 1 (CTNNBL1), mRNA /cds=(95,1786) /gb=NM_030877	NM_030877	Hs.178576	NP_110517
		/gi=18644733 /ug=Hs 178576 /len=1900			
13355	0.042048	mRNA; cDNA DKFZp313E1815 (from clone DKFZp313E1815) /gb=AL833098	AL833098	Hs.125031	
		/gi=21733689 /ug=Hs.125031 /len=1937			
13366	0.014265	hypothetical protein DKFZp434I1916	NM_032245	Hs.334641	NP_115621
		(DKFZp434I1916), mRNA /cds=(144,563) /gb=NM_032245 /gi=14149959 /ug=Hs.334641 /len=800			
13376	0.025072	hypothetical protein FLJ20276	NM_017738	Hs.270502	NP_060208
		(FLJ20276), mRNA /cds=(134,3388) /gb=NM_017738 /gi=8923250 /ug=Hs.270502 /len=4790			
13379	0.031002		NM_007218	Hs.28285	NP_009149
		/cds=(215,2209) /gb=NM_007218 /gi=21314653 /ug=Hs.28285 /len=2481		ing a stage	
13391	0.038054	chondroitin sulfate GalNAcT-2	NM_018590	Hs.180758	NP_061060
		(GALNACT-2), mRNA /cds=(336,1964) /gb=NM_018590 /gi=24429591 /ug=Hs.180758 /len=3745			
13441	0.025072	hypothetical protein FLJ10769 (FLJ10769), mRNA /cds=(15,1187)	NM_018210	Hs.8083	NP_060680
	, e	/gb=NM_018210 /gi=8922653 /ug=Hs.8083 /len=2659			
13477	0.032415	cytoplasmic FMR1 interacting protein 1 (CYFIP1), mRNA /cds=(53,3814)	NM_014608	Hs.77257	NP_055423
		/gb=NM_014608 /gi=24307968 /ug=Hs.77257 /len=4394			
13478	0.04638	EST(xd92a04.x1 Soares_NFL_T_GBC_S1 clone	AW117454		NP_073592
		IMAGE:2605038 3')			
13483	0.031002	EST(oy85h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 clone IMAGE:1672661 3')	AI038280		
13485	0.01798	UI-H-FE1-bdt-o-02-0-UI.s1 NCI_CGAP_FE1 cDNA clone UI-H-FE1-	BU630228	Hs.402266	
		bdt-o-02-0-UI 3', mRNA sequence /clone=UI-H-FE1-bdt-o-02-0-UI			
		/clone_end=3' /gb=BU630228 /gi=23296993 /ug=Hs.402266 /len=703		•	

Spot	p-valu	D scription	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
13486	0.04638	catenin (cadherin-associated protein),	NM_003798	Hs.58488	NP_003789
		alpha-like 1 (CTNNAL1), mRNA			
		/cds=(44,2248) /gb=NM_003798			
		/gi=4503128 /ug=Hs.58488 /len=2446	· · · · · · · · · · · · · · · · · · ·		
13491	0.04638	hypothetical protein MGC33602	NM_152391	Hs.274415	NP_689604
-		(MGC33602), mRNA /cds=(140,748)	٠ .		-
		/gb=NM_152391 /gi=22748836	•		
		/ug=Hs.274415 /len=1790			
13514	0.027906	cDNA FLJ39478 fis, clone	AK096797	Hs.372680	
		PROST2013605. /gb=AK096797	•		
		/gi=21756367 /ug=Hs.372680 /len=2507		•	
13516	0.025072		Al268689		
		IMAGE:1911689 3')			
13523	0.012669	UI-H-DI0-auw-o-12-0-UI.s1	BM997944	Hs.444026	
		NCI_CGAP_DI0 cDNA clone			
	· ·	IMAGE:5875427 3', mRNA sequence			
		/clone=IMAGE:5875427 /clone_end=3'			
		/gb=BM997944 /gi=19722845	•		
		/ug=Hs.444026 /len=753		<u>'</u>	
13545	0.044138	yg03b02.s1 Soares infant brain 1NIB	R42618	Hs.12700	
		cDNA clone IMAGE:30959 3', mRNA			•
		sequence /clone=IMAGE:30959			
		/clone_end=3' /gb=R42618 /gi=817379			
		/ug=Hs.12700 /len=441			
13550	0.038054	cDNA FLJ39435 fis, clone	AK096754	Hs.376116	
		PROST2004727. /gb=AK096754	· ·		
, 1		/gi=21756318 /ug=Hs.376116 /len=2450			'
13558	0.022485	DKFZP564O0823 protein	NM_015393	Hs.105460	NP_056208
		(DKFZP564O0823), mRNA			
		/cds=(171,905) /gb=NM_015393			
		/gi=7661631 /ug=Hs.105460 /len=2155		• .	- 1
13560	0.031002	EST (tz36f03.x1 NCI_CGAP_Ut2 cDNA	AI783534		
		clone IMAGE:2290685 3')			
13562	0.011228	AGENCOURT_6653840	BM924828	Hs.181174	
		NIH_MGC_116 cDNA clone			1
	· .	IMAGE:5761286 5', mRNA sequence			
		/clone=IMAGE:5761286 /clone_end=5'			,
		/gb=BM924828 /gi=19375207			
		/ug=Hs.181174 /len=1422			
13569	0.031002	EST (tu41c10.x1 NCI_CGAP_Pr28	AI686385		
		cDNA clone IMAGE:2253618 3' similar		,	
		to contains Alu repetitive element;)			
13582	0.01798	mRNA; cDNA DKFZp586M1819 (from	AL834255	Hs.355753	NP_848934
		clone DKFZp586M1819) /cds=(1,795)		j ;	
-		/gb=AL834255 /gi=21739805			
		/ug=Hs.355753 /len=1723			

Sp	ot	p-value	Description	Gene	Unigene	Protein
'	Į	•		Accession	Accession	Accession
				No.	No.	No.
135	598	0.025072	PP3731 mRNA sequence	AF258562	Hs.352231	
1			/cds=(1443,1751) /gb=AF258562			
			/gi=10834669 /ug=Hs.352231 /len=1946			
			3			1
136	300	0.04638	Cdc42 guanine nucleotide exchange	NM 015185	Hs.54697	NP_056000
			factor (GEF) 9 (ARHGEF9), mRNA	=		
1			/cds=(802,2352) /gb=NM 015185			
			/gi=7662107 /ug=Hs.54697 /len=5413			2 45 7 7 7
136	312	0.04638	poly(rC) binding protein 2 (PCBP2),	NM 005016	Hs.63525	NP 114366
			transcript variant 1, mRNA			
	- 1		/cds=(89,1189) /gb=NM_005016	,		
)			/gi=14141167 /ug=Hs.63525 /len=1362			•
1			3			
136	618	0.027906	B-cell CLL/lymphoma 10 (BCL10),	NM 003921	Hs.193516	NP_003912
			mRNA /cds=(706,1407)			
		· · ·	/gb=NM 003921 /gi=20336470			
			/ug=Hs.193516 /len=2809		·	
136	334	0.009931	non-SMC (structural maintenance of	NM 145080	Hs.284295	NP_659547
			chromosomes) element 1 protein	<u> </u>		
1		•	(NSE1), mRNA /cds=(24,794)		Ì	
1 .		•	/gb=NM_145080 /gi=21489972		,	
			/ug=Hs.284295 /len=992			
136	646	0.011228	FLJ13090 fis, clone NT2RP3002142	AK023152	Hs.287955	
			/cds=UNKNOWN /gb=AK023152			
Į.			/gi=10434945 /ug=Hs.287955 /len=2182			
ŀ					•	4.1
130	659	0.027906	hypothetical protein (HSPC016), mRNA	NM_015933	Hs.397853	NP_057017
			/cds=(39,233) /gb=NM_015933			-
l			/gi=7705430 /ug=Hs.397853 /len=384			
130	662	0.008765	hypothetical protein FLJ14936	NM_032864	Hs.5301	NP_116253
1		·	(FLJ14936), mRNA /cds=(187,1125)			1
1		÷	/gb=NM_032864 /gi=24762235			
			/ug=Hs 5301 /len=2613			
130	665	0.004545	ubiquitin-conjugating enzyme E2 variant	NM_003350	Hs.79300	NP_003341
ı	,		2 (UBE2V2), mRNA /cds=(22,459)			
ļ			/gb=NM_003350 /gi=12025664			
1			/ug=Hs.79300 /len=1535			·
130	086	0.009931	transforming, acidic coiled-coil	NM_006997	Hs.272023	NP_008928
1			containing protein 2 (TACC2), mRNA	}		}
1			/cds=(87,3167) /gb=NM_006997			44
	,		/gi=11119413 /ug=Hs.272023 /len=3686			
L	٠				<u> </u>	
130	90	0.044138	mRNA; cDNA DKFZp566G1424 (from	AL122043	Hs.19221	
]			clone DKFZp566G1424) /gb=AL122043]
			/gi=6093233 /ug=Hs.19221 /len=4410]
			\\.	<u> </u>	l	<u></u>

Spot	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
			No.	No	No.
13691	0.006784	POP4 (processing of precursor , S. cerevisiae) (POP4), mRNA	NM_006627	Hs.421667	NP_006618
	14	/cds=(26,688) /gb=NM_006627			
		/gi=5729985 /ug=Hs.421667 /len=1133			-
13700	0.014265	DJ467N11.1 protein, FLJ13127 fis,	AK023189	Hs.143917	NP 071374
, , , , , ,		clone NT2RP3002911 /cds=UNKNOWN			r -
		/gb=AK023189 /gi=10435003			* .
		/ug=Hs.143917 /len=3073		*	
13709	0.04638	hypothetical protein MGC2560	NM_031452	Hs.80624	NP 113640
		(MGC2560), mRNA /cds=(195,551)			_
		/gb=NM_031452 /gi=13899288			
		/ug=Hs.80624 /len=1229		200	
13718	0:029136	hypothetical protein MGC5370	NM_032739	Hs.332938	NP_116128
l		(MGC5370), mRNA /cds=(189,269)			N. C.
		/gb=NM 032739 /gi=14249363			
		/ug=Hs.332938 /len=974			
13722	0.044138	cDNA FLJ13032 fis, clone	AK023094	Hs.110956	:
		NT2RP3001120, moderately similar to			
		ZINC FINGER PROTEIN 136.			
		/cds=(120,1730) /gb=AK023094			•
		/gi=10434855 /ug=Hs.110956 /len=2316	. "		
					ı
13731	0.025072	diacylglycerol O-acyltransferase	NM_032564	Hs.334305	NP_115953
2	1 1	homolog 2 (mouse) (DGAT2), mRNA		•	
	۷.	/cds=(777,1670) /gb=NM_032564			
		/gi=14211870 /ug=Hs.334305 /len=2713			
			10-		No. 25 10
13761	0.016031		NM_130837	Hs.147946	NP_570850
		(OPA1), nuclear gene encoding			
		mitochondrial protein, transcript variant			
		8, mRNA /cds=(56,3103)			
		/gb=NM_130837 /gi=18860844		•	
		/ug=Hs.147946 /len=6029			
13782	0.014265	citrate synthase (CS), nuclear gene	NM_004077	Hs.239760	NP_004068
		encoding mitochondrial protein, mRNA	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	;	
		/cds=(1,1401) /gb=NM_004077	* 1		
		/gi=4758075 /ug=Hs.239760 /len=1401			
13783	0.027906	centrin, EF-hand protein, 2 (CETN2),	NM 004344	Hs.82794	NP 004335
[mRNA /cds=(48,566) /gb=NM_004344	_		_
		/gi=4757901 /ug=Hs.82794 /len=1087			
13803	0.038054	Rho-related BTB domain containing 3	NM_014899	Hs.10432	NP_055714
		(RHOBTB3), mRNA /cds=(336,2171)	_		- -
		/gb=NM_014899 /gi=7662355			
		/ug=Hs.10432 /len=4099			

Spot	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
12010	0.031003	hypothotical protoin EL 111577	No. NM_025159	No.	No.
13810	v.os i voš	hypothetical protein FLJ11577 (FLJ11577), mRNA /cds=(277,1182)	IAINI_059 (98	Hs.289065	NP_079435
l .	ا ماشنام در جاملا				
		/gb=NM_025159 /gi=13376758		ren en en en en en en en en en en en en e	
12011	0.042049	/ug=Hs.289065 /len=1808	NINE 047702	Ho 26424	ND 0600E0
13811	0.042048	hypothetical protein FLJ20360	NM_017782	Hs.26434	NP_060252
,		(FLJ20360), mRNA /cds=(80,2305)			
		/gb=NM_017782 /gi=8923334			
12027	0.042040	/ug=Hs.26434 /len=3041	NIM OCCOO	110 4745	ND 002702
13827	0.042046	proteasome (prosome, macropain) 26S	NM_002802	Hs.4745	NP_002793
		subunit, ATPase, 1 (PSMC1), mRNA		,	
		/cds=(49,1371) /gb=NM_002802			
		/gi=24430150 /ug=Hs.4745 /len=1586			
40000	0.04000	DKE7 5045040	NIVA 000400	11 400050	ND 005405
13860	0.04638	hypothetical protein DKFZp564F013	NM_020432	Hs.128653	NP_065165
		(DKFZP564F013), mRNA		<u> </u>	
		/cds=(107,2194) /gb=NM_020432			
		/gi=24308192 /ug=Hs.128653 /len=4572			
10070	0.004070	 	1100000		
13878	0.034378	EST(yr18g03.r1 cDNA clone 205684 5')	H63006		j .
40044	0.000405		NIM 040050*	11- 454040	ND 000000
13914	0.022485 	hypothetical protein FLJ11193	NM_018356	Hs.151046	NP_060826
		(FLJ11193), mRNA /cds=(115,1443)			
		/gb=NM_018356 /gi=8922930			} .
40000	0.000054	/ug=Hs.151046 /len=2719	44000700		ND 000000
13932	0.038054	EST(zr99b03.r1 NCI_CGAP_GCB1	AA236732		NP_690869
10000	0.000.405	clone IMAGE:683789 5')	1100007	,	ND 000400
13939		EST(ys82e11.r1 clone 221324 5')	H92037	11 00000	NP_803133
13953	0.04638	hypothetical protein FLJ20287	NM_017746	Hs.26369	NP_060216
		(FLJ20287), mRNA /cds=(132,2921)	* 4.		·
		/gb=NM_017746 /gi=8923268	· ·		
40054	0.000400	/ug=Hs.26369 /len=3043	4.4700500		
13954	0.020126	EST nw48e08.s1 NCI_CGAP_Ew1	AA730589		
40004	0.040040	IMAGE:1249862	11001500	11. 400005	· · ·
13984	0.042048	to90d01.x1 NCI_CGAP_Gas4 cDNA	Al801509	Hs.436925	
		clone IMAGE:2185537 3' similar to			
	1.	contains L1.t1 L1 repetitive element;		1	<u> </u>
		mRNA sequence]	
1	1	/clone=IMAGE:2185537 /clone_end=3'			<u> </u>
		/gb=Al801509 /gi=5366981			
4 4635	0.000.15=	/ug=Hs.436925 /len=446	10.71055		ND 001055
14015	J 0.022485	EST(AV713804 DCB cDNA clone	AV713804		NP_004853
1 4 2 2 2	0.00000	DCBAXA05 5')	1.0000		ND 000545
14018	0.009931	1	AI086864	: ' '	NP_002517
		(Soares_senescent_fibroblasts_NbHSF		,	
	1	clone IMAGE:1682209 3')		L	l

14021 0.034378 UI-E-EJO-ahg-j-09-0-UI-f UI-E-EJO BM712784 Hs.278378 CDNA clone UI-E-EJO-ahg-j-09-0-UI f Ms.278378 Ms.278378 GDNA clone UI-E-EJO-ahg-j-09-0-UI f GDNA clone Glone-UI-E-EJO-ahg-j-09-09-UI clone, end-5 / gb=BM712784 gi=19026042 /ug=Hs.278378 /len=1255 Ms.27239 GDNA sequence FLJ12285 fis, clone AK022347 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545 Ms.27239 /len=4545	Spot	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
CDNA clone UI-E-EJ0-ahg-j-09-0-UI 5; mRNA sequence /clone=UI-E-EJ0-ahg-j-09-0-UI /clone_end=5 / jp-BM712784 /gi=19026042 /ug=Hs 278378 /len=1255	14024	0.024279	ULE E10 obs : 00 0 UL d ULE E10			No.
mRNA sequence /clone=UI-E-EJ0-ahg-j 09-0-UI /clone_end=5' /gb=BM712784 /gi=19026042 /ug=Hs_278378 /len=1255	14021	0.034370 		DIVI7 12704	IDS.210310	
09-0-UJ /clone_end=5' /gb=BM712784						
/gi=19026042 / ug=Hs.278378 /len=1255		•				
14023 0.04638 cDNA sequence FLJ12285 fis, clone MAMMA1001764 14056 0.04638 mRNA for KIAA1748 protein, partial cds. /cds=(1120,3396) /gb=AB051535 /gi=12698040 /ug=Hs.27239 /len=4545 14057 0.027906 cDNA FLJ90553 fis, clone OVARC1000853 /cds=(116,748) /gb=AK075034 /gi=22760867 /ug=Hs.406158 /len=1673 14060 0.004545 beta-amyloid binding protein precursor (BBP); mRNA /cds=(304,927) /gb=NM_032027 /gi=17738309 /ug=Hs.333541 /len=1250 14060 0.016031 cDNA sequence FLJ13663 fis, clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE1011646, highly similar to H. sapiens clone PLACE101646, highly similar to H. sapiens clone PLACE101646, highly similar to H. sapiens clone PLACE101646, highly similar to H. sapiens clone PLACE101646, highly similar to H. sapiens clone PLACE101646, highly similar to H. sapiens clone PLACE101646, highly similar to H. sapiens clone PLACE101646, highly similar to H. sapiens clone PLACE101646, highly similar to H. sapiens clone PLACE101646, highly similar to H. sapiens clone PLACE101646, highly similar to H. sapiens clone PLACE101646, highly similar to H. sapiens clone H. sapiens clone PLACE101646, highly similar to H. sapi						,
MAMMA1001764			/gi=19026042 /ug=Hs.278378 /len=1255			
MAMMA1001764	14023	0.04638	cDNA sequence FL 112285 fis. clone	AK022347		
14056	14023	0.04000		7.11.0220-17	. <i>:</i>	
/cds=(1120,3396) /gb=AB051535 /gi=12698040 /ug=Hs 27239 /len=4545	14056	0.04638		AB051535	Hs.27239	7
/gi=12698040 /ug=Hs.27239 /len=4545						2.5
14057						
OVARC100853. /cds=(116,748) /gb=AK075034 /gi=22760867 /ug=Hs. 406158 /lein=1673 NM_032027 Ng=Hs. 406158 /lein=1673 NM_032027 Ng=Hs. 406158 /lein=1673 NM_032027 NM_032027 Ng=Hs. 406158 /lein=1673 NM_032027 NM_032027 NM_032027 Np=NMA /cds=(304,927) /gb=NM_032027 /gi=177738309 /ug=Hs. 333541 /lein=1250 NM_032027 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03			/g. 120000 to rag the 21 200 non-to-10			
/gb=AK075034 /gi=22760867 /ug=Hs.406158 /len=1673	14057	0.027906	cDNA FLJ90553 fis, clone	AK075034	Hs 406158	,
14060 0.004545 beta-arryloid binding protein precursor (BBP), mRNA /cds=(304,927) /gb=NM_032027 (gi=17738309) /ug=Hs.333541 /len=1250 NP_032027 (gi=17738309) /ug=Hs.333541 /len=1250 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03817 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_03818 NP_038			OVARC1000853. /cds=(116,748)		-	
14060 0.004545 beta-amyloid binding protein precursor (BBP), mRNA /cds=(304,927) /gb=NM_032027 /gi=17733309 /ug=Hs.333541 /len=1250 NP_032027 /gi=17733309 /ug=Hs.333541 /len=1250 NP_033541 /len=1250 NP_033541 /len=1250 NP_033541 /len=1250 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517 NP_033517		· ·				
14060 0.004545 beta-amyloid binding protein precursor (BBP); mRNA /cds=(304,927) /gb=NM_032027 /gi=17738309 /ug=Hs_333541 /len=1250 NP_032027 MRNA /cds=(304,927) /gb=NM_032027 /gi=17738309 /ug=Hs_333541 /len=1250 NP_003817 NP_003817 NP_003817 NP_003478 ST_(2h68h11_r1 Soares_fetal_liver_spleen_1NFLS_S1 clone IMAGE:417285_5) NR_08789 NR_08789 NR_08789 NR_08789 NR_08789 NR_08789 NR_08789 NR_08789 NR_08789 NR_088789 NR_0888888888888888888888888888888888888	[
(BBP); mRNA /cds=(304,927) /gb=NM_032027 /gi=17738309 /ug=Hs_333541 /len=1250 14066	14060	0.004545		NM 032027	Hs.333541	NP 114416
International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color International Color	1 1 7 7 7					_
Aug=Hs.333541 /len=1250	* 1		1,			
14066 0.016031 cDNA sequence FLJ13663 fis, clone PLACE1011646, highly similar to H sapiens clone AK023725 NP_003817 14067 0.034378 EST (zh68h11.r1 Soares_fetal_liver_spleen_1NFLS_S1 clone IMAGE:417285 5') W87789 W87789 14085 0.034378 EST (np87f03.s1 NCl_CGAP_Thy1 IMAGE:1133309) AA632677 IMAGE:1133309) AA668159 NP_054767 14087 0.042048 EST ab74g12.s1 Stratagene fetal retina 937202 H.sapiens cDNA clone IMAGE:852742 3' AA668159 NP_054767 14097 0.04638 MR0-HT0559-290500-027-d10 HT0559 cDNA clone IMAGE:3571677 sl. mRNA sequence /gb=BE708268 /gi=10096533 /ug=Hs.209224 /len=619 BE708268 Hs.209224 len=619 14100 0.00772 7n87e11.x1 NCI_CGAP_Ov18 cDNA clone IMAGE:3571677 /lclone_end=3' /gb=BF195714 /gi=11082893 /ug=Hs.439426 /len=458 BF195714 Hs.439426 14109 0.013065 wq35e02.x1 NCI_CGAP_GC6 cDNA clone IMAGE:2473274 /lclone_end=3' /gb=Al950442 /gi=5742752 /ug=Hs.176956 /len=496 Al950442 Hs.176956 /len=496 Hs.176956 14134 0.038054 EST (602302386F1 NIH_MGC_87 cDNA clone IMAGE:4403877 5') BG034307 cDNA clone IMAGE:4403877 5') NP_001943 cDNA clone IMAGE:4403877 5') 14144 0.006784 EST (AU143964 HEMBA1 cDNA clone IMAGE) AU1	J.,					
PLACE1011646, highly similar to H. sapiens clone	14066	0.016031		AK023725	· · · · · · · · · · · · · · · · · · ·	NP 003817
H.sapiens clone	1 1000	0.010001	•	, (020120		-0000
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Clone IMAGE:417285 5')	14007	0.004370		VV07703		
14085 0.034378 EST (np87f03.s1 NCI_CGAP_Thy1 IMAGE:1133309) 14087 0.042048 EST ab74g12.s1 Stratagene fetal retina 937202 H.sapiens cDNA clone IMAGE:852742 3' 14097 0.04638 MR0-HT0559-290500-027-d10 HT0559 BE708268 cDNA, mRNA sequence /gb=BE708268 /gi=10096533 /ug=Hs.209224 /len=619 EF195714 Hs.439426 Clone IMAGE:3571677 3', mRNA sequence /clone=IMAGE:3571677 7' /clone_end=3' /gb=BF195714 /gi=11082893 /ug=Hs.439426 /len=458 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.176956 Hs.17	'					
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14087 0.042048 EST ab74g12.s1 Stratagene fetal retina 937202 H.sapiens cDNA clone IMAGE:852742 3' AA668159 NP_054767 937202 H.sapiens cDNA clone IMAGE:852742 3' 14097 0.04638 MR0-HT0559-290500-027-d10 HT0559 cDNA, mRNA sequence /gb=BE708268 /gi=10096533 /ug=Hs.209224 /len=619 BE708268 Hs.209224 14100 0.00772 7n87e11.x1 NCI_CGAP_Ov18 cDNA clone IMAGE:3571677 3', mRNA sequence /clone=IMAGE:3571677 //clone_end=3' /gb=BF195714 /gi=11082893 /ug=Hs.439426 /len=458 Hs.439426 Hs.439426 14109 0.013065 wq35e02.x1 NCI_CGAP_GC6 cDNA clone IMAGE:2473274 //clone_end=3' /gb=Al950442 /gi=5742752 /ug=Hs.176956 /len=496 Al950442 Hs.176956 /len=496 Hs.176956 14134 0.038054 EST (602302386F1 NIH_MGC_87 cDNA clone IMAGE:4403877 5') BG034307 cDNA clone IMAGE:4403877 5') NP_001943 cDNA clone AU143964 NP_057535	14003	0.034376 		JAA032011		
937202 H.sapiens cDNA clone IMAGE:852742 3' 14097	14087	0.042048		AA668159	\ 	NP 054767
IMAGE:852742 3'	14007	0.072070		7 0 1000 100		1111 _004707
14109					· ·	
cDNA, mRNA sequence /gb=BE708268 /gi=10096533 /ug=Hs.209224 /len=619 14100	14097	0.04638		BF708268	Hs 209224	
/gi=10096533 /ug=Hs.209224 /len=619 14100	1.00	0.0.1000			110.20022	
14100 0.00772 7n87e11.x1 NCI_CGAP_Ov18 cDNA clone IMAGE:3571677 3', mRNA sequence /clone=IMAGE:3571677 /clone_end=3' /gb=BF195714 /gi=11082893 /ug=Hs.439426 /len=458 14109 0.013065 wq35e02.x1 NCI_CGAP_GC6 cDNA clone IMAGE:2473274 3', mRNA sequence /clone=IMAGE:2473274 /clone_end=3' /gb=Al950442 /gi=5742752 /ug=Hs.176956 /len=496 14134 0.038054 EST (602302386F1 NIH_MGC_87 cDNA clone IMAGE:4403877 5') 14144 0.006784 EST (AU143964 HEMBA1 cDNA clone AU143964 NP_057535	1				,	1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.
Clone IMAGE:3571677 3', mRNA sequence /clone=IMAGE:3571677 /clone_end=3' /gb=BF195714 /gi=11082893 /ug=Hs.439426 /len=458	<u> </u>		/g = 10090000 /dg=113.200224 /icii=010		· ·	
Clone IMAGE:3571677 3', mRNA sequence /clone=IMAGE:3571677 /clone_end=3' /gb=BF195714 /gi=11082893 /ug=Hs.439426 /len=458	14100	0.00772	7n87e11 x1 NCL CGAP Ov18 cDNA	BF195714	Hs 439426	-
Sequence /clone=IMAGE:3571677 /clone_end=3' /gb=BF195714 /gi=11082893 /ug=Hs.439426 /len=458						
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clone IMAGE:2473274 3', mRNA sequence /clone=IMAGE:2473274 /clone_end=3' /gb=Al950442 /gi=5742752 /ug=Hs.176956 /len=496	1		/g =110020007ug=113.4034207ich=400			
clone IMAGE:2473274 3', mRNA sequence /clone=IMAGE:2473274 /clone_end=3' /gb=Al950442 /gi=5742752 /ug=Hs.176956 /len=496	14109	0.013065	wq35e02.x1 NCI CGAP GC6 cDNA	AI950442	Hs.176956	
sequence /clone=IMAGE:2473274 /clone_end=3' /gb=Al950442 /gi=5742752 /ug=Hs.176956 /len=496 14134 0.038054 EST (602302386F1 NIH_MGC_87 BG034307 NP_001943 CDNA clone IMAGE:4403877 5') 14144 0.006784 EST (AU143964 HEMBA1 cDNA clone AU143964 NP_057535						
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cDNA clone IMAGE:4403877 5')	14134	0.038054		BG034307		NP 001943
14144 0.006784 EST (AU143964 HEMBA1 cDNA clone AU143964 NP_057535		5.555554				
l	14144	0.006784		AU143964		NP 057535
			HEMBA1000519-3')			

Spot	p-value	Description	Gene	Unigene	Protein
	,		Accession	Accession	Accession
			No.	No.	No.
14168	0.020126	7j81h05.x1	BF055560	Hs.298968	
		Soares_NSF_F8_9W_OT_PA_P_S1			
		cDNA clone IMAGE:3392889 3', mRNA	e e e e		
		sequence /clone=IMAGE:3392889			
		/clone_end=3' /gb=BF055560			
		/gi=10809456 /ug=Hs.298968 /len=506			
,)		
14173	0.044138	Wilms' tumour 1-associating protein	NM 004906	Hs.119	NP 690597
		(WTAP), transcript variant 1, mRNA			_
		/cds=(223,1413) /gb=NM_004906			
		/gi=23199972 /ug=Hs.119 /len=2143			
14174	0.034378	mitochondrion, complete genome	NC 001807	*	
14178		EST(cDNA PM4-EN0063-051100-003-	BF848451	, , , , , , , , , , , , , , , , , , , ,	
14 17 0	.0.0-20-0	g09 EN0063)			
14200	0.011228	EST(wf59e08.x1	AI809898		V
17200	0.011220	Soares_NFL_T_GBC_S1 cDNA clone	711000000		
\$ 10 m		IMAGE:2359910 3')	, and		
14201	0.011004	EST(te67a08.x1	Al377927		No. 1 Personal Property of
14201	0.0 1904		A1311921	.*	
,		Soares_NFL_T_GBC_S1 cDNA clone			*
44000	0.005070	IMAGE:2091734 3')	DV400460	Un 200002	
14209	0.025072	BX109160 Soares_NhHMPu_S1 cDNA	BX109160	Hs.308982	
		clone IMAGp998H024744, mRNA			
	s :	sequence			
	*	/clone=IMAGp998H024744_;_IMAGE:1			
		933489 /gb=BX109160 /gi=27877586			and the second
		/ug=Hs.308982 /len=483			1 7 7 7 7 7 7 7 7
14235	0.025072	hypothetical protein MGC45400	NM_153333	Hs.389734	NP_699164
	***	(MGC45400), mRNA /cds=(245,598)			
1		/gb=NM_153333 /gi=23503246			
		/ug=Hs.389734 /len=1290			
14243	0.022485	cDNA FLJ36574 fis, clone	AK093893	Hs.356595	•
		TRACH2012376. /gb=AK093893		<u>'</u>	
		/gi=21752845 /ug=Hs.356595 /len=1952			
			To the		
14250	0.027906	ferritin, light polypeptide (FTL), mRNA	NM_000146	Hs.430150	NP_000137
		/cds=(189,716) /gb=NM_000146			
		/gi=20149497 /ug=Hs.430150 /len=878			
14272	0.04638	nuclear protein double minute 1	NM 017440	Hs.12871	NP_064513
		(MDM1), mRNA /cds=(93,2237)	_		
		/gb=NM 017440 /gi=24586654			
, ,		/ug=Hs.12871 /len=2942	1		
14279	0.01798	AL535026 LTI FL013 FBrn1 cDNA	AL535026	Hs.268474	
	5.550	clone CS0DF007YJ21 3 prime, mRNA			
		sequence /clone=CS0DF007YJ21			
		/clone_end=3' /gb=AL535026			
		/gi=12798519 /ug=Hs.268474 /len=921	· ·		
1.		1/91 121 000 10 /49 113.200414 /1011=021			, .
	<u> </u>	<u> </u>	L	L	L

Spot	p-value		Gene Accession No.	Unigene Accession No.	Protein Acc ssion No.
14284	0.027906	hypothetical protein FLJ23751	NM_152282	Hs.37443	NP_689495
		(FLJ23751), mRNA /cds=(121,1563)			i
		/gb=NM_152282 /gi=22748648			
•	,	/ug=Hs.37443 /len=2994			
14288	0.034378	small acidic protein (SMAP), mRNA	NM_014267	Hs.78050	NP_055082
		/cds=(137,688) /gb=NM_014267	, , , , , , , , , , , , , , , , , , , ,	•	
		/gi=20070245 /ug=Hs.78050 /len=1504			
14380	0.042048		NM_004545	Hs.183435	NP_004536
		beta subcomplex, 1, 7kDa (NDUFB1),			
, s	; 4,	mRNA /cds=(34,210) /gb=NM_004545			
	1	/gi=27597086 /ug=Hs.183435 /len=290			
14382	0.038054	mRNA; cDNA DKFZp434P1018 (from	AL137527	Hs.289038	NP_116162
		clone DKFZp434P1018), partial cds			
		/cds=UNKNOWN /gb=AL137527			
		/gi=6808195 /ug=Hs.289038 /len=3327			
14409	0.04638	ESTs, cDNA, 3' end	AA709133	Hs.180144	
		/clone=IMAGE:384992 /clone end=3'			* .
-		/gb=AA709133 /gi=2719051		and the second	
		/ug=Hs.180144 /len=428			1
14425	0.00772	wc34a07.x1 NCI_CGAP_Pr28 cDNA	Al745524	Hs.205153	A TOTAL CONTRACTOR
		clone IMAGE:2317044 3' similar to			
		contains element MSR1 repetitive	,		
		element ;, mRNA sequence			
,		/clone=IMAGE:2317044 /clone_end=3'		į.	
	•	/gb=AI745524 /gi=5113812		•	
		/ug=Hs.205153 /len=398			
14487	0.038054	Cloning vector pAS2, complete	U30496		
		sequence			115
14520	0.01798	cDNA FLJ90504 fis, clone	AK074985	Hs.171802	NP_775918
		NT2RP3004090, weakly similar to			•
		GOLIATH PROTEIN. /cds=(103,1305)	4.	. /	C.
	,	/gb=AK074985 /gi=22760786			
Ta Ta min no		/ug=Hs.171802 /len=2452	1170700		<u> </u>
14522		EST(Soares fetal liver spleen	N72700		NID 070000
14529	0.04638	hypothetical protein FLJ23033	NM_024686	Hs.96423	NP_078962
		(FLJ23033), mRNA /cds=(108,1826)			
		/gb=NM_024686 /gi=13375957		1	1
44550	0.005070	/ug=Hs.96423 /len=2115	NIM 047540	110 202000	ND 000040
14553	0.0250/2	hypothetical protein H41 (H41), mRNA	NM_017548	Hs.283690	NP_060018
		//cds=(324,1100) /gb=NM_017548			
		/gi=24475997 /ug=Hs.283690 /len=3346			
14559	0.004596	EST hb88d08.x1 NCI_CGAP_Ut2 cDNA	AW439829		NP_620128
		clone IMAGE:2890287 3'			

Spot	p-value	Description	Gene	Unigene	Protein
•			Accession	Accession	Accession
			No.	No.	No.
14560	0.016031	TRAM-like protein (KIAA0057), mRNA	NM_012288	Hs.153954	NP_036420
		/cds=(76,1188) /gb=NM_012288			
		/gi=6912449 /ug=Hs.153954 /len=6974			
14571	0.020912	EST(xx31a10.x1 NCI_CGAP_Ut1 clone	AW571469		NP_055260
		IMAGE:2839098 3')			
14596	0.038054	AGENCOURT_8819408 NIH_MGC_18	BQ941317	Hs.443078	
		cDNA clone IMAGE:6422878 5', mRNA		•	
	,	sequence /clone=IMAGE:6422878			
	;	/clone_end=5' /gb=BQ941317		}	1
		/gi=22356795 /ug=Hs.443078 /len=929		{	
<u> </u>		<u></u>			
14618	0.005206	EST (UI-H-BI2-agh-g-08-0-UI.s1	AW291353		NP_061049
		NCI_CGAP_Sub4 cDNA clone			1
<u> </u>		IMAGE:2724303 3')			
14623	0.042048	hypothetical protein FLJ35779	NM_152408	Hs.432726	NP_689621
		(FLJ35779), mRNA /cds=(42,1694)	[
ľ		/gb=NM_152408 /gi=22748864			
		/ug=Hs.432726 /len=1698			
14631	0.027906	EST(12h2 retina cDNA randomly primed	W26795		
		sublibrary)	1		
14642	0.038054	aa51h10.s1 NCI_CGAP_GCB1 cDNA	AA490540	Hs 336686	}
		clone IMAGE:824515 3' similar to			
		contains MER30.b1 MER30 repetitive	Lagran Company		
∤ 2 .		element ;, mRNA sequence	1		
1		/clone=IMAGE:824515 /clone_end=3'			
1	 	/gb=AA490540 /gi=2219713		{ ·	[
	<u> </u>	/ug=Hs.336686 /len=378	1		
14650	0.04638	clone IMAGE:4139786, mRNA, partial	BC007901	Hs.433279	
		cds /cds=(1,625) /gb=BC007901			
ļ	· ·	/gi=14043927 /ug=Hs.433279 /len=1493		<i>t</i>	
1 12	2 2 3 1 1 2 2	 			
14677	0.044138	cDNA, 5' end /clone=IMAGE:158873	R75776	Hs.302485	NP_004356
	·	/clone_end=5' /gb=R75776 /gi=850458		l e e e e	
11000	2 2 2 2 2 2 2	/ug=Hs.302485 /len=522			100 0000
14686	J U.U12669	chromosome 20 open reading frame 52	NM_080748	Hs.401703	NP_542786
		(C20orf52), mRNA /cds=(164,403)	1	ľ	
		/gb=NM_080748 /gi=18152784	(
44000	0.04000	/ug=Hs 401703 /len=602	1,1,000,050	11- 450440	
14690	U.04638	cDNA FLJ35033 fis, clone	AK092352	Hs.156113	.
		OCBBF2016590, weakly similar to			
,		CELL SURFACE ANTIGEN 114/A10)	
1		PRECURSOR. /cds=(407,934)		ļ	ļ
		/gb=AK092352 /gi=21750925	1.		
L	L	/ug=Hs.156113 /len=2884	J .	L	<u> </u>

Spot	p-value	Description	Gene	Unigene	Protein
)			Accession	Accession	Accession
	. <u></u>	<u> </u>	No	No.	No.
14777	0.038054	UI-E-EJ0-ahn-c-06-0-UI s1 UI-E-EJ0	BM674956	Hs.131705	
• *		cDNA clone UI-E-EJ0-ahn-c-06-0-UI 3',			
		mRNA sequence /clone=UI-E-EJ0-ahn-			
	6.	c-06-0-UI /clone_end=3' /gb=BM674956		All Marie Control	
		/gi=18984854 /ug=Hs.131705 /len=1017			
				÷ .	
14779	0.016031	UI-H-BI2-ahk-c-12-0-UI.s1	AW294558	Hs.437134	
		NCI_CGAP_Sub4 cDNA clone			
		IMAGE:2727166 3', mRNA sequence			
		/clone=IMAGE:2727166 /clone_end=3'			
		/gb=AW294558 /gi=6701194			1
		/ug=Hs.437134 /len=888	f		
14799	0.04638	DKFZp586J021 (from clone	AL110197	Hs.6441	NP_003246
		DKFZp586J021) /cds=UNKNOWN			
1		/gb=AL110197 /gi=5817115			1.
		/ug=Hs.6441 /len=1896		<u> </u>	
14804	0.014741	splicing factor, arginine/serine-rich 12	NM_139168	Hs.381165	NP_631907
		(SFRS12), mRNA /cds=(342,1868)			
		/gb=NM_139168 /gi=21040254			
	<u> </u>	/ug=Hs.381165 /len=3811	,		
14882	0.038054	DKFZp434C022_s1 434 (synonym:	AL044366	Hs.165805	2 2122
		htes3) cDNA clone DKFZp434C022 3',			
ŀ	}	mRNA sequence			
		/clone=DKFZp434C022 /clone_end=3'			
		/gb=AL044366 /gi=5432588			
		/ug=Hs.165805 /len=668			
14934	0.026138	No significant match			
L		(ORF:+1:1~102[102])	SEQ.ID.No.59		
14941	0.01798	brain cDNA clone:QmoA-10474, full	AB062971		
:		insert sequence			:

		TABLE 30			
Genes Co	rr spondir	ng To Diff rentially Expressed Genes in I	Figure 22 - Os	teoarthritis	
Spot	p-value	Description	Accession	Unigene	Protein
				_	Accession
					No
8	0.000153	calreticulin (CALR), mRNA	NM_004343	Hs.353170	NP 004334
		/cds=(69,1322) /gb=NM_004343			-
4		/gi=5921996 /ug=Hs.353170 /len=1899			
21	0.000298	telomeric repeat binding factor (NIMA-	NM 017489	Hs.194562	NP 059523
<u>-</u> '	0.000200	interacting) 1 (TERF1), transcript variant	11111_017400	1113.10-1002	-0000020
		1, mRNA /cds=(16,1335) /gb=NM_017489			
	4.1	/gi=9257245 /ug=Hs.194562 /len=2686			
		/g -925/245/ug=Hs.194502/lef1=2000			
01	0.004446	VDA hinding protein 4, putoting ATD/CTD)	NIM 007066	Un 10050	ND 000407
91	0.001116	XPA binding protein 1; putative ATP(GTP)	14141_007266	Hs.18259	NP_009197
		binding protein (NTPBP), mRNA			
		/cds=(25,1149) /gb=NM_007266	;		
*		/gi=14149628 /ug=Hs.18259 /len=1829			
146	0.001393	similar to hypothetical protein (L1H 3	NM_145302	Hs.343206	NP_660345.1
		region) - human (LOC201853), mRNA		The second state	
		/cds=(500,820) /gb=NM_145302			
	1 2 .	/gi=21699085 /ug=Hs.343206 /len=8 <u>51</u>		<u> </u>	
176	0.000508	nuclear autoantigenic sperm protein	NM_172164	Hs.380400	NP_751896
		(histone-binding) (NASP), transcript		1	
	, , , , , , , , , , , , , , , , , , ,	variant 1, mRNA /cds=(170,2542)			ri .
		/gb=NM 172164 /gi=27262633	·		
	1	/ug=Hs.380400 /len=3396			
192	0.000809	mRNA for KIAA0570 protein, partial cds.	AB011142	Hs.180948	BAA25496.2
	0.90000	/cds=(480,10718) /gb=AB011142			
	1	/gi=20521084 /ug=Hs.180948 /len=11269		1	
		/gi-20021004/dg-113.100040/lci1-11200			
195	0.000346	X-ray repair complementing defective	NM 021141	Hs.84981	NP 066964
133	0.0000	repair in Chinese hamster cells 5 (double-	021141	1113.04301	111 _000004
		strand-break rejoining; Ku autoantigen,			
		80kDa) (XRCC5), mRNA /cds=(34,2232)			
					ļ: · · · !
		/gb=NM_021141 /gi=12408650			
<u> </u>	0.0000	/ug=Hs.84981 /len=3310		11 70450	ND 000404
301	0.000333	chaperonin containing TCP1, subunit 4	NM_006430	HS. 79150	NP_006421
	· · · · ·	(delta) (CCT4), mRNA /cds=(1,1620)			
1		/gb=NM_006430 /gi=5453604			
		/ug=Hs.79150 /len=1883			
328		EST(yj40f11.r1 clone 151245 5')	H02533		NP_705833
331	0.000492	dihydropyrimidinase-like 2 (DPYSL2),	NM_001386	Hs.173381	NP_001377
		mRNA /cds=(275,1993) /gb=NM_001386			
		/gi=19923654 /ug=Hs.173381 /len=4459			
		<u></u>	<u> </u>	·	
333	8.88E-06	chaperonin containing TCP1, subunit 8	NM_006585	Hs.15071	NP_006576
		(theta) (CCT8), mRNA /cds=(29,1675)	_		
1		/gb=NM_006585 /gi=6005726	1		1 .
1	1	/ug=Hs.15071 /len=1821			·
361	0.001546	THO complex 1 (THOC1), mRNA	NM 005131	Hs.1540	NP_005122
	0.001040	/cds=(15,1988) /gb=NM_005131	1.111_000101	1.10.7070	-000122
		/gi=4826881 /ug=Hs.1540 /len=2092	· .		
		1/91-702000 1 /uy-113, 1340 /le11-2032		1	1

Sp	ot	p-value	Description	Accession	Unigene	Protein Accession
		 	 			No.
40)5	0.001541	ATPase, Ca_transporting, plasma	NM_001682	Hs.78546	NP_001673
-			membrane 1 (ATP2B1), mRNA		-	
	.		/cds=(182,3844) /gb=NM_001682		***	المتأثر ورووي
		·	/gi=4502286 /ug=Hs.78546 /len=4398			Liii gaaa
42	25	7.47E-05		NM_002432	Hs.153837	NP_002423
1			(MNDA), mRNA /cds=(201,1424)			
X	l		/gb=NM_002432 /gi=4505226		,	
		ا	/ug=Hs.153837 /len=1670			<u></u>
45	59	0.000298	X-ray repair complementing defective	NM_022550	Hs.150930	NP_072044
			repair in Chinese hamster cells 4		·	Section 1
	}		(XRCC4), transcript variant 3, mRNA		į	
			/cds=(176,1180) /gb=NM_022550			
		<u> </u>	/gi=12408648 /ug=Hs.150930 /len=1707			
46	55	0.000636	hypothetical protein, estradiol-induced	NM_014367	Hs.5243	NP_055182
:			(E2IG5), mRNA /cds=(71,643)	1		
	1		/gb=NM_014367 /gi=21361426			
		·	/ug=Hs.5243 /len=1215			<u> </u>
52	25	0.000356	KDEL (Lys-Asp-Glu-Leu) containing 1	NM_024089	Hs.44970	NP_076994
	· }		(KDELC1), mRNA /cds=(338,1846)			
			/gb=NM_024089 /gi=13129085			
			/ug=Hs.44970 /len=2082			
. 70	00	8.5E-06	major histocompatibility complex, class II,	NM_019111	Hs.409805	NP_061984
			DR alpha (HLA-DRA), mRNA			
			/cds=(65,829) /gb=NM_019111			
	}		/gi=18641378 /ug=Hs.409805 /len=1237			
73	31	5.82E-05	mitochondrial ribosomal protein S21	NM_018997	Hs.81281	NP_114107
	. [(MRPS21), transcript variant 2, nuclear		1	
			gene encoding mitochondrial protein,	1	ł	,
			mRNA /cds=(519,782) /gb=NM_018997			
	`		/gi=16950592 /ug=Hs.81281 /len=939	. '		
79	93	0.000356	glyoxalase I (GLO1), mRNA	NM_006708	Hs.75207	NP_006699
		. * .	/cds=(88,642) /gb=NM_006708	7		
			/gi=5729841 /ug=Hs.75207 /len=1993			
79	96	0.000948	poly(rC) binding protein 2 (PCBP2),	NM 005016	Hs.63525	NP 114366
;			transcript variant 1, mRNA /cds=(89,1189)			-
			/gb=NM 005016 /gi=14141167	1		1
-		1	/ug=Hs.63525 /len=1362		er.	
8	52	0.001638	mannosidase, beta A, lysosomal	AF224669		AAF35233.1
		.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	(MANBA) gene, and ubiquitin-conjugating			
			enzyme E2D 3 (UBE2D3) genes,		,	.:
			complete cds			
9	19	0.000117		U93051	Hs.356062	NP_000305
Ĭ	-		(PTEN) mRNA, complete cds			
			/cds=(1,1212) /gb=U93051 /gi=1916351		1	
			/ug=Hs.356062 /len=1212	1, 2, 2		1
10	39	5.44F-07	CDNA FLJ13779 fis, clone	AK023841	Hs.172069	T12506
	,50	0.142.07	PLACE4000445, highly similar to mRNA;		1	.2555
				1	}	1 11
			CDNA DKEZn434C212 (from clone	j	3	1
			cDNA DKFZp434C212 (from clone DKFZp434C212). /gb=AK023841			

Spot	p-value	Description	Accession	Unigene	Protein
					Accession
1064	2.57E-05	mitochondria solute carrier protein	AY032628		No. NP 061049
1004	2.07 €-09	(MSCP)	A 1 0 3 2 0 2 0		147_001049
1113	0.001393	nischarin (NISCH), mRNA /cds=(27,4541)	NM 007184	Hs.26285	NP 009115
		/gb=NM_007184 /gi=6005787	=	,	
		/ug=Hs 26285 /len=5132			
1134	0.000326	cDNA FLJ30093 fis, clone	AK054655	Hs.349261	
		BNGH41000033. /gb=AK054655			
		/gi=16549241 /ug=Hs.349261 /len=2926			
1196	0.000492	FK506 binding protein 14, 22 kDa	NM_017946	Hs.264636	NP_060416
		(FKBP14), mRNA /cds=(146,781)			
	• .	/gb=NM_017946 /gi=8923658			
· · · · · · · · · · · · · · · · · · ·	; .	/ug=Hs.264636 /len=2248		 	
1241	0.000164	netrin 4 (NTN4), mRNA /cds=(452,2338)	NM_021229	Hs.102541	NP_067052
	* *	/gb=NM_021229 /gi=24475651]		; ·
4050	4.455.05	/ug=Hs.102541 /len=3607	NIN 445700	11 40507	ND 000700
1259	4,15E-05	desmuslin (DMN), transcript variant A,	NM_145728	Hs.10587	NP_663780
		mRNA /cds=(121,4818) /gb=NM_145728 /gi=22027637 /ug=Hs.10587 /len=7343	; ** .		
		/gi-2202/63/ /ug-ns.1056/ /ieii-/545			
1290	0.000050	synaptic nuclei expressed gene 1 (SYNE-	NM 015293	Hs.192102	NP_598411
1290	0.000333	1), transcript variant beta, mRNA	14141_013233	113.132102	141 _ 3304 11
		/cds=(121,10086) /gb=NM_015293	}		
		/gi=19526752 /ug=Hs.192102 /len=10742		•	
	*	13 110020102703			
1303	5.82E-05	imageqc_6_2001/snk86bdrr81.y1	BQ109159	Hs.433575	
		NIH_MGC_12 cDNA clone	}		
		IMAGE:5110111 5', mRNA sequence		· ·	1
	1	/clone=IMAGE:5110111 /clone_end=5'		1	
		/gb=BQ109159 /gi=20158813	[
	<u> </u>	/ug=Hs.433575 /len=604			
1340	0.000326	structure specific recognition protein 1	NM_003146	Hs.79162	NP_003137
		(SSRP1), mRNA /cds=(275,2404)	1	ł	
		/gb=NM_003146 /gi=4507240		1	
1 - 2 - 2		/ug=Hs.79162 /len=2839	1001000	100054	110 110 570
1581	0.000521	SH3 domain binding glutamic acid-rich	NM_031286	Hs 109051	NP_112576
		protein like 3 (SH3BGRL3), mRNA			
		/cds=(72,353) /gb=NM_031286	1		1
1673	2.765.05	/gi=13775197 /ug=Hs.109051 /len=764 endoplasmic reticulum stress-inducible,	NM_014685	Hs.146393	NP_055500
1073	2.70⊑-00	ubiquitin-like domain member 1	LAINI-O 14000	113.140383	_00000
		(HERPUD1), mRNA /cds=(96,1271))	
		//gb=NM_ 014685 /gi=7661869		1	
	,	/ug=Hs.146393 /len=1884			
1804	0.000109	serine (or cysteine) proteinase inhibitor,	NM_006216	Hs.21858	NP_006207
		clade E (nexin, plasminogen activator	1		
		inhibitor type 1), member 2 (SERPINE2),)	
	, ·	mRNA /cds=(210,1406) /gb=NM_006216		1	
,	}	/gi=24307906 /ug=Hs.21858 /len=2129	1	1 .	

Spot	p-value	Description	Accession	Unigene	Protein
. 1					Accession No.
1813	0.000659	chromosome 14 open reading frame 80 (C14orf80), mRNA /cds=(330,1076)	NM_173608	Hs.72363	NP_775879
		/gb=NM_173608 /gi=27734692			
1843	0.000492	/ug=Hs.72363 /len=1419 CDK2-associated protein 1 (CDK2AP1),	NM 004642	Hs.433201	NP 004633
10,10	0.000-102	mRNA /cds=(523,870) /gb=NM_004642 /gi=17978492 /ug=Hs.433201 /len=1627		. 10. 10020 1	
1946	4.31E-05	sphingolipid activator protein 1	J03015		NP 002769
1982		ATP synthase, H transporting, mitochondrial F0 complex, subunit c	NM_005176	Hs.89399	NP_005167
		(subunit 9), isoform 2 (ATP5G2), mRNA /cds=(60,485) /gb=NM_005176 /gi=6671590 /ug=Hs.89399 /len=746			
2013	4.31E-05	actinin, alpha 2 (ACTN2), mRNA /cds=(174,2858) /gb=NM_001103	NM_001103	Hs.83672	NP_001094
·		/gi=4501892 /ug=Hs.83672 /len=4181			
2065	1.38E-05	tenascin C (hexabrachion) (TNC), mRNA /cds=(314,6919) /gb=NM_002160	NM_002160	Hs.289114	NP_002151
0705	0.004500	/gi=4504548 /ug=Hs.289114 /len=7560	NINA 004005	11- 454000	ND 000507
2135	0.001538	hypothetical protein MDS025 (MDS025), mRNA /cds=(363,1127) /gb=NM_021825	NM_021825	Hs.154938	NP_068597
		/gi=21361605 /ug=Hs.154938 /len=1585			
2164	0.0012	KIAA1074 protein (KIAA1074), mRNA	NM_014915	Hs.129218	NP_055730
		/cds=(151,5280) /gb=NM_014915 /gi=7662473 /ug=Hs.129218 /len=5360			
2340	0.001393	mRNA, cDNA DKFZp434F2311 (from clone DKFZp434F2311) /gb=AL137603	AL137603	Hs.233890	
		/gi=6808349 /ug=Hs.233890 /len=842			<u> </u>
2394	0.000164	RAN, member RAS oncogene family (RAN), mRNA /cds=(115,765)	NM_006325	Hs.10842	NP_006316
		/gb=NM_006325 /gi=6042206 /ug=Hs.10842 /len=1656			
2418	5.82E-05	RAN binding protein 1 (RANBP1), low match	NM_002882		NP_002873
2434	0.000316	small nuclear ribonucleoprotein D3	NM_004175	Hs.1575	NP_004166
		polypeptide 18kDa (SNRPD3), mRNA /cds=(88,468) /gb=NM_004175 /gi=4759159 /ug=Hs.1575 /len=626			
2490	0.000417	gonadotropin-releasing hormone receptor	NM_000406	Hs.73064	NP_000397
		(GNRHR), mRNA /cds=(1749,2735) /gb=NM_000406 /gi=4504058 /ug=Hs.73064 /len=2735			
2584	0.000316	mRNA for KIAA0627 protein, partial cds. /cds=(1,3976) /gb=AB014527	AB014527	Hs.108614	BAA31602.1
2748	0.00051	/gi=3327067 /ug=Hs 108614 /len=5614 serologically defined colon cancer antigen 1 (SDCCAG1)	NM_004713		NP_004704

Spot	p-value	Description	Accession	Unigene	Protein Accession
					No.
2773	0.000326	nucleosome assembly protein 1-like 1	NM_139207	Hs.302649	NP_631946
,		(NAP1L1), transcript variant 1, mRNA		[· ·	
		/cds=(125,1300) /gb=NM_139207	, i	i.	
		/gi=21327707 /ug=Hs.302649 /len=3582		,	
2790	2.76E-05	choroideremia (Rab escort protein 1)	NM_000390	Hs.2010	NP_000381
		(CHM), transcript variant 2950156, mRNA			
[[/cds=(31,1992) /gb=NM_000390		[· ·	· ·
		/gi=9966760 /ug=Hs.2010 /len=2115		<u> </u>	
2847	1.38E-05	lysosomal-associated membrane protein	NM_013995	Hs.8262	NP_054701
	,	2 (LAMP2), transcript variant LAMP2B,			
		mRNA /cds=(138,1370) /gb=NM_013995	1 4		
		/gi=7669502 /ug=Hs.8262 /len=4006			
·	· · · · · · · · · · · · · · · · · · ·				
2912	0.000492	KIAA0690 protein (KIAA0690), mRNA	NM_015179	Hs.60103	NP_055994
		/cds=(87,3980) /gb=NM_015179]]
	1 105 00	/gi=15987120 /ug=Hs.60103 /len=4396	NINA 000444	455000	ND 005447
2926	1.12E-06	DEAD/H (Asp-Glu-Ala-Asp/His) box	NM_020414	Hs.155986	NP_065147
	,	polypeptide 24 (DDX24), mRNA			
		/cds=(100,2679) /gb=NM_020414			
2012	2 245 00	/gi=14251213 /ug=Hs.155986 /len=2967	NM 018466	Hs.110853	NP_060936
3013	3.34⊑-00	uncharacterized hematopoietic stem/progenitor cells protein MDS031		10000	ME_000930
		(MDS031), mRNA /cds=(35,532)			
		/gb=NM_018466 /gi=20070304			
		/ug=Hs.110853 /len=1358			
3017	0.0012	DC6 protein (DC6), mRNA /cds=(162,467)	NM 020189	Hs.283740	NP_064574
0017	0.0012	/gb=NM_020189 /gi=9910185			,
		/ug=Hs.283740 /len=676			<i>i</i>
3029	0.000927	Yip1p-interacting factor (YIF1P), mRNA	NM 020470	Hs.406422	NP_065203
		/cds=(116,997) /gb=NM_020470	-		-
		/gi=9994168 /ug=Hs.406422 /len=1078	<u> </u>		1
3062	0.000117	myosin, light polypeptide, regulatory, non-	NM_006471	Hs.180224	NP_006462
	, , ,	sarcomeric (20kD) (MLCB), mRNA			
		/cds=(115,630) /gb=NM_006471			
		/gi=5453739 /ug=Hs.180224 /len=944			
3137	0.00121	yp24c06.s1 Soares breast 3NbHBst cDNA	H43642	Hs.418241	
		clone IMAGE:188362 3' similar to			
	ŀ	gb:M10942_cds1 metallothionein-le gene	A**		•
		mRNA sequence /clone=IMAGE:188362			
[[· .	/clone_end=3' /gb=H43642 /gi=919694			
,		/ug=Hs.418241 /len=452			
2404	0.00050	Upratain phoophatas 2A resulation	NM 024424	He 400740	NP 821070
3181	0.000521	protein phosphatase 2A, regulatory	NM_021131	Hs.400740	NP_02 10/0
		subunit B' (PR 53) (PPP2R4), mRNA			
		/cds=(190,1161) /gb=NM_021131 /gi=10880986 /ug=Hs.400740 /len=2661			
3185	3.075.06	mRNA for repressor protein, partial cds.	D30612	Hs.58167	NP_003566
7103	3.07 = 00	/cds=(1,2157) /gb=D30612 /gi=2723456		10.00107	
		/ug=Hs.58167 /len=3737		**	
	L	1/49 113.00 101 /1011-0701	<u> </u>		1

Spot	p-value	Description	Accession	Unigene	Protein Accession
	,				No.
3246	0.000295	UI-E-EJ0-ail-e-04-0-UI.r1 UI-E-EJ0 cDNA	BM727687	Hs.446532	NP 079466.1
		clone UI-E-EJ0-ail-e-04-0-UI 5', mRNA		1.10.11.10002	
i kaj Si ski		sequence /clone=UI-E-EJ0-ail-e-04-0-UI			
		/clone_end=5' /gb=BM727687			
		/gi=19049020 /ug=Hs.446532 /len=1103			
3266	0.000386	DKFZP564C186 protein	NM 015658	Hs.134200	NP_056473
		(DKFZP564C186), mRNA /cds=(16,2265)			
*		/gb=NM_015658 /gi=7661605			
		/ug=Hs.134200 /len=2762	,		
3308	3.33E-05	putative breast adenocarcinoma marker	NM_014453	Hs 12107	NP 055268
		(32kD) (BC-2), mRNA /cds=(130,798)			
		/gb=NM_014453 /gi=7656921			
* * * * * * * * * * * * * * * * * * * *		/ug=Hs.12107 /len=903			
3321	0.000448	KIAA0097 gene product (KIAA0097),	NM 014756	Hs 76989	NP 055571
	1	mRNA /cds=(27,5945) /gb=NM 014756		:	
		/gi=24307972 /ug=Hs.76989 /len=6449			
3331	0.001616	ectonucleotide	NM 006208	Hs.11951	NP_006199
		pyrophosphatase/phosphodiesterase 1	_		
•		(ENPP1), mRNA /cds=(173,2794)		,	
*		/gb=NM 006208 /gi=13324676			
		/ug=Hs.11951 /len=3493	1 m	\	
3385	5.44E-07	SMC4 structural maintenance of	NM 005496	Hs.50758	NP 005487
	1.5	chromosomes 4-like 1 (yeast) (SMC4L1),	-		
		mRNA /cds=(233,4099) /gb=NM_005496	Fig. 1		3.
		/gi=21361251 /ug=Hs.50758 /len=5261			
	3.0	<u> </u>			
3396	3.64E-05	CGI-121 protein (CGI-121), mRNA	NM_016058	Hs.433212	NP_057142
		/cds=(107,634) /gb=NM_016058			-
	,	/gi=7705589 /ug=Hs.433212 /len=703			
3418	0.001449	syntaxin 4A (placental) (STX4A), mRNA	NM_004604	Hs.83734	NP_004595
		/cds=(234,1127) /gb=NM_004604			-
		/gi=20149559 /ug=Hs.83734 /len=1412			
3561	0.000636	IkB kinase-b (IKK-beta) mRNA, complete	AF080158	Hs.226573	AAD08997.1
,		cds /cds=(144,2414) /gb=AF080158			
		/gi=4185274 /ug=Hs.226573 /len=3058			
	• ,		*		
3625	0.001021	UI-E-CQ1-aev-g-12-0-UI.s1 UI-E-CQ1	BM666437	Hs.279806	JC1087
		cDNA clone UI-E-CQ1-aev-g-12-0-UI 3',			
		mRNA sequence /clone=UI-E-CQ1-aev-g-			
		12-0-UI /clone_end=3' /gb=BM666437			
<u> </u>		/gi=18974127 /ug=Hs.279806 /len=1103			
3650	0.00143	hypothetical protein FLJ10326	NM_018060	Hs.262823	NP_060530
		(FLJ10326), mRNA /cds=(3,2297)			_
		/gb=NM_018060 /gi=8922355			
		/ug=Hs:262823 /len=3016			

Spot	p-value	Description	Accession	Unigene	Protein Accession No.
3685		SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 (SMARCE1), mRNA /cds=(122,1357) /gb=NM_003079 /gi=21264354 /ug=Hs.332848 /len=1576		Hs.332848	NP_003070
3686	3.07E-05	autism susceptibility candidate 2 (AUTS2), mRNA /cds=(322,4101) /gb=NM_015570 /gi=17864089 /ug=Hs.32168 /len=5972	NM_015570	Hs.32168	NP_056385
3701	0.000356	nudix (nucleoside diphosphate linked moiety X)-type motif 9 (NUDT9), mRNA /cds=(326,1378) /gb=NM_024047 /gi=20127621 /ug=Hs.301789 /len=1718	NM_024047	Hs.301789	NP_076952
3721	0.001393	apoptosis-associated speck-like protein containing a CARD (ASC), transcript variant 1, mRNA /cds=(241,828) /gb=NM_013258 /gi=22035618 /ug=Hs.71869 /len=936	NM_013258	Hs.71869	NP_660184
3731	0.000521	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA /cds=(39,1613) /gb=NM_002778 /gi=11386146 /ug=Hs.406455 /len=2767	NM_002778	Hs.406455	NP_002769
3792	1.38E-05	guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA /cds=(333,1355) /gb=NM_002074 /gi=20357526 /ug=Hs.215595 /len=3147	NM_002074	Hs.215595	NP_002065
3903	0.000356	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 (CHST1), mRNA /cds=(367,1602) /gb=NM_003654 /gi=4502840 /ug=Hs.104576 /len=2415	NM_003654	Hs.104576	NP_003645
3941		pinin, desmosome associated protein (PNN), mRNA /cds=(31,2262) /gb=NM_002687 /gi=4505922 /ug=Hs 44499 /len=2617	NM_002687		NP_002678
4142		chromosome 14 open reading frame 92 (C14orf92), mRNA /cds=(33,1898) /gb=NM_014828 /gi=7662273 /ug=Hs.194035 /len=4174	NM_014828	Hs.194035	NP_055643
4177	0.000356	connective tissue growth factor (CTGF), mRNA /cds=(146,1195) /gb=NM_001901 /gi=4503122 /ug=Hs.75511 /len=2312	NM_001901	Hs.75511	NP_001892
 4209	7.4E-05	cDNA FLJ39491 fis, clone PROST2015924, weakly similar to Opa- interacting protein OIP2 mRNA. /gb=AK096810 /gi=21756383 /ug=Hs.274170 /len=2835	AK096810	Hs.274170	NP_852480

Spot	p-value	Description	Accession	Unigen	Protein
			₩	-	Accession No.
4227	0.000298	ribosomal protein S15 (RPS15), mRNA /cds=(47,484) /gb=NM_001018	NM_001018	Hs.406683	NP_001009
	e Antonio de la composición de la composición de la composición de la composición de la composición de la composición	/gi=14591911 /ug=Hs:406683 /len=515			
4229	8.62E-05	chaperonin containing TCP1, subunit 5 (epsilon) (CCT5), mRNA /cds=(92,1717)	NM_012073	Hs.1600	NP_036205
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		/gb=NM_012073 /gi=24307938 /ug=Hs.1600 /len=1961			
4400	/ 15E-05	mRNA; cDNA DKFZp762O1615 (from	AL359558	Hs.284252	
4400	H. 10JE-00	clone DKFZp762O1615) /gb=AL359558 /gi=8655613 /ug=Hs.284252 /len=2340	AE339330	115.204232	jork i Nerio
4447	0.000521	runt-related transcription factor binding protein 2 (RUNXBP2), mRNA	NM_006766	Hs.82210	NP_006757
		/cds=(394,6408) /gb=NM_006766 /gi=5803097 /ug=Hs.82210 /len=7869			
4631	1.38E-05	chemokine (C-X-C motif) ligand 9 (CXCL9), mRNA /cds=(40,417)	NM_002416	Hs.77367	NP_002407
9		/gb=NM_002416 /gi=4505186 /ug=Hs.77367 /len=2545			
4689	0.000659		NM_006520	Hs.446392	NP_006511
		/gb=NM_006520 /gi=5730086 /ug=Hs.446392 /len=2156			
4770	0.000569	endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	NM_014685	Hs.146393	NP_055500
		(HERPUD1), mRNA /cds=(96,1271) /gb=NM_014685 /gi=7661869	,		
*.		/ug=Hs.146393 /len=1884	1		
4845	0.000356	melanoma antigen, family D, 1 (MAGED1), mRNA /cds=(143,2479)	NM_006986	Hs.5258	NP_008917
		/gb=NM_006986 /gi=14195633 /ug=Hs.5258 /len=2713			
4858	0.001393	AGENCOURT_8819408 NIH_MGC_18 cDNA clone IMAGE:6422878 5', mRNA	BQ941317	Hs.443078	
		sequence /clone=IMAGE:6422878 /clone_end=5' /gb=BQ941317			
4927	0.000153	/gi=22356795 /ug=Hs.443078 /len=929 palmdelphin (PALMD), mRNA	NM_017734	Hs.14606	NP_060204
		/cds=(286,1941) /gb=NM_017734 /gi=16306484 /ug=Hs.14606 /len=2581		1	
4975	2.54E-05	hypothetical protein MGC2747 (MGC2747), mRNA /cds=(93,248) /gb=NM_024104 /gi=13129111	NM_024104	Hs.194017	NP_077009
	-	/ug=Hs.194017 /len=1171			
5090		U3 small nuclear RNA gene	M14061		
5117	2.76E-05	dynein, cytoplasmic, light polypeptide 1 (DNCL1), mRNA /cds=(94,363)	NM_003746	Hs.5120	NP_003737
1.5		/gb=NM_003746 /gi=4505812 /ug=Hs.5120 /len=643			

Spot	p-value	Description	Acc ssion	Unigen	Protein Accession
=00.			NIN 1 0 (500)	1111 SOFTEO	No.
5204	0.000882	stathmin-like 3 (STMN3), mRNA	NM_015894	Hs.285753	NP_056978
		/cds=(83,625) /gb=NM_015894			
5207	0.000746	/gi=14670374 /ug=Hs.285753 /len=2255	NIM OOFSCO	He 20250	ND 005254
5207	0.000746	v-maf musculoaponeurotic fibrosarcoma oncogene (avian) (MAF), mRNA	NM_005360	Hs.30250	NP_005351
		/cds=(808,2019) /gb=NM_005360			
		/gi=5453735 /ug=Hs.30250 /len=2145	1. 1		
5243	0.000326	chromosome 14 open reading frame 2	NM 004894	Hs.109052	NP_004885
0240	0.000020	(C14orf2), mRNA /cds=(61,237)	14111_004054	113.103002	141 _004000
		/gb=NM 004894 /gi=4758939			
		/ug=Hs.109052 /len=627			
5338	0.000356	thyroid hormone receptor interactor 3	NM 004773	Hs.2210	NP_004764
	0.0000	(TRIP3), mRNA /cds=(39,506)			
		/gb=NM_004773 /gi=22094078			+ 1
		/ug=Hs.2210 /len=950			
5383	0.001449	ADP-ribosylation factor GTPase activating	NM 014570	Hs.13014	NP_055385
7777		protein 3 (ARFGAP3), mRNA			
		/cds=(39,1589) /gb=NM_014570			
		/gi=20070254 /ug=Hs.13014 /len=2666			
5396	0.000951	Hypothetical protein(cDNA: FLJ23122 fis,	AK026775		NP_003608
		clone LNG08008)			
5411	0.000569	DKFZp566J2446 (from clone	AL050082		NP_008944
		DKFZp566J2446)			-
5653	2.57E-05	glypican 3 (GPC3), mRNA	NM_004484	Hs.119651	NP_004475
	1	/cds=(191,1933) /gb=NM_004484	7 :		
	* .	/gi=5360213 /ug=Hs.119651 /len=2382			
5654	0.000882	Tis11d	U07802		AAA91778.1
5767	2.61E-05	hypothetical gene supported by AL449243	NM_033318	Hs.306083	NP_201575
,		(LOC91689), mRNA /cds=(80,403)			
1. 7		/gb=NM_033318 /gi=21314768]		4
	ĵ.	/ug=Hs.306083 /len=1586			
5810	3.64E-05	non-metastatic cells 2, protein (NM23B)	NM_002512	Hs.433416	NP_002503
		expressed in (NME2), nuclear gene	* * * * * * * * * * * * * * * * * * * *		
		encoding mitochondrial protein, mRNA			
1	- 14 · 1	/cds=(73,531) /gb=NM_002512			
		/gi=4505408 /ug=Hs.433416 /len=670	<u> </u>		
5826	0.001616	ribosomal protein L13a (RPL13A), mRNA	NM_012423	Hs.389335	NP_036555
	,	/cds=(23,634) /gb=NM_012423			•
		/gi=14591905 /ug=Hs.389335 /len=1142			* :
5941	8.5E-06	ubiquitin-protein isopeptide ligase (E3)	NM_014671	Hs.155287	NP_055486
		(KIAA0010), mRNA /cds=(304,3555)			
		/gb=NM_014671 /gi=7661855	ŀ		
		/ug=Hs.155287 /len=5160			
6027	0.000356	mesenchyme homeo box 2 (growth arrest	NM_005924	Hs.77858	NP_005915
		specific homeo box) (MEOX2), mRNA			
		/cds=(182,1093) /gb=NM_005924			:
		/gi=21396478 /ug=Hs.77858 /len=2284			
	1	<u> </u>			F .

	Spot	p-value	Description	Accession	Unigene	Protein Accession No.
	6046	0.000711	KIAA0092 gene product (KIAA0092), mRNA /cds=(54,1478) /gb=NM_014679 /gi=7661899 /ug=Hs.151791 /len=2913	NM_014679	Hs.151791	NP_055494
-	6202	0.000492	Si-1-8-16 mRNA, partial cds	AB044752		NP 061130
	6360		heterogeneous nuclear ribonucleoprotein D-like (HNRPDL), transcript variant 1, mRNA /cds=(581,1843) /gb=NM_005463 /gi=14110410 /ug=Hs.372673 /len=3514	NM_005463	Hs 372673	NP_112740
\vdash	6458	9 46F-06	mitochondrion, complete genome	NC 001807		
	6491		RecQ protein-like (DNA helicase Q1-like) (RECQL), transcript variant 1, mRNA /cds=(472,2421) /gb=NM_002907 /gi=14591903 /ug=Hs.235069 /len=2866	NM_002907	Hs.235069	NP_116559
	6510	0.001449	UI-H-DT0-atx-f-13-0-UI.s1 NCI_CGAP_DT0 cDNA clone IMAGE:5865612 3', mRNA sequence	BM994157	Hs.406666	
-			/clone=IMAGE:5865612 /clone_end=3' /gb=BM994157 /gi=19719058 /ug=Hs.406666 /len=1283			
74	6526	0.001021	sequestosome 1 (SQSTM1), mRNA /cds=(41,1363) /gb=NM_003900 /gi=19923742 /ug=Hs.182248 /len=2870	NM_003900	Hs.182248	NP_003891
	6595	8.62E-05	H factor 1 (complement) (HF1), mRNA /cds=(74,3769) /gb=NM_000186 /gi=4504374 /ug=Hs.250651 /len=3926	NM_000186	Hs.250651	NP_000177
	6622	0.000669	aquaporin 1 (channel-forming integral protein, 28kDa) (AQP1), mRNA /cds=(39,848) /gb=NM_000385 /gi=4755121 /ug=Hs.76152 /len=1662	NM_000385	Hs.76152	NP_000376
	6663		PRO0461 protein (PRO0461), mRNA /gb=NM_031268 /gi=20588827 /ug=Hs 25063 /len=1100	NM_031268	Hs.25063	Q9UI25
	6733	1.38E-05	putative transmembrane protein (NMA), mRNA /cds=(373,1155) /gb=NM_012342 /gi=6912533 /ug=Hs.78776 /len=1521	NM_012342	Hs.78776	NP_036474
	6901	0.000983	cDNA FLJ34353 fis, clone FEBRA2011665. /cds=(178,573) /gb=AK091672 /gi=21750096 /ug=Hs.13477 /len=3517	AK091672	Hs.13477	BAC03718.1
	6925	0.000298	mitochondrial ribosomal protein S22 (MRPS22), nuclear gene encoding mitochondrial protein, mRNA /cds=(9,1091) /gb=NM_020191 /gi=16554602 /ug=Hs.107127 /len=1155	NM_020191	Hs.107127	NP_064576

Spot	p-valu	Description	Accession	Unigene	Protein Accession
-					No.
6962	2.03E-05	hypothetical protein FLJ10377	NM_018077	Hs.274263	NP_060547
		(FLJ10377), mRNA /cds=(116,2395)			
2		/gb=NM_018077 ⁻ /gi=8922387 ⁻			
		/ug=Hs.274263 /len=2809		· · · · <u> </u>	- <u> </u>
6999	0.000298	ring finger protein 20 (RNF20), mRNA	NM_019592	Hs.168095	NP_062538
		/cds=(91,3018) /gb=NM_019592			
,*		/gi=16554452 /ug=Hs.168095 /len=3936		•	
7030	1.38E-05	CD74 antigen (invariant polypeptide of	NM_004355	Hs.84298	NP_004346
		major histocompatibility complex, class II			<u> </u>
-		antigen-associated) (CD74), mRNA	<u>.</u>		
		/cds=(8,706) /gb=NM_004355			
	1	/gi=10835070 /ug=Hs.84298 /len=1304			
7142	0.001116	eukaryotic translation elongation factor 1	NM_001402	Hs.422118	NP_001393
		alpha 1 (EEF1A1), mRNA /cds=(63,1451)			1 · · · · · ·
		/gb=NM_001402 /gi=25453469			
,		/ug=Hs.422118 /len=1837		1	
7287	0.000492	mRNA; cDNA DKFZp586E1624 (from	AL110152	Hs.94030	
		clone DKFZp586E1624) /gb=AL110152			
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	,	/gi=5817054 /ug=Hs.94030 /len=1341			
7382	0.000316	cortactin binding protein 2 (CORTBP2),	NM 033427	Hs.293539	NP_219499
		mRNA /cds=(93,5084) /gb=NM_033427		7	
		/gi=16975495 /ug=Hs.293539 /len=5975			
7398	0.000463	laminin, alpha 2 (merosin, congenital	NM 000426	Hs.75279	NP_000417
		muscular dystrophy) (LAMA2), mRNA			,
	* .	/cds=(50,9382) /gb=NM_000426	•		· ·
		/gi=4557708 /ug=Hs.75279 /len=9534			
7420	0.001021	UDP-N-acetyl-alpha-D-	NM 020474	Hs.80120	NP_065207
J		galactosamine:polypeptide N-	· · · ·		_ : : : :
		acetylgalactosaminyltransferase 1			
		(GalNAc-T1) (GALNT1), mRNA			
		/cds=(32,1711) /gb=NM_020474			
	*	/gi=13124890 /ug=Hs.80120 /len=3778			
7556	0.000173	interleukin enhancer binding factor 1	NM_004514	Hs.296281	NP 852096
<i>े इंस्</i>		(ILF1), mRNA /cds=(198,2165)		1 7 7 7 1	_ · · · = · · · · · · · · · · · · · · ·
		/gb=NM_004514 /gi=4758599			
		/ug=Hs.296281 /len=3059		1	
7725	8.5F-06	proteasome (prosome, macropain)	NM 002794	Hs.432607	NP 002785
		subunit, beta type, 2 (PSMB2), mRNA			
	100	/cds=(111,716) /gb=NM_002794	,		
		/gi=22538463 /ug=Hs.432607 /len=850			
7899	0.000117	UI-E-DW0-agk-i-01-0-UI.r1 UI-E-DW0	BM696546	Hs.356149	-
	3.555117	cDNA clone UI-E-DW0-agk-i-01-0-UI 5',			1
		mRNA sequence /clone=UI-E-DW0-agk-i-			
		01-0-UI /clone_end=5' /gb=BM696546			
	``	/gi=19009804 /ug=Hs.356149 /len=1200			1
7906	0.001071	cDNA FLJ30587 fis, clone	AK055149	Hs.367639	··· · · · · · · · · · · · · · · · · ·
/ 900	0.001071		1,11000149	13.307039	
		BRAWH2007800, weakly similar to Ovo		}	1
:		protein. /gb=AK055149 /gi=16549814			
	L	/ug=Hs.367639 /len=2529	<u> </u>	L	1

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7915	
/cds=(185,1636) /gb=NM_020198 /gi=9910241 /ug=Hs.8207 /len=3294 7927	
/gi=9910241 /ug=Hs.8207 /len=3294 Rollong UI-H-EZ1-bca-n-05-0-UI s1 NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-bca-n-05-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bca-n-05-0-UI /lene_end=3' /gb=BQ774356 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=3' /gb=BQ774356 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=3' /gb=BQ774356 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=3' /gb=BQ774356 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=3' /gb=BQ774356 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=3' /gb=BQ774356 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=3' /gb=BQ774356 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=3' /gb=BQ774356 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=3' /gb=BQ774356 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=3' /gb=BQ774356 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=3' /gb=BQ774356 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=3' /gb=BQ774356 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI /lene_end=2276 Rollong UI-H-EZ1-bca-n-05-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0-UI-H-EZ1-bca-n-0	3
7927 0.0003 UI-H-EZ1-bca-n-05-0-UI.S1 NCI_CGAP_Ch2 cDNA clone UI-H-EZ1- bca-n-05-0-UI.31, mRNA sequence /clone=UI-H-EZ1-bca-n-05-0-UI /clone_end=31/gb=BQ774356 /gi=21982825 /ug=Hs.43227 /len=1083 7947 3.9E-07 EST (AV690707 GKC H.sapiens cDNA AV690707 NP_00457 7952 0.000793 EST (Al683276 tx02h12.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2268071 3') 8043 0.000173 hypothetical protein from BCRA2 region (CG005), mRNA /cds=(166,1917) //gb=NM_014887 /gi=7656970 //ug=Hs.23518 /len=2825 8069 0.001021 Similar to nuclear localization signals binding protein 1, clone MGC:21810 IMAGE:4183576, mRNA, complete cds //cds=(58,375) /gb=BC016981 //gi=16877469 /ug=Hs.244624 /len=2059 8134 0.000104 CGI-204 mRNA, complete cds //cds=(41,799) /gb=AF285120 /gi=9858830 //ug=Hs.283734 /len=2865 8179 0.000364 karyopherin (importin) beta 3 (KPNB3), mRNA /cds=(139,3486) /gb=NM_002271 //gi=24797085 /ug=Hs.113503 /len=5977 8202 0.000364 transcription factor Dp-1 (TFDP1), mRNA NM_007111 Hs.79353 NP_009045)	
NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-bca-n-05-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bca-n-05-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bca-n-05-0-UI /Clone_end=3' /gb=BQ774356 /gi=21982825 /ug=Hs.43227 /len=1083	
bca-n-05-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bca-n-05-0-UI /clone_end=3' /gb=BQ774356 /gi=21982825 /ug=Hs.43227 /len=1083 /gi=21982825 /ug=Hs.43227 /len=1083 /gi=21982825 /ug=Hs.43227 /len=1083 /gi=21982825 /ug=Hs.43227 /len=1083 /gi=21982825 /ug=Hs.43227 /len=1083 /gi=21982825 /ug=Hs.43227 /len=1083 /gi=21982825 /ug=Hs.2318 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /ug=Hs.23518 /us=219 /ug=Hs.23518 /us=219 /ug=Hs.23518 /us=219 /ug=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=Hs.23518 /us=219 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419 /us=419	
/clone=UI-H-EZ1-bca-n-05-0-UI /clone_end=3' /gb=BQ774356 /gi=21982825 /ug=Hs.43227 /len=1083 7947	
/clone_end=3' /gb=BQ774356 /gi=21982825 /ug=Hs.43227 /len=1083 7947	٠.
/gi=21982825 /ug=Hs.43227 /len=1083 7947 3.9E-07 EST (AV690707 GKC H.sapiens cDNA AV690707 NP_00457 7952 0.000793 EST (Al683276 tx02h12.x1 Al683276 NCI_CGAP_Ut4 cDNA clone IMAGE:2268071 3') Round NM_014887 Al683276 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887 NM_014887	
3.9E-07 EST (AV690707 GKC H.sapiens cDNA AV690707 NP_004577	
7952	
NCI_CGAP_Ut4 cDNA clone IMAGE:2268071 3')	<u> </u>
IMAGE:2268071 3') 8043 0.000173 hypothetical protein from BCRA2 region (CG005), mRNA /cds=(166,1917) /gb=NM_014887 /gi=7656970 /ug=Hs.23518 /len=2825 Similar to nuclear localization signals binding protein 1, clone MGC:21810 IMAGE:4183576, mRNA, complete cds /cds=(58,375) /gb=BC016981 /gi=16877469 /ug=Hs.244624 /len=2059 R134 0.000104 CGI-204 mRNA, complete cds /cds=(41,799) /gb=AF285120 /gi=9858830 /ug=Hs.283734 /len=2865 R179 0.000364 karyopherin (importin) beta 3 (KPNB3), mRNA /cds=(139,3486) /gb=NM_002271 /gi=24797085 /ug=Hs.113503 /len=5977 MM_007111 Hs.79353 NP_009045 /cds=(222,1454) /gb=NM_007111 NM_007111 Hs.79353 NP_009045 /cds=(222,1454) /gb=NM_007111 NM_007111 Hs.79353 NP_009045 /cds=(222,1454) /gb=NM_007111 NM_007111 Hs.79353 NP_009045 /cds=(222,1454) /gb=NM_007111 NM_007111 Hs.79353 NP_009045 /cds=(222,1454) /gb=NM_007111 NM_007111 Hs.79353 NP_009045 /cds=(222,1454) /gb=NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_007111 NM_0007111 NM_007111 NM_007111 NM_0007111 NM_0007111 NM_000711	·
8043	
(CG005), mRNA /cds=(166,1917) /gb=NM_014887 /gi=7656970 /ug=Hs.23518 /len=2825 8069	
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8069 0.001021 Similar to nuclear localization signals binding protein 1, clone MGC:21810 IMAGE:4183576, mRNA, complete cds /cds=(58,375) /gb=BC016981 /gi=16877469 /ug=Hs.244624 /len=2059 8134 0.000104 CGI-204 mRNA, complete cds. /cds=(41,799) /gb=AF285120 /gi=9858830 /ug=Hs.283734 /len=2865 8179 0.000364 karyopherin (importin) beta 3 (KPNB3), mRNA /cds=(139,3486) /gb=NM_002271 /gi=24797085 /ug=Hs.113503 /len=5977 8202 0.000364 transcription factor Dp-1 (TFDP1), mRNA NM_007111 Hs.79353 NP_009043 /cds=(222,1454) /gb=NM_007111	
binding protein 1, clone MGC:21810 IMAGE:4183576, mRNA, complete cds /cds=(58,375) /gb=BC016981 /gi=16877469 /ug=Hs.244624 /len=2059 8134	
IMAGE:4183576, mRNA, complete cds /cds=(58,375) /gb=BC016981 /gi=16877469 /ug=Hs.244624 /len=2059	.1
/cds=(58,375) /gb=BC016981 /gi=16877469 /ug=Hs.244624 /len=2059 8134	
/gi=16877469 /ug=Hs.244624 /len=2059	
8134	- 11 -
/cds=(41,799) /gb=AF285120 /gi=9858830 /ug=Hs.283734 /len=2865 8179	
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8179 0.000364 karyopherin (importin) beta 3 (KPNB3), mRNA /cds=(139,3486) /gb=NM_002271	
mRNA /cds=(139,3486) /gb=NM_002271 /gi=24797085 /ug=Hs.113503 /len=5977 8202	
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8202	
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	2
8315 0.000448 UI-H-ED0-awz-g-17-0-UI.s1 BM994952 Hs.15702	
NCI_CGAP_ED0 cDNA clone	
IMAGE:5825704 3', mRNA sequence	
/clone=IMAGE:5825704 /clone_end=3'	
/gb=BM994952 /gi=19719853	
/ug=Hs.15702 /len=1200	
8334 0.000272 EST (MR4-ST0070-051099-009-e09 AW387240 NP_03654	3
ST0070)	
8351 0.000806 EST zr46h01.s1 Soares NhHMPu S1 AA233076	
cDNA clone 666481 3'	
8360 0.000521 EST(zf51h11.r1 Soares retina N2b4HR AA044938	
clone IMAGE:380517 5' contains	
MER17.b2 MER17 repeat)	
8466 0.000625 Tho2 mRNA, complete cds /cds=(1,4437) AF441770 Hs.16411 AAM28436	_
/gb=AF441770 /gi=20799317	.1
/ug=Hs.16411 /len=4452	.1

Spot	p-value	Description	Accession	Unigene	Protein
	,		-1.1	: .	Accession
8580	0.001546	BX096173 Soares_testis_NHT cDNA	BX096173	Hs.188780	No.
0000	0.001540	clone IMAGp998F151793, mRNA	DX090173	115.100700	
		sequence			
		/clone=IMAGp998F151793_;_IMAGE:730			
100		766 /gb=BX096173 /gi=27842669			to the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second se
		/ug=Hs.188780 /len=556			
8622	0.001393	FLJ30623 fis, clone CTONG2001748	AK055185	Hs.351574	NP 079050
0022	0.001000	/cds=UNKNOWN /gb=AK055185	/ " 1000 100	110,00107	-070000
		/gi=16549855 /ug=Hs.351574 /len=2870			a financia
8663	.0.000326	hypothetical protein BC018453	NM_138798	Hs.14222	NP_620153
	0.0000	(LOC129531), mRNA /cds=(49,798)			_020 (00
		/gb=NM_138798 /gi=20270348			
**		/ug=Hs.14222 /len=963			7 t
8706	0.000164	cDNA FLJ31306 fis, clone	AK055868	Hs.442335	NP_071431.1
		LIVER1000111. /gb=AK055868			
	,	/gi=16550703 /ug=Hs.442335 /len=2360			1
8717	8.5F-06	EST(cDNA clone IMAGE:2622241 3')	AW131141		NP 055262
8770		UI-H-DF0-bey-f-20-0-UI.s1	CA427170	Hs.27996	
37.7	0.0007770	NCI CGAP DF0 cDNA clone UI-H-DF0-			
2		bey-f-20-0-UI 3', mRNA sequence			
		/clone=UI-H-DF0-bey-f-20-0-UI			
		/clone_end=3' /gb=CA427170			
	·	/gi=24789896 /ug=Hs.27996 /len=1082			
8771	0.000298	mitochondrion, complete genome	NC 001807		
8804		E2F transcription factor 5, p130-binding	NM_001951	Hs.2331	NP_001942
·		(E2F5), mRNA /cds=(35,1075)			
,		/gb=NM_001951 /gi=12669916	<u>.</u>		
	•	/ug=Hs.2331 /len=1752			
8843	3.07E-05	No significant match, ORF-1(69~499)low			
		complexity	12 5		
8853	0.000153	No significant match			1.
	4	(ORF:+1:13~144[132], +2:50~151[102])		0.4	
8856	0.000625				
8862	0.000326	cDNA FLJ14368 fis, clone	AK027274	Hs.330716	
		HEMBA1001122. /gb=AK027274			
		/gi=140 <u>41848</u> /ug=Hs.330716 /len=1543			
8865	3.07E-05	cDNA FLJ12091 fis, clone	AK022153		
		HEMBB1002582			
8875	0.000326	No significant match, ORF+2(131~292)			
8951	0.000569	PTK2 protein tyrosine kinase 2 (PTK2),	NM_153831	Hs.740	NP_722560
		transcript variant 1, mRNA			
		/cds=(231,3389) /gb=NM_153831			
		/gi=27886591 /ug=Hs.740 /len=4453	<u> </u>		
9026	0.000105	df118f01.w1 Morton Fetal Cochlea cDNA	BI495496	Hs.345508	
		clone IMAGE:2539897 3', mRNA	·		
,		sequence /clone=IMAGE:2539897			
		/clone_end=3' /gb=BI495496			
	<u> </u>	/gi=15334840 /ug=Hs.345508 /len=553			<u> </u>

Spot	p-value	D scription	Accession	Unigene	Protein Accession
					No.
9065	0.000983	UI-H-BI0p-abb-b-05-0-UI.s1	AW015262	Hs.440665	
		NCI_CGAP_Sub2 cDNA clone			
		IMAGE:2711001 3', mRNA sequence			
		/clone=IMAGE:2711001 /clone_end=3'	· ·		
		/gb=AW015262 /gi=5863949			
		/ug=Hs.440665 /len=854			ie La companya de la companya de la companya de la companya de la companya de la companya de la companya de la co
9078	0.000959	cDNA FLJ13207 fis, clone	AK023269	Hs.14355	
		NT2RP4000023. /gb=AK023269			
•		/gi=10435128 /ug=Hs.14355 /len=2633			_
9142	0.000492	cDNA FLJ38449 fis, clone	AK095768	Hs.146312	NP_071431.1
	·	FEBRA2019389. /gb=AK095768	1.1		
		/gi=21755098 /ug=Hs.146312 /len=2628	1		
9161	2.07E-05	cDNA FLJ31107 fis, clone	AK055669	Hs.405954	
		IMR322000152. /gb=AK055669			
		/gi=16550452 /ug=Hs.405954 /len=2250			
9271	2.8E-05	fj53d02.x1 adult brain Danio rerio cDNA 3'	AW281691	**************************************	EFHU2
		similar to SW:EF2_CHICK Q90705			
	1 :	ELONGATION FACTOR 2 ;			
9364	8.5E-06	FLJ12419 fis, clone MAMMA1003047,	AK022481	Hs.105779	NP_056981
		highly similar to Homo sapiens protein			
		inhibitor of activated STAT protein PIASy			
	, .	mRNA /cds=UNKNOWN /gb=AK022481			
		/gi=10433892 /ug=Hs.105779 /len=3054			
9376	0.000928	tenascin XB (TNXB), transcript variant	NM_019105	Hs 169886	NP_115859
		XB, mRNA /cds=(205,13074)	at .		
		/gb=NM_019105 /gi=20544188			
		/ug=Hs.169886 /len=13268		*	
9451	5.82E-05	phospholipase A2-activating protein	NM_004253	Hs.27182	NP_004244
		(PLAA), mRNA /cds=(29,2245)			
		/gb=NM_004253 /gi=21361288			
		/ug=Hs.27182 /len=3240	*.		
9463	0.000521	tropomyosin 3 (TPM3), mRNA	NM_153649	Hs.85844	NP_705935
		/cds=(52,798) /gb=NM_153649			
4. 1	•	/gi=24119202 /ug=Hs.85844 /len=2089		<u> </u>	
9488	3.07E-05	UDP-N-acteylglucosamine	NM_003115	Hs.21293	NP_003106
		pyrophosphorylase 1 (UAP1), mRNA		"	
		/cds=(312,1829) /gb=NM_003115			
		/gi=19923738 /ug=Hs.21293 /len=2332			
9535	0.001449	Hypothetical protein 669, cDNA FLJ32614	BC000819	Hs.180378	NP_062556
[' ·		fis, clone STOMA2000121, moderately			
,		similar to Fugu rubripes CCBL1 gene			,
		(AK057176.1) (=CG6950 gene,			3
		BC000819.1)			
9573	0.000326	cDNA FLJ39084 fis, clone	AK096403	Hs.356835	BAC04779.1
		NT2RP7018871. /cds=(491,1024)			
		/gb=AK096403 /gi=21755888	,		
		/ug=Hs.356835 /len=2242			

	Spot	p-value	D scription	Accession	Unigene	Protein
						Accession No.
Ī	9633	0.000298	U7 snRNP-specific Sm-like protein LSM10 (LSM10), mRNA /cds=(151,522)	NM_032881	Hs.3496	NP_116270
			/gb=NM_032881 /gi=14249631			
l			/ug=Hs.3496 /len=869	1		
٠	9634	4.31E-05	cDNA PSEC0070 fis, clone	AK075380	Hs.183454	NP_849193
	·	• • •	NT2RP2001508, moderately similar to			
		• .	OLIGOSACCHARYL TRANSFERASE	,		
1			STT3 SUBUNIT. /cds=(94,954)			
			/gb=AK075380 /gi=22761428			
L	-		/ug=Hs.183454 /len=2510	*		
	9771	0.000521	EST(oo43e04.s1 NCI_CGAP_Lu5 clone	AA973377		
i			IMAGE:1568958 3' contains L1.t1 L1			
Ļ			repeat)	the second		
I	9862	0.001393	component of oligomeric golgi complex 1	NM_018714	Hs.283109	NP_061184
١			(COG1), mRNA /cds=(27,2969)			
	***		/gb=NM_018714 /gi=21237782			
L		4	/ug=Hs.283109 /len=3047			
١	9895	4.31E-05	FLJ23227 fis, clone CAE00645, highly	AK026880	Hs.6580	NP_031397.1
ı			similar to AF052138 Homo sapiens clone		* .	
ı			23718 mRNA sequence /cds=UNKNOWN			
ı	. 4		/gb=AK026880 /gi=10439841		4	
L	** .		/ug=Hs.6580 /len=1729			
1	9975	0.000298	RAB6A, member RAS oncogene family	NM_002869	Hs.5636	NP_002860
1			(RAB6A), mRNA /cds=(427,1053)			
1		2.14	/gb=NM_002869 /gi=19923230			
L			/ug=Hs.5636 /len=3079			
ſ	9995	0.000659	UDP-Gal:betaGlcNAc beta 1,3-	NM_003781	Hs.267695	NP_149359
.	**		galactosyltransferase, polypeptide 3			_
1			(B3GALT3), transcript variant 1, mRNA			
1			/cds=(399,1394) /gb=NM_003781			
L			/gi=15451873 /ug=Hs.267695 /len=3210			
	9998	3.07E-05	chromosome 20 open reading frame 14	NM_012469	Hs.31334	NP_036601
			(C20orf14), mRNA /cds=(100,2925)			
ı			/gb=NM_012469 /gi=6912731			
ļ			/ug=Hs.31334 /len=3060			
	10021	. 3.07E-05	RalGDS-like gene (RGL), mRNA	NM_015149	Hs 79219	NP_055964
1			/cds=(450,2861) /gb=NM_015149	. •		
L		A CONTRACTOR	/gi=20127535 /ug=Hs.79219 /len=5111			
	10024	1.38E-05	DnaJ (Hsp40) subfamily B, member 11	NM_016306	Hs.278605	NP_057390
1			(DNAJB11), mRNA /cds=(160,1236)	ř		
			/gb=NM_016306 /gi=25014110			'
L		1	/ug=Hs.278605 /len=1621	<u> </u>		
	10044	2.76E-05	ER-resident protein ERdj5 (ERdj5),	NM_018981	Hs.1098	NP_061854
			mRNA /cds=(416,2797) /gb=NM_018981			
			/gi=24308126 /ug=Hs.1098 /len=4193			
L			t			

Spot	p-value	Description	Accession	Unigene	Protein Accession
10050	0.000164	FLJ10765 fis, clone NT2RP4000111,	AK001627	Hs.224961	No
1,0000	0.000104	highly similar to CLEAVAGE AND	AR001027	1115.224501	
		POLYADENYLATION SPECIFICITY			
		FACTOR, 100 KD SUBUNIT			
		/cds=UNKNOWN /gb=AK001627			
10001	5 005 05	/gi=7022996 /ug=Hs.224961 /len=4352	50404004	177000	
10061	5.82E-05	UI-H-EU0-azv-c-01-0-UI.s1	BQ181694	Hs.177936	
		NCI_CGAP_Car1 cDNA clone IMAGE:		• •	
•		5854008 3', mRNA sequence			
	;	/clone=IMAGE:_5854008 /clone_end=3!	. 1		
		/gb=BQ181694 /gi=20357186			
		/ug=Hs.177936 /len=1076			
10069	5.82E-05	hypothetical protein FLJ20297	NM_017751	Hs.94491	NP_060421
	-	(FLJ20297), mRNA /cds=(111,2507)			İ
		/gb=NM_017751 /gi=8923276			
	-	/ug=Hs.94491 /len=3682	,		
10087	2.07E-05	cDNA FLJ30064 fis, clone	AK054626	Hs.188504	BAB70777.1
		ADRGL2000323. /cds=(118,516)			
		/gb=AK054626 /gi=16549205			
		/ug=Hs.188504 /len=2081			
10094	8 88F-06	nuclear factor of kappa light polypeptide	NM 013432	Hs.323834	NP 038460
10034	0.002.00	gene enhancer in B-cells inhibitor-like	14111_010402	113.020004	141-20090
	-	2(NFKBIL2), mRNA /cds=(473,4132)			
		/gb=NM_013432/gi=15718771		·	
]				·
40000	0.000744	/ug=Hs.323834 /len=4501	AF004045		A A COO 42C 4
10099	0.000711	intersectin (ITSN) gene, exons and short	AF064245		AAC80436.1
		form, partial cds	 		
10105	2.76E-05	programmed cell death 2 (PDCD2),	NM_144781	Hs.367900	NP_659005
		transcript variant 2, mRNA /cds=(80,766)			-
		/gb=NM_144781 /gi=21735593			
		/ug=Hs.367900 /len=2066		<u> </u>	
10126	0.000356	mRNA for KIAA0647 protein, partial cds	AB014547	Hs.141727	NP_004678
		/cds=UNKNOWN /gb=AB014547			
		/gi=20521118 /ug=Hs.141727 /len=5719			
10163	1.46E-05	KIAA0062 mRNA, partial cds	D31887	Hs.89868	BAA06685.1
	ł	/cds=(1,1598) /gb=D31887 /gi=505101			1
		/ug=Hs.89868 /len=4573	1	,	
10183	5 82F-05	cDNA: FLJ20924 fis, clone ADSE00928.	AK024577	Hs.306692	JC5238
	0.022	/gb=AK024577 /gi=10436889		:	
	{	/ug=Hs.306692 /len=1516			
10228	0.001440	hypothetical protein FLJ10342	NM 018064	Hs.101514	NP_060534
10220	0.001448	(FLJ10342), mRNA /cds=(534,1145)	14141_010004	113.101314	_000004
	((FL310342), MKNA/cds=(334,1143) //gb=NM 018064/gi=14149717		ļ.:	,
		10 - 0			
40000	0.000000	/ug=Hs.101514 /len=1506	NIM 004544	He 404054	ND 070707
10236	0.000882	hypothetical protein MGC4701	NM_024511	Hs.421054	NP_078787
		(MGC4701), mRNA /cds=(149,1585)		,	
	ľ	/gb=NM_024511 /gi=24308290	1	1	
		/ug=Hs.421054 /len=1686	1	 	
10302	0.000427	EST CM4-CT0343-301199-052-d11	AW363671		NP_000998
	I	CT0343	I		·

Spot	p-value	Description	Accession	Unigene	Protein Accession
			·		
10348	0.000533	BX103634	BX103634	Hs.134848	No.
10346	0.000523	Soares NSF F8 9W OT PA P S1	DX 103034	FIS. 13#040	•
	_	cDNA clone IMAGp998O213969, mRNA			
		· · · · · · · · · · · · · · · · · · ·		1.	
		sequence			
		/clone=IMAGp998O213969_;_IMAGE:156			
		6572 /gb=BX103634 /gi=27845812			
40400	0.000004	/ug=Hs.134848 /len=554	BC041379	11-407040	
10428	0.000694	clone IMAGE:5275048, mRNA	BC041379	Hs.187646	
•		/gb=BC041379 /gi=27552809			
70470	0.075.05	/ug=Hs 187646 /len=3258	DE500007	11 40000=	NID 000074.0
10479	3.07E-05	UI-H-BI4-aos-c-04-0-UI.s1	BF508907	Hs.433695	NP_003874.2
		NCI_CGAP_Sub8 cDNA clone			
		IMAGE:3085830 3', mRNA sequence			
		/clone=IMAGE:3085830 /clone_end=3'			Ĭ ·
a de la compa		/gb=BF508907 /gi=11592205		1.5	
11 11 12 13 13 13 13 13 13 13 13 13 13 13 13 13		/ug=Hs.433695 /len=932			
10484	3.64E-05	hypothetical protein FLJ20255	NM_017728	Hs.15797	NP_060198
		(FLJ20255), mRNA /cds=(146,1090)			.
		/gb=NM_017728 /gi=8923229	, ,		
		/ug=Hs.15797 /len=1769			
10501	2.76E-05	UI-E-DW0-agg-d-24-0-UI.r1 UI-E-DW0	BM706154	Hs.433446	P51003
•		cDNA clone UI-E-DW0-agg-d-24-0-UI 5',			
. •		mRNA sequence /clone=UI-E-DW0-agg-d	•		
		24-0-UI /clone_end=5' /gb=BM706154			
		/gi=19019412 /ug=Hs.433446 /len=1003		1	
10528	0.000104	FLJ32238 fis, clone PLACE6004993	AK056800	Hs.183161	NP_036595
		/cds=UNKNOWN /gb=AK056800			
·		/gi=16552307 /ug=Hs.183161 /len=2204		<u> </u>	
10533	5.82E-05	EST(Normalized Human Islet 4 N4-HIS 1	BI964140	- :	NP_006531
	<u> </u>	Homo sapiens cDNA 5')		ļ.,	
10594	0.000791	UI-H-EZ1-bbh-j-15-0-UI.s1	BQ575990	Hs.445509	
		NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-		- '	
		bbh-j-15-0-UI 3', mRNA sequence	2.4) .	
•	,	/clone=UI-H-EZ1-bbh-j-15-0-UI			
		/clone_end=3' /gb=BQ575990			
		/gi=21479307 /ug=Hs.445509 /len=1032		ļ	
10606	0.001387	EST(fp43g05.x1 zebrafish gridded kidney	BG891931		
		Danio rerio cDNA clone 4759496 3'			
		similar to contains element MER21			
	ļ	repetitive element ;)			
10657	1.01E-05	cDNA FLJ34771 fis, clone	AK092090	Hs.433010	NP_060312.1
		NT2NE2003150. /gb=AK092090			
		/gi=21750599 /ug=Hs.433010 /len=2424		<u> </u>	
10684		EST(cDNA clone IMAGE:4090855 3')	BF447403		NP_002806
10783	0.000298	EST (nm30c04.s1 NCI_CGAP_Lip2	AA569171]	
· .		IMAGE:1061670)			
10786	0.001289	EST (MR0-SN0040-060400-001-h09	AW867719		
		SN0040)			1
10864	0.000492	EST (ab81d11.s1 Stratagene fetal retina	AA663308	-	
<i>i</i>	-	937202 IMAGE:853365 3')		· [

Spot	p-value	Description	Accession	Unigene	Protein Accession
					No.
10967	0.000681	cDNA /clone=cD622 /gb=AF107454 /gi=5052209 /ug=Hs.107537 /len=4850	AF107454	Hs.107537	NP_071903
11107	8.5E-06	cDNA FLJ11041 fis, clone	AK001903	Hs.28792	
		PLACE1004405. /gb=AK001903		-	
		/gi=7023457 /ug=Hs.28792 /len=1932			
11139	0.000298	ESTs, cDNA, 3' end	BF593483	Hs.235860	Q9H334
	7.3	/clone=IMAGE:3676432 /clone_end=3'			
		/gb=BF593483 /gi=11685729			
• •		/ug=Hs.235860 /len=582	· ·		
11183	0.000298	No significant match			
11276		FLN29 gene product (FLN29), mRNA	NM 006700	Hs.5148	NP_006691
	1.002	/cds=(55,1803) /gb=NM_006700			
		/gi=5729827 /ug=Hs.5148 /len=2618			
11279	0.000298	cDNA FLJ11660 fis, clone	AK021722	Hs.281895	- 01 11-11 - CH -
	0.000200	HEMBA1004610. /gb=AK021722	111021722	1.10.201000	
		/gi=10432962 /ug=Hs.281895 /len=1769			
11323	0.001393	inhibitor of kappa light polypeptide gene	XM_032491		†
11020	0.001000	enhancer in B-cells, kinase beta (IKBKB),	J002 10 1		
		mRNA		F	
11345	0.000719	HT001 protein (HT001), mRNA	NM 014065	Hs.279040	NP_054784
110-10	0.0007 10	/cds=(242,1204) /gb=NM_014065	11111_014000	113.2730.10	111 _004704
1	;	/gi=7661837 /ug=Hs.279040 /len=1402			
11357	3.07F-05	splicing factor 3a, subunit 1, 120kDa	NM 005877	Hs 406277	NP_005868
11007	0.07 L-00	(SF3A1), mRNA /cds=(132,2513)	14141_000077	113.400277	
		/gb=NM_005877 /gi=20127483			<u>,</u>
		/ug=Hs.406277 /len=2944			4.5
11414	1 38F-05	solute carrier family 25 (mitochondrial	NM 002635	Hs.78713	NP_005879
11717	1.002-00	carrier; phosphate carrier), member 3	TIM_002000	113.707 10	
		(SLC25A3), nuclear gene encoding		İ	
		mitochondrial protein, transcript variant	1,		
		11b, mRNA /cds=(49,1134)			
		/gb=NM_002635 /gi=4505774	er to provide		
		/ug=Hs.78713 /len=1330			Ì .
11462	3.07E=05	ta10c07.x1	AI581285	Hs.309697	
11-102	3.07E-00	Soares_total_fetus_Nb2HF8_9w cDNA	71001200	113.505057	
		clone IMAGE:2043660 3', mRNA		(
]	sequence /clone=IMAGE:2043660			٠.
		/clone_end=3' /gb=Al581285 /gi=4565661			·
	,	/ug=Hs 309697 /len=467	·.		
11595	0.000173	hypothetical protein FLJ22104	NM_022918	Hs.183887	NP_075069
11000	0.000170	(FLJ22104), mRNA /cds=(63,1127)	1401_022310	113.103007	_0/0000
		/gb=NM_022918 /gi=12597666	,		1
		/ug=Hs.183887 /len=2952		* -	
11684	0.001001	cDNA: FLJ21311 fis, clone COL02167.	AK024964	Hs.173933	NP 005586
11004	0.001001	/gb=AK024964 /gi=10437390	711024304	1113, 170300	
		/ug=Hs.173933 /len=3216			
11688	0.000173	hypothetical protein from clone 24796	NM 020422	Hs.27191	NP 065155
11000	0.000 173	(LOC57146), mRNA /cds=(113,598)	INIVI_UZU4ZZ	113.21 131	145 700 150
		/gb=NM_020422 /gi=21361853			
				.	
		/ug=Hs 27191 /len=1683	<u> </u>	<u> </u>	

Spot	oot p-valu Description		Accession	Unigene	Protein Accession	
			·		No	
11693	0.001001	cell adhesion molecule-related/down-	NM_016952	Hs.159565	NP_058648	
		regulated by oncogenes (CDON), mRNA	-		* 4	
		/cds=(1,3723) /gb=NM_016952				
		/gi=8393083 /ug=Hs.159565 /len=3986		,		
11751	3.07E-05	NADH dehydrogenase (ubiquinone) 1,	NM 004549	Hs.193313	NP_004540	
		subcomplex unknown, 2, 14.5kDa			 ·	
		(NDUFC2), mRNA /cds=(151,510)				
		/gb=NM 004549 /gi=19923255		\$		
		/ug=Hs.193313 /len=2168				
11807	0.000681		NM 016059	Hs.27693	NP 057143	
	0.0000	1 (PPIL1), mRNA /cds=(222,722)	11111_01000	113.27 000	-007 1 10	
	3	/gb=NM_016059 /gi=22035675				
		/ug=Hs.27693 /len=1723				
11834	0.000274	hypothetical protein LOC93550	NM 174890	Hs.377945	NP 777550	
1.1054	0.000274		17469U	∏5.3779 4 5	INP_///550	
		(LOC93550), mRNA /cds=(217,2400)				
	•	/gb=NM_174890 /gi=28376663				
		/ug=Hs.377945 /len=3256				
11909	3.07E-05	HRD1 protein (HRD1), transcript variant 2,	NM_172230	Hs.334819	NP_757385	
		mRNA /cds=(95,1948) /gb=NM_172230		A		
100		/gi=27436926 /ug=Hs.334819 /len=3074				
11912	9.46E-06	hypothetical protein MGC40157	NM_152350	Hs.295362	NP_689563	
		(MGC40157), mRNA /cds=(106,498)				
		/gb=NM_152350 /gi=22748758			· .	
		/ug=Hs.295362 /len=1250				
11939	1.38E-05	tyrosine 3-monooxygenase/tryptophan 5-	NM 012479	Hs.25001	NP_036611	
	}	monooxygenase activation protein,	_	1		
	2	gamma polypeptide (YWHAG), mRNA	. , ,	*		
•		/cds=(192,935) /gb=NM_012479				
		/gi=21464100 /ug=Hs.25001 /len=3747				
11962	8 88E 06	aquaporin 3 (AQP3), mRNA	NM_004925	Hs.234642	NP_004916	
11302	0.002-00	/cds=(63,941) /gb=NM_004925	14141_004925	113.234042	_004910	
	İ		1		1	
40005	0.000450	/gi=22165421 /ug=Hs 234642 /len=1835	A A COO 2 FO	 		
12005	0.000153	EST(no44e03.s1 NCI_CGAP_Pr23 cDNA	AA622352	1		
1000=	1 2 2 2 2 5	clone IMAGE:1103548)	1.05450			
12037	2.07E-05	EST(EST58819 Infant brain 3' contains	AA351153			
<u> </u>		Alu repeat)				
12056	4.31E-05	EST(ak48e09.s1 Soares testis NHT clone	AA860225			
		IMAGE:1409224 3')				
12112	0.000326	EST(xu58f03.x1 NCI_CGAP_Ut1 clone	AW511419		NP_073572	
		IMAGE:2805917 3' TR:O35371 O35371		,	<u> </u>	
		PERIPHERIAL BENZODIAZEPINE	, .		1.	
		RECEPTOR ASSOCIATED PROTEIN)			1	
12182	0.000328	Williams-Beuren Syndrome critical region	NM 145645	Hs 406306	NP 663620	
· · • •		protein 20 copy B (WBSCR20B), mRNA				
]	/cds=(984,1448) /gb=NM 145645				
•,		/gi=21717802 /ug=Hs.406306 /len=1634			1	
5.5	1	191-211 11002 109-115,400300 Nett-1034		1	1	

Spot	p-value	Description	Accession	Unigene	Protein
·. •				* **	Accession
40004	0,004004	100 E EQ. 11 80 0 10 4 10 E EQ.	DM077540	11- 440000	No.
12261	0.001021	UI-E-EO1-aid-o-06-0-UI s1 UI-E-EO1	BM677516	Hs.443680	
		cDNA clone UI-E-EO1-aid-o-06-0-UI 3',		. N	
		mRNA sequence /clone=UI-E-EO1-aid-o-			
		06-0-UI /clone_end=3' /gb=BM677516			
,		/gi=18987412 /ug=Hs 443680 /len=1044			
12383	0.000356	Saccharomyces cerevisiae chromosome	NC_001144		
	* = * = = = = = =	XII, complete chromosome sequence			
12390	3.07E-05	UI-H-ED0-awy-a-01-0-UI s1	BQ017647	Hs.124747	
		NCI_CGAP_ED0 cDNA clone			
		IMAGE:5825160 3', mRNA sequence			
		/clone=IMAGE:5825160 /clone_end=3'			
		/gb=BQ017647 /gi=19752924		* .	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -
1		/ug=Hs.124747 /len=1445			
12426	0.000636	602590145F1 NIH_MGC_76 cDNA clone	BG564169	Hs.444093	
	.'	IMAGE:4724074 5', mRNA sequence	* * **	1	
		/clone=IMAGE:4724074 /clone_end=5			
		/gb=BG564169 /gi=13571821			
		/ug=Hs.444093 /len=792			1 1 1 1 1 1
12477	0.000117	602022714F1 NCI_CGAP_Brn67 cDNA	BF347758	Hs.280146	
		clone IMAGE:4158098 5', mRNA			
		sequence /clone=IMAGE:4158098			
		/clone_end=5' /gb=BF347758			
		/gi=11295353 /ug=Hs.280146 /len=738		<u> </u>	
12512	0.000158	nx84b05.s1 NCI_CGAP_GCB1 cDNA	AA720890	Hs.291473	
		clone IMAGE:1268913 3', mRNA		<u>'</u>	1
		sequence /clone=IMAGE:1268913			
		/clone_end=3' /gb=AA720890			
		/gi=2737025 /ug=Hs.291473 /len=268			
12515	0.000158	stress 70 protein chaperone, microsome-	NM_006948	Hs.352341	NP_008879
		associated, 60kDa (STCH), mRNA			
		/cds=(37,1452) /gb=NM_006948			
Page 1		/gi=24431965 /ug=Hs.352341 /len=3998			· · ·
12544	0.001164	cDNA FLJ33247 fis, clone	AK090566	Hs.349938	NP_076936.1
		ASTRO2004974. /gb=AK090566			
		/gi=21748752 /ug=Hs.349938 /len=3175			
12583		Novel, ORF+3(45~300)			
12603	0.001116	BX094154 Soares fetal liver spleen	BX094154	Hs.12962	
		1NFLS cDNA clone IMAGp998P17654,			,
		mRNA sequence			
		/clone=IMAGp998P17654_;_IMAGE:2936		1	
	· ·	32 /gb=BX094154 /gi=27826950		1	
		/ug=Hs.12962 /len=758]].	
12608	8.81E-05	mRNA; cDNA DKFZp586L081 (from clone	AL080234	Hs.432862	NP 060312.1
		DKFZp586L081) /gb=AL080234		F	-
		/gi=5262727 /ug=Hs.432862 /len=2159			
12615	0.000153	No significant match, low complexity			
12794		ribosomal protein L12 (RPL12), mRNA	NM 000976	Hs.405042	NP_000967
		/cds=(89,586) /gb=NM_000976			========
	•		I .	1	1

Spot	p-valu	Description	Accession	Unigene	Protein
			1		Accession
					No.
12835	3.64E-05	AGENCOURT_8856629	BQ947179	Hs.356605	-
		Lupski_sciatic_nerve cDNA clone			
		IMAGE:6200636 5', mRNA sequence			
,		/clone=IMAGE:6200636 /clone_end=5'	1		
	*y - 1	/gb=BQ947179 /gi=22362657			
		/ug=Hs.356605 /len=1277			
12880		EST(cDNA clone IMAGE:1470581 3')	AA873731		NP_004087
12901	0.000659	ESTs, cDNA /clone=IMAGE:1203867	AA640737	Hs.336767	
		/gb=AA640737 /gi=2565987		1	
	<i>2</i> *	/ug=Hs.336767 /len=416			<u> </u>
12918	0.000295	cDNA: FLJ21962 fis, clone HEP05564.	AK025615	Hs.7567	W. T. T. T. T. T. T. T. T. T. T. T. T. T.
		/gb=AK025615 /gi=10438186			
		/ug=Hs.7567 /len=3323			
12952	3.07E-05	cDNA: FLJ21265 fis, clone COL01584.	AK024918	Hs.306728	The second second second
		/gb=AK024918 /gi=10437333			
		/ug=Hs.306728 /len=2233			
12981	6.97E-05	selenoprotein H (SELH), mRNA	NM 170746	Hs.290874	NP 734467
		/cds=(243,611) /gb=NM_170746			
		/gi=25014108 /ug=Hs.290874 /len=834			
13047	0.000295				
13058		No significant match, ORF+1(1~237),-	-		
	0.022	3(47~832)			
13064	1.38F-05	No significant match (ORF:-			
		1:37~186[150])			
13095	0.000316	No significant match, ORF-3(30~198)		 	
13197		similar to rat nuclear ubiquitous casein	NM_022731	Hs.118064	NP_073568
10107	0.000200	kinase 2 (NUCKS), mRNA /cds=(67,558)	022701	113.110004	
		/gb=NM_022731 /gi=12232386		1.	
		/ug=Hs.118064 /len=1811			
13230	0.000295	ATP-binding cassette, sub-family E	NM 002940	Hs.12013	NP_002931
10200	0.000200	(OABP), member 1 (ABCE1), mRNA	14101_0025#0	113.12010	
		/cds=(118,1917) /gb=NM_002940			
		/gi=4506558 /ug=Hs.12013 /len=3568			
13330	0.001164	bridging integrator 2 (BIN2), mRNA	NM_016293	He 14770	NP_057377
13330	0.001104	/cds=(39,1736) /gb=NM_016293	14141_0 10293	1113.14770	NF_037377
1 .		/gi=7706486 /ug=Hs.14770 /len=2206			
13338	0.000522	solute carrier family 30 (zinc transporter),	NM 022902	Hs.129445	NP_076960
13336	0.000323	member 5 (SLC30A5), mRNA	14141_022902	ITS. 129445	INP_0/0900
		/cds=(202,2499) /gb=NM 022902	÷		
		/gi=20070322 /ug=Hs 129445 /len=2952			
13364	Q EE OC	hypothetical protein PC000519	NIM 120262	Ho 125265	ND 612272
13364	0.515-06	hypothetical protein BC009518	NM_138363	Hs.135265	NP_612372
	[(LOC90799), mRNA /cds=(59,2524)			
		/gb=NM_138363 /gi=19923898		1	
40540	0.00000	/ug=Hs.135265 /len=2705	A14/070004		ND 070000
13512	0.000928	EST EST384986 MAGE resequences,	AW972891		NP_078939
L ·		MAGL	l		L

Spot	p-value	Description	Accession	Unigen	Protein Accession
			٠		No.
13761	6.73E-05	optic atrophy 1 (autosomal dominant). (OPA1), nuclear gene encoding	NM_130837	Hs.147946	NP_570850
		mitochondrial protein, transcript variant 8,	<u> </u>		
		mRNA /cds=(56,3103) /gb=NM_130837			
		/gi=18860844 /ug=Hs.147946 /len=6029	. 4		
13789	0.000357	cDNA FLJ31372 fis, clone	AK055934	Hs.89388	7
		NB9N42000281. /gb=AK055934	,	113.0000	
		/gi=16550786 /ug=Hs.89388 /len=2606	· ·		
13812	0.001554	plasminogen activator, tissue (PLAT),	NM 000930	Hs 274404	NP 127509
.00,12	0.001001	transcript variant 1, mRNA	11111_000500	113.27 - 1-0-1	111 _127000
		/cds=(209,1897) /gb=NM 000930			
		/gi=14702165 /ug=Hs.274404 /len=2653	,		
13818	3.07E-05	bladder cancer-related protein (LHX)	AY034106		NP_002856
, ,	J.07 L=00	gene, partial 3'UTR sequence	1/1/00-100		1.41 _002000
13854	3.07E-05	palmdelphin (PALMD), mRNA	NM_017734	Hs.14606	NP 060204
12004	3.07 L-03	/cds=(286,1941) /gb=NM_017734	VIVI_U1/134	115.14000	NF_000204
		/gi=16306484 /ug=Hs.14606 /len=2581	:		
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10000	0.001021	PLACE1000133, highly similar to	JAK027730	NS.33740	DA600042.1
		TRANSCRIPTION FACTOR BTF3.			
		/cds=(91,567) /gb=AK027750			
	, i	/gi=14042660 /ug=Hs.93748 /len=2203			
13869	0.00135	peptidylprolyl isomerase C (cyclophilin C)	NM 000943	Hs.110364	NP 000934
13009	0.00133	(PPIC), mRNA /cds=(88,726)	14141_000943	П5.110304	INF_000934
		/gb=NM_000943 /gi=20149506		1	
				* * .	
13903	0.000701	/ug=Hs 110364 /len=1015 cDNA FLJ32300 fis, clone	AK056862	Hs.201676	ND 005700
13903	(0.000791		 \vec{V}\n20005	I	NP_005782
		PROST2002227, highly similar to M- PHASE PHOSPHOPROTEIN 10.		·	
		/gb=AK056862 /gi=16552379			
		/gb=AK056662 /gi= 16552379 /ug=Hs.201676 /len=2334	•		
13954	0.000400		A A 720500	·	
		EST nw48e08.s1 NCI_CGAP_Ew1 IMAGE:1249862	AA730589		,
14039	9.46E-06	hypothetical protein FLJ10038	NM_017976	Hs 181202	NP_060446
	,	(FLJ10038), mRNA /cds=(167,577)			
		/gb=NM_017976 /gi=8922197			
		/ug=Hs.181202 /len=1461		-	
14081	0.000316	mRNA; cDNA DKFZp434H2019 (from	AL137535	Hs.15806	NP_116212.1
,]	clone DKFZp434H2019) /gb=AL137535			
· · ·		/gi=6808211 /ug=Hs.15806 /len=1974		<u> </u>	
14094	0.000112	EST (wh67d04.x1 NCI_CGAP_Kid11	AI766049		T08781
		IMAGE:2385799 3')			
14166	0.001443	cDNA FLJ38536 fis, clone	AK095855	Hs.30089	
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		/gi=21755199 /ug=Hs.30089 /len=2950_		<u>L</u> _	
14247	2.76E-05	clone IMAGE:4836898, mRNA	BC042527	Hs.434231	
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		/ug=Hs.434231 /len=2935			

Spot	p-value	D scription	Acc ssion	Unigene	Protein Accession No.	
14291	0.000377	calmodulin 2 (phosphorylase kinase,	NM_001743	Hs.425808	NP_001734	
		delta) (CALM2), mRNA /cds=(69,518)				
		/gb=NM_001743 /gi=20428653				
		/ug=Hs.425808 /len=1128				
14371	0.000356	EST391381 MAGE resequences, MAGP	AW979271	Hs.293184		
		cDNA, mRNA sequence /gb=AW979271				
		/gi=8170559 /ug=Hs.293184 /len=577				
14399	3.37E-06	EST, clone 25032 mRNA sequence	AF131764	Hs.396998	NP_071919	
·		/cds=UNKNOWN /gb=AF131764			– ·	
		/gi=4406586 /ug=Hs.13399 /len=1798				
14427	0.000463	EST(cDNA clone IMAGE:2420325 3')	Al814793		NP_005617	
14455	0.001532	No significant match, ORF+3(135~404)				
14501	0.000716	No significant match				
14517	0.000295	xq09e02.x1 NCI_CGAP_Ut1 cDNA clone	AW517395	Hs.445194	NP_064622.1	
		IMAGE:2750138 3' similar to contains Alu				
		repetitive element;, mRNA sequence				
		/clone=IMAGE:2750138 /clone_end=3'				
		/gb=AW517395 /gi=7155477	, '			
		/ug=Hs.445194 /len=519				
14626	0.000949	cDNA FLJ31439 fis, clone	AK056001	Hs.349656	NP_060312.1	
, .		NT2NE2000707. /gb=AK056001				
		/gi=16550873 /ug=Hs.349656 /len=2009	1			
14784	0.000882	ak04g10.s1	AA845596	Hs.275849	NP_060312.1	
,	\	Soares_parathyroid_tumor_NbHPA cDNA	:	` ·		
		clone IMAGE:1405026 3' similar to				
••		contains Alu repetitive element, mRNA	, · · · ·	1		
	r - e	sequence /clone=IMAGE:1405026		l .	•	
	٠,	/clone_end=3' /gb=AA845596				
		/gi=2933355 /ug=Hs.275849 /len=525	\ .	•		
14705	0.000400	-DNA 51 127500 51	A1600 4005	Up 141000	+	
14785	0.000492	cDNA FLJ37586 fis, clone	AK094905	Hs.141269		
		BRCOC2005903. /gb=AK094905	-			
14024	0.000742	/gi=21754065 /ug=Hs.141269 /len=2373	NIM 019714	Ha 202100	ND 061194	
14834	0.000743	component of oligomeric golgi complex 1	NM_018714	Hs.283109	NP_061184	
	, ,	(COG1), mRNA /cds=(27,2969)				
35 g		/gb=NM_018714 /gi=21237782				
14849	0.000125	/ug=Hs.283109 /len=3047 cDNA FLJ11469 fis, clone	AK021531	Hs.224398		
14049	0.000135	CDNA FLJ 1469 fis, cione HEMBA1001658. /gb=AK021531	ANUZ 1991 -	115.224390	. 1	
14020	0.000400	/gi=10432731 /ug=Hs.224398 /len=1665	ļ		 	
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W. P. Carlotte						t
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:	and the second						
			4		•		
caaata	aaca aa	aacttcca	atctccattt	aaaat			155
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gttctg	ggna acgggcaatg d	gggcttgca	acgggnggaa	naaaaacagn	cccaaaagaa	240
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tg						242
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			*** **********************************			
			\$		·	
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	at the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of					
gcaggg	agct gagattgcgc (cactgccctc	catcctgggc	gacagagcaa	gaacetgtet	180
c						181
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